



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:00 PM GMT

PDB ID : 4B2T
Title : The crystal structures of the eukaryotic chaperonin CCT reveal its functional partitioning
Authors : Kalisman, N.; Schroeder, G.F.; Levitt, M.
Deposited on : 2012-07-17
Resolution : 5.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

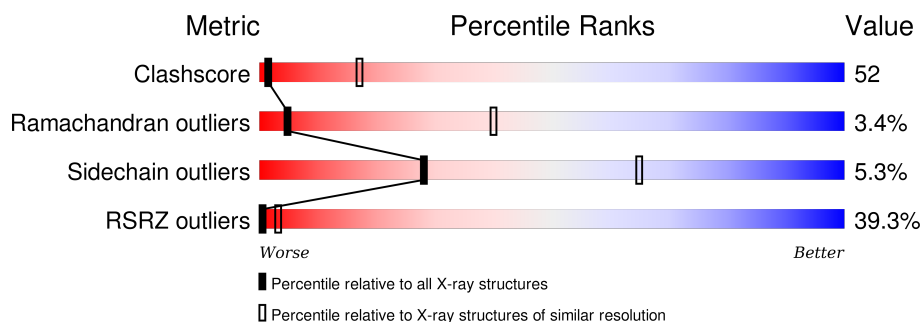
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1020 (7.10-3.70)
Ramachandran outliers	100387	1014 (7.36-3.64)
Sidechain outliers	100360	1013 (7.38-3.62)
RSRZ outliers	91569	1014 (7.38-3.62)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	556	<div> <div>26%</div> <div>29% 51% 6% 13%</div> </div>
1	a	556	<div> <div>29%</div> <div>57% 6% 35%</div> </div>
2	B	535	<div> <div>44%</div> <div>35% 52% 10%</div> </div>
2	b	535	<div> <div>31%</div> <div>62% 5% 33%</div> </div>
3	D	542	<div> <div>31%</div> <div>28% 55% 5% 11%</div> </div>
3	d	542	<div> <div>26%</div> <div>61% 5% 34%</div> </div>
4	E	541	<div> <div>22%</div> <div>32% 50% 7% 11%</div> </div>

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Mol	Chain	Length	Quality of chain
4	e	541	
5	G	545	
5	g	545	
6	H	543	
6	h	543	
7	Q	548	
7	q	548	
8	Z	531	
8	z	531	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 51877 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	0	0
			3625	2280	633	692	20			
1	a	359	Total	C	N	O	S	0	0	0
			2705	1703	469	520	13			

- Molecule 2 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	481	Total	C	N	O	S	0	0	0
			3602	2258	629	696	19			
2	b	359	Total	C	N	O	S	0	0	0
			2658	1652	469	524	13			

- Molecule 3 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT DELTA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	481	Total	C	N	O	S	0	0	0
			3610	2259	627	703	21			
3	d	359	Total	C	N	O	S	0	0	0
			2690	1671	473	532	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	158	VAL	GLU	CONFLICT	UNP Q2T9X2
D	510	LEU	GLN	CONFLICT	UNP Q2T9X2
d	1158	VAL	GLU	CONFLICT	UNP Q2T9X2
d	1510	LEU	GLN	CONFLICT	UNP Q2T9X2

- Molecule 4 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT EPSILON.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	481	Total	C	N	O	S	0	0	0
			3674	2299	644	703	28			
4	e	359	Total	C	N	O	S	0	0	0
			2724	1688	486	528	22			

- Molecule 5 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT GAMMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	481	Total	C	N	O	S	0	0	0
			3719	2326	661	705	27			
5	g	359	Total	C	N	O	S	0	0	0
			2735	1711	480	523	21			

- Molecule 6 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT ETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	481	Total	C	N	O	S	0	0	0
			3671	2320	633	693	25			
6	h	359	Total	C	N	O	S	0	0	0
			2724	1719	472	517	16			

- Molecule 7 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT THETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	Q	481	Total	C	N	O	S	0	0	0
			3673	2317	628	703	25			
7	q	359	Total	C	N	O	S	0	0	0
			2739	1729	467	526	17			

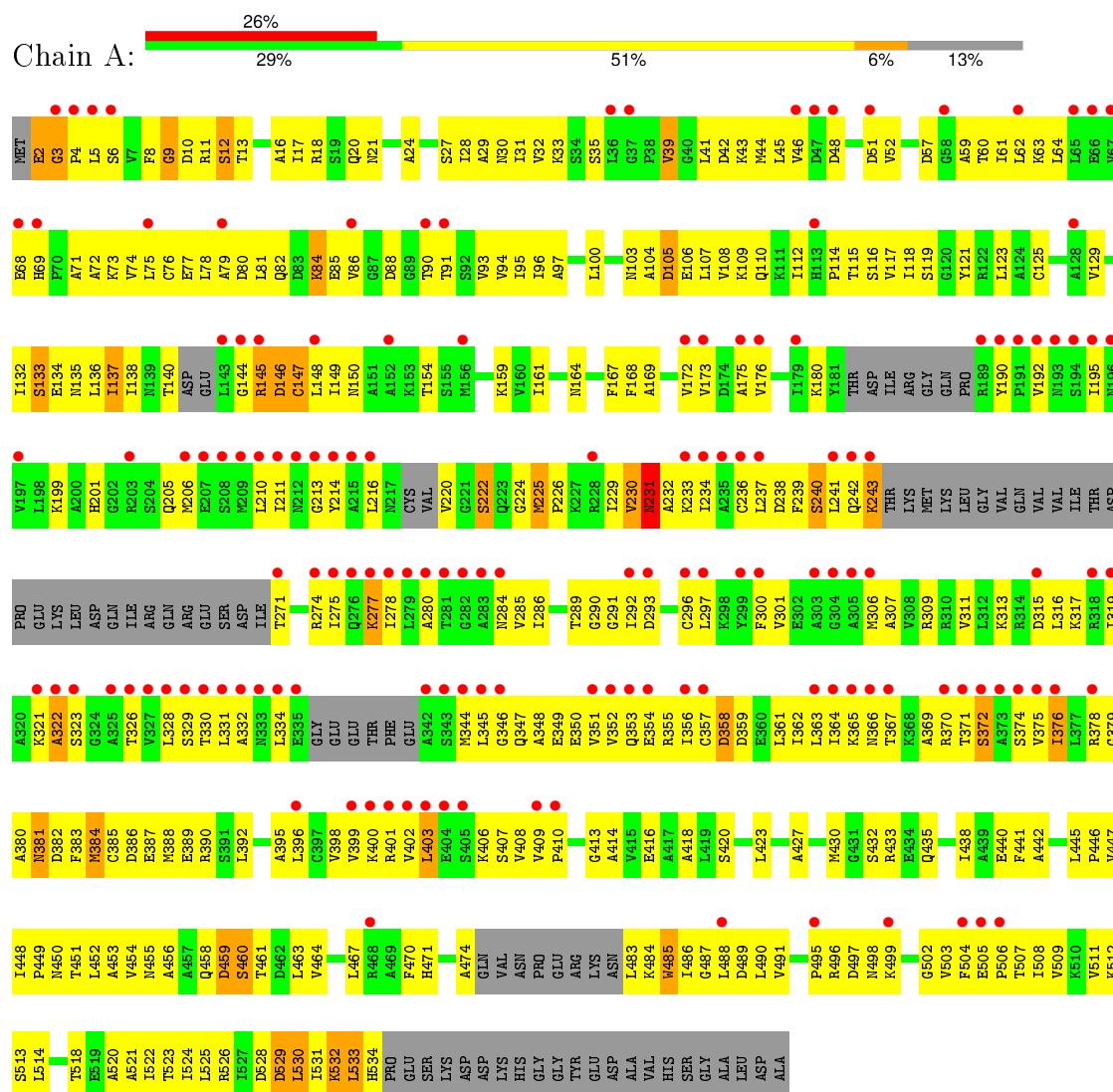
- Molecule 8 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT ZETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	Z	481	Total	C	N	O	S	0	0	0
			3664	2310	638	697	19			
8	z	481	Total	C	N	O	S	0	0	0
			3664	2310	638	697	19			

3 Residue-property plots

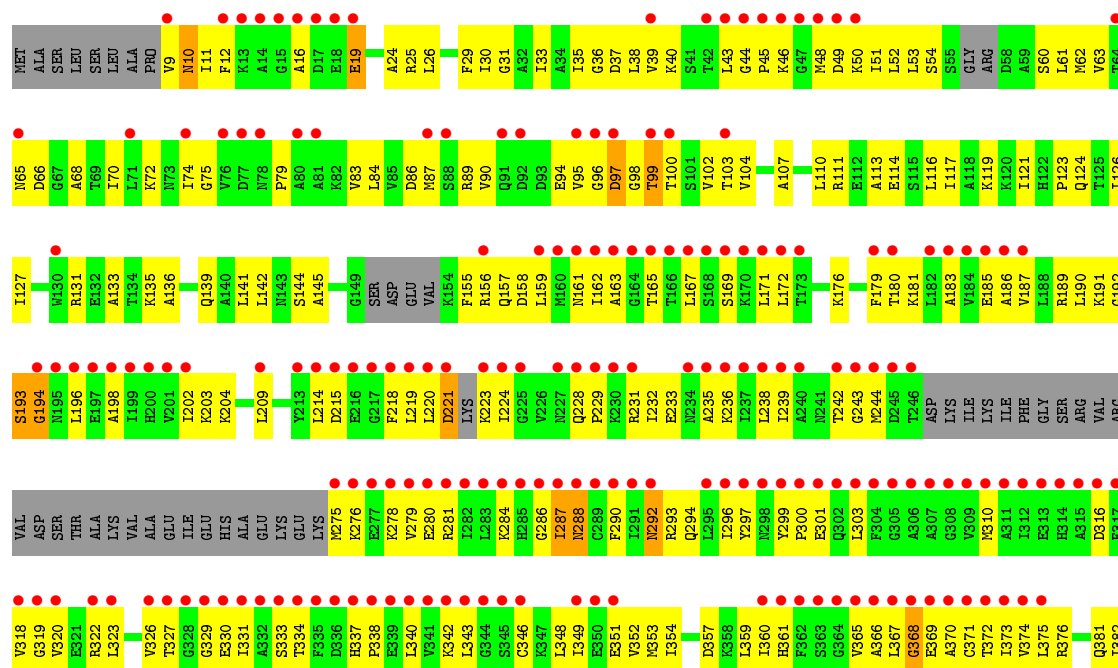
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT ALPHA

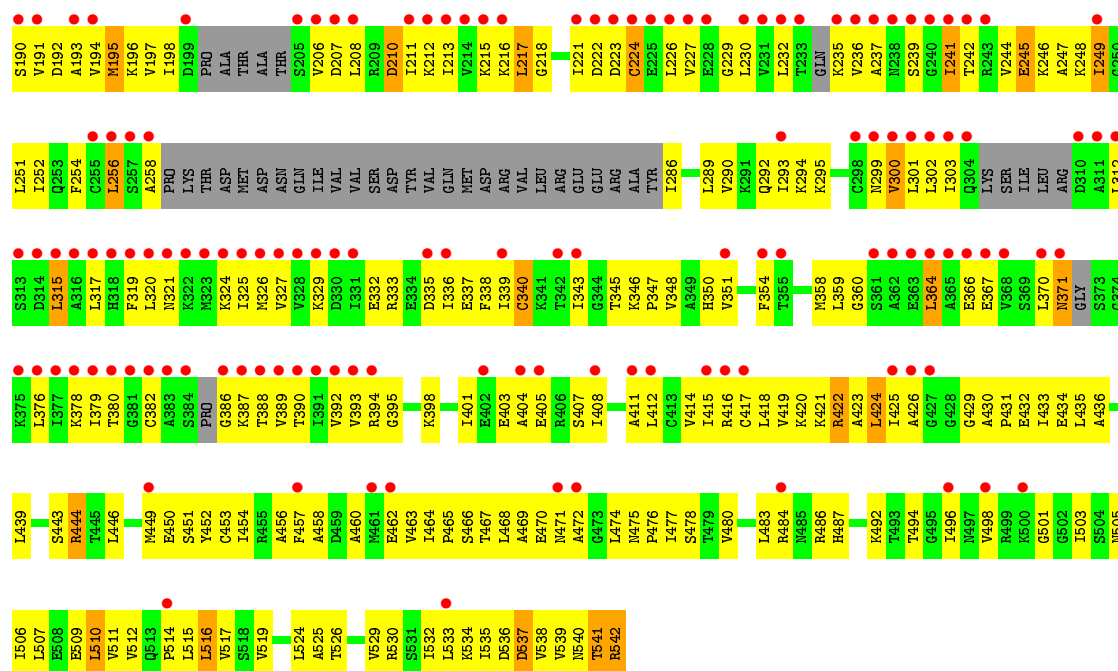


• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT ALPHA

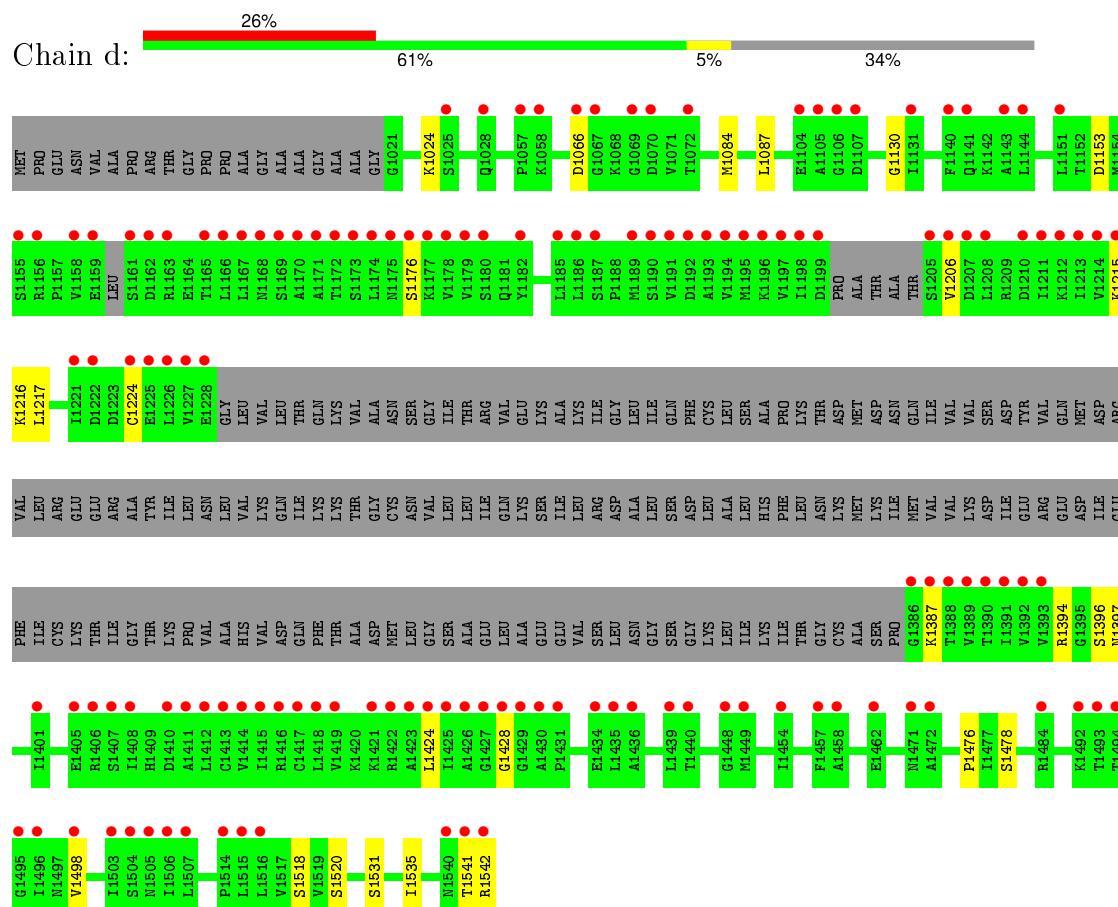






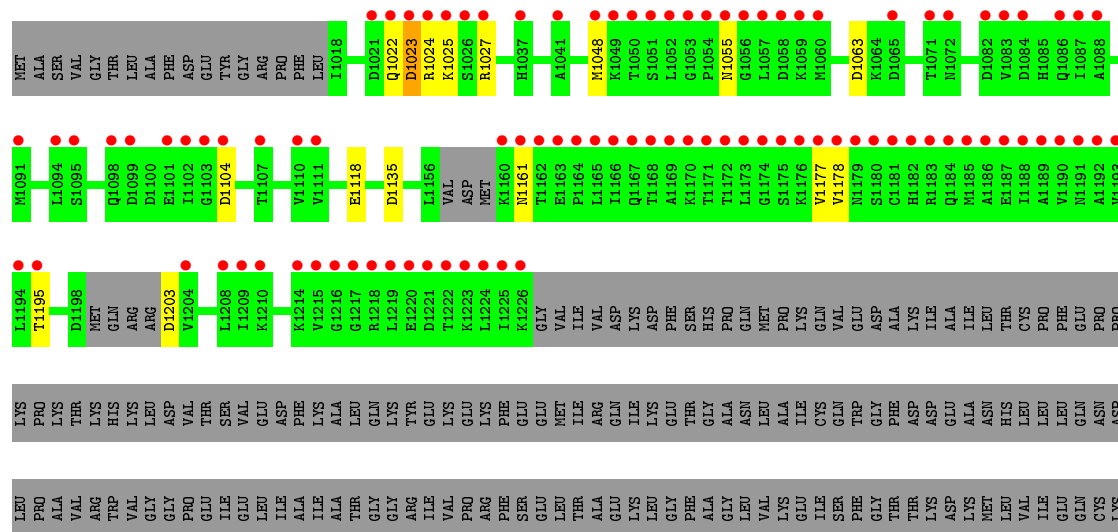


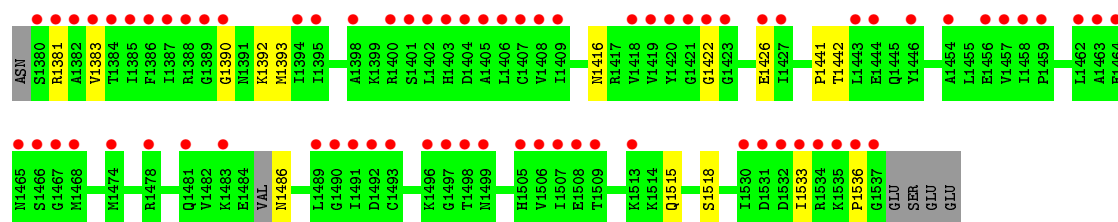
• Molecule 3: T-COMPLEX PROTEIN 1 SUBUNIT DELTA



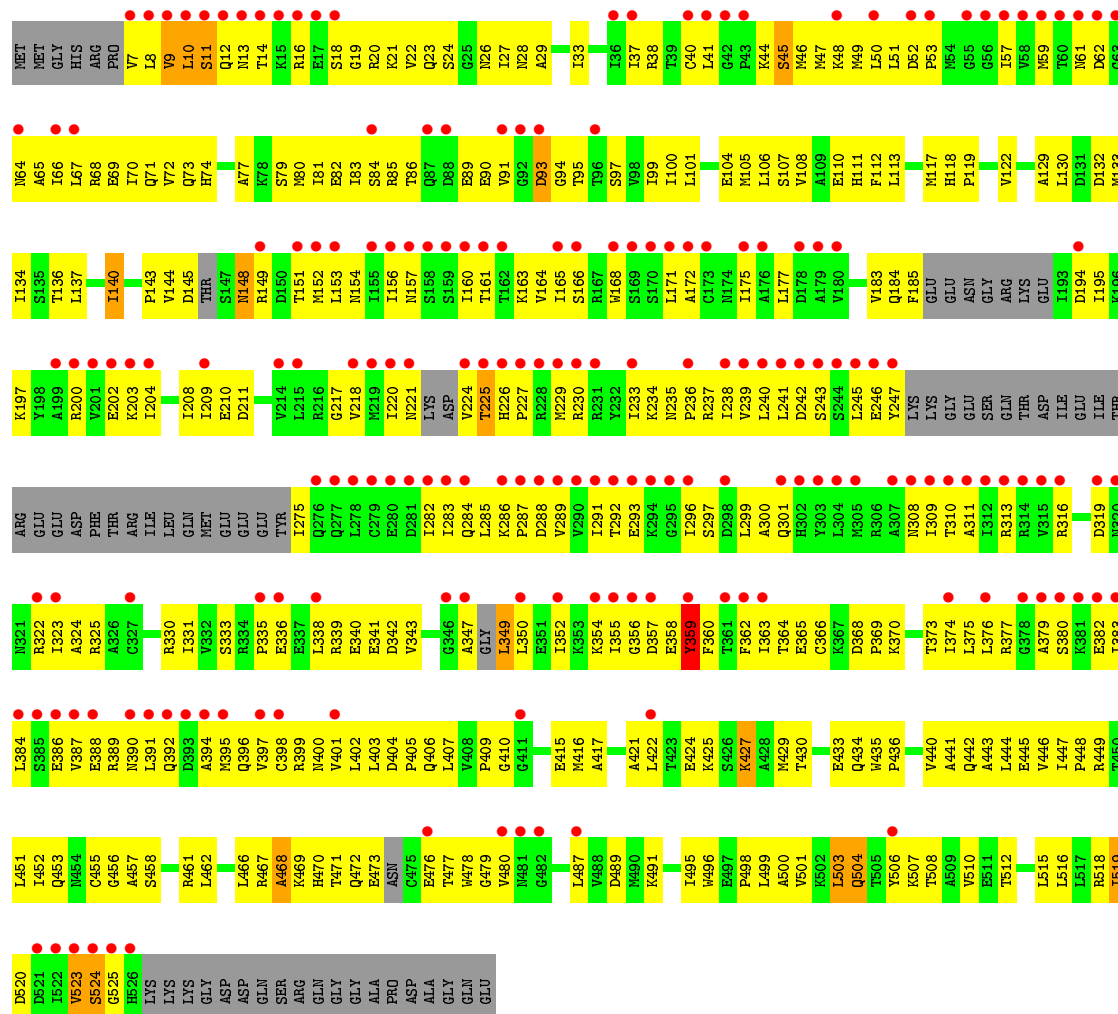
• Molecule 4: T-COMPLEX PROTEIN 1 SUBUNIT EPSILON





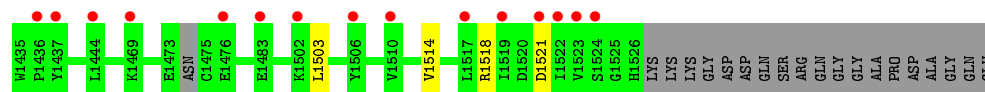
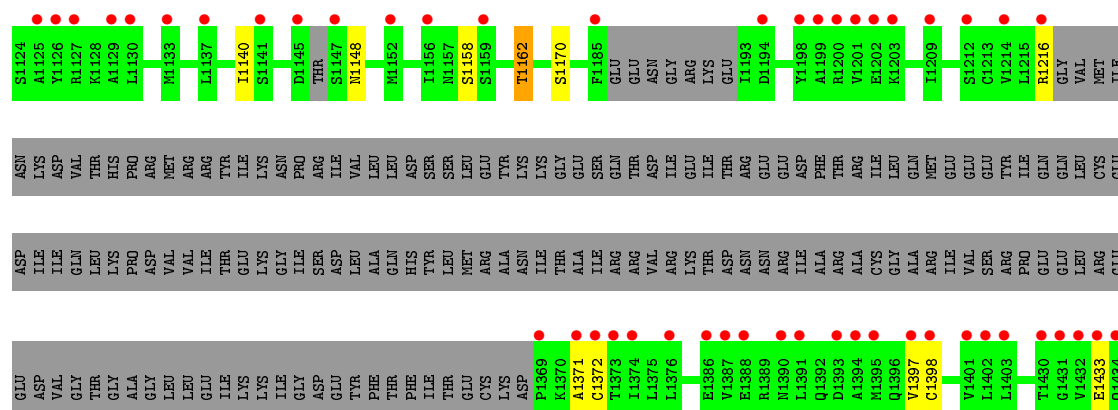


• Molecule 5: T-COMPLEX PROTEIN 1 SUBUNIT GAMMA

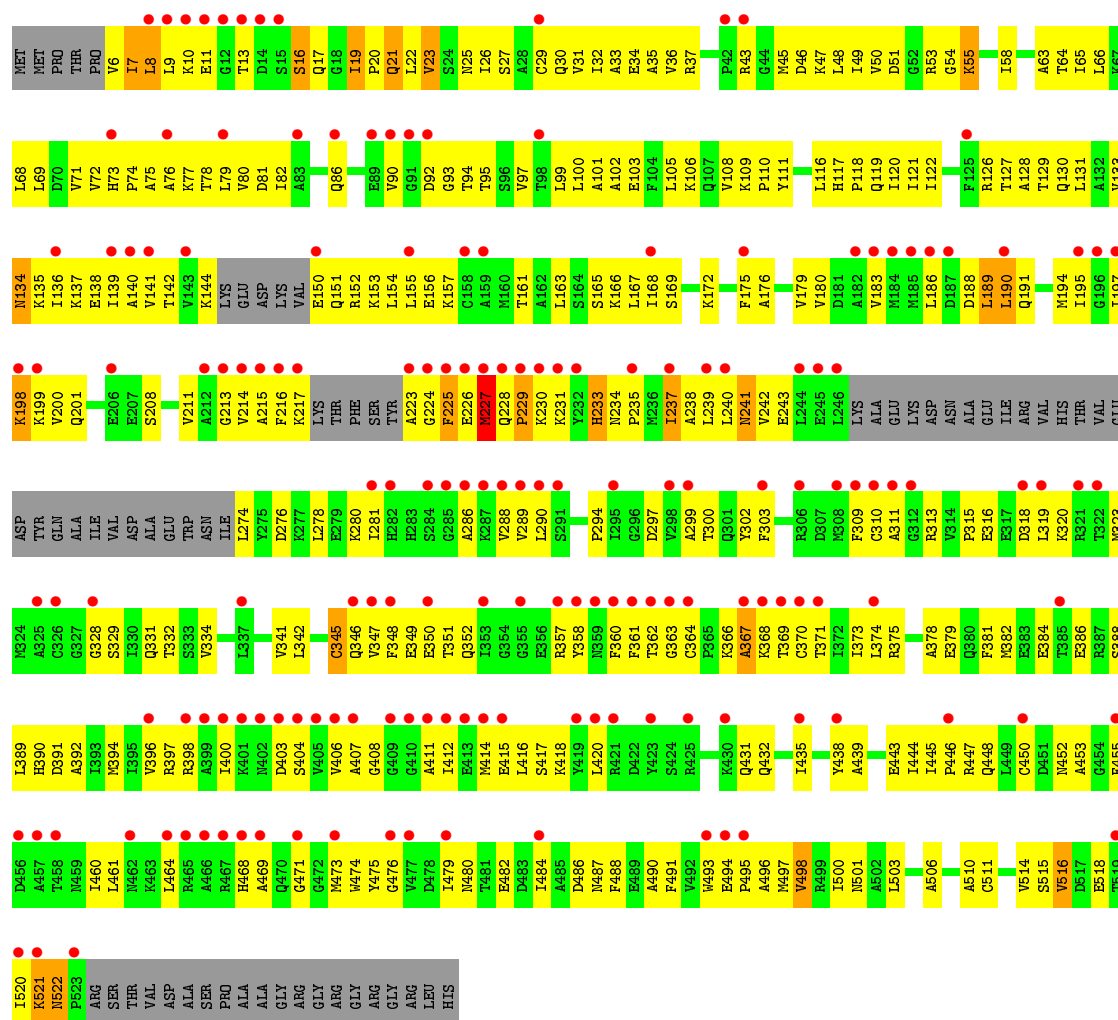


• Molecule 5: T-COMPLEX PROTEIN 1 SUBUNIT GAMMA

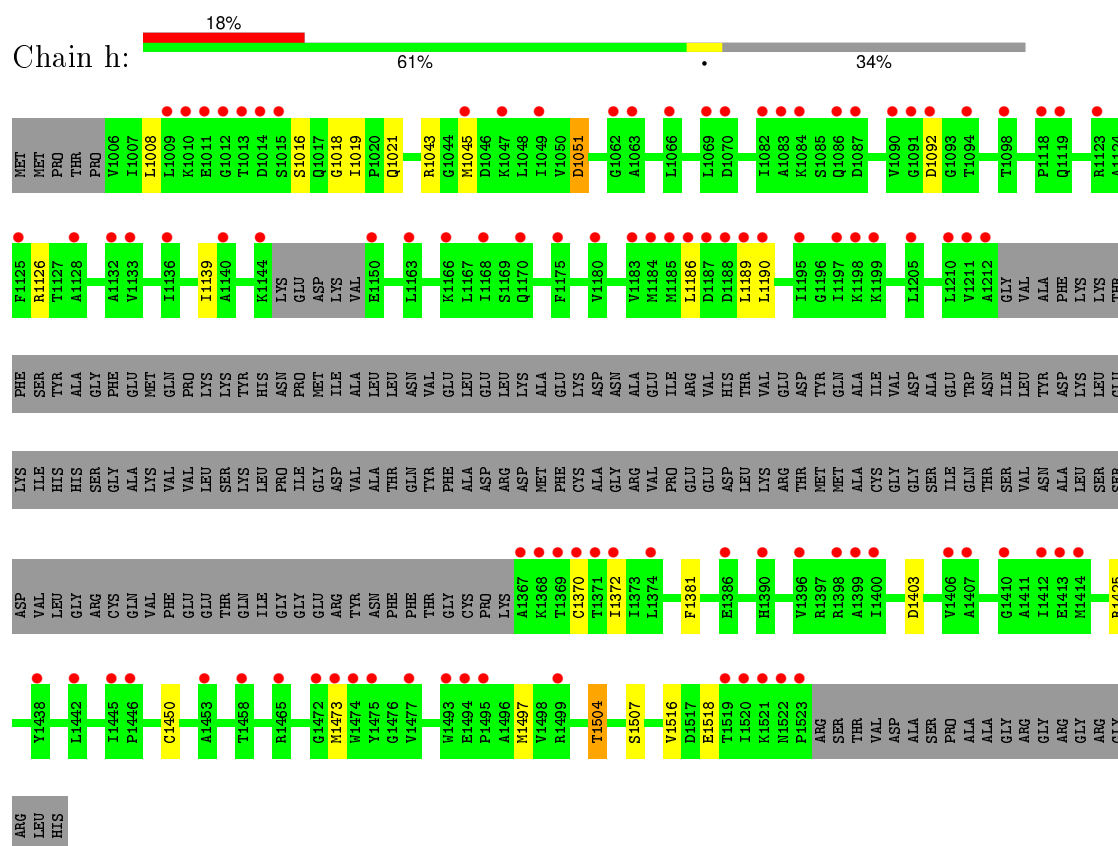




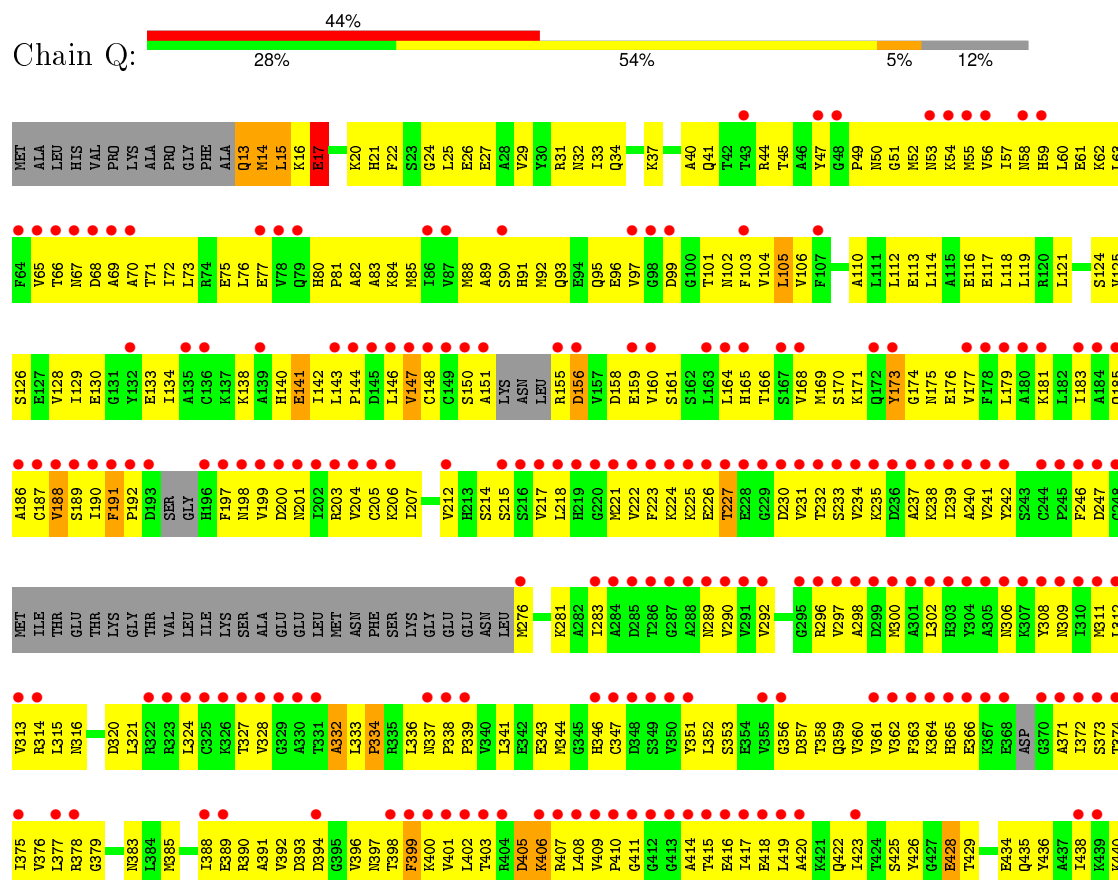
• Molecule 6: T-COMPLEX PROTEIN 1 SUBUNIT ETA

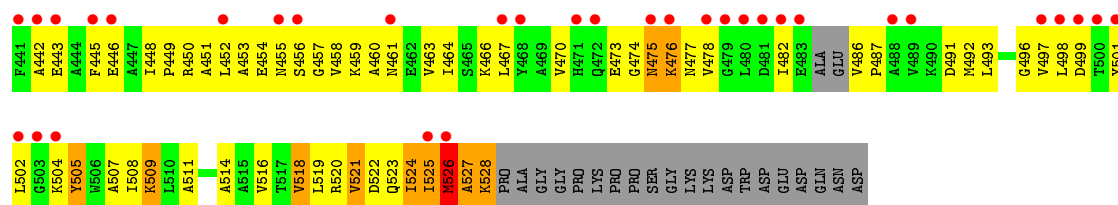


- Molecule 6: T-COMPLEX PROTEIN 1 SUBUNIT ETA

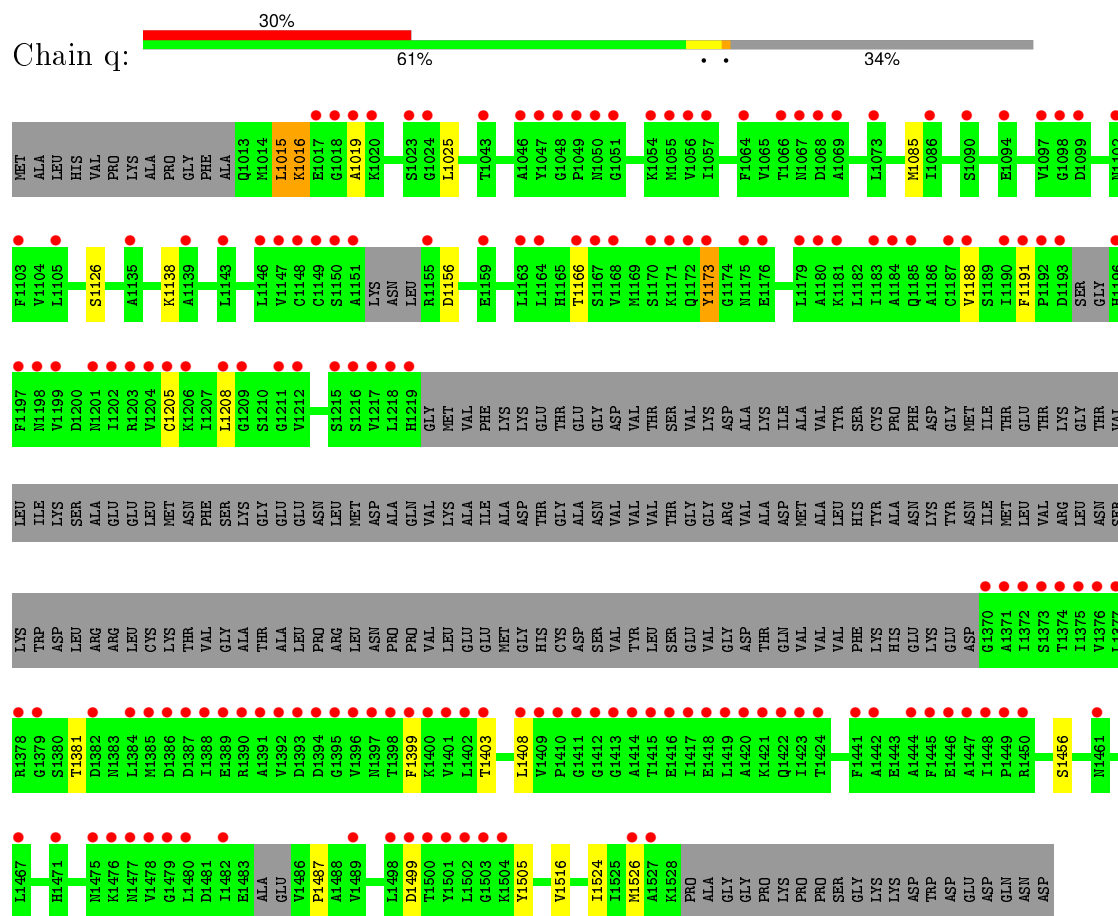


- Molecule 7: T-COMPLEX PROTEIN 1 SUBUNIT THETA

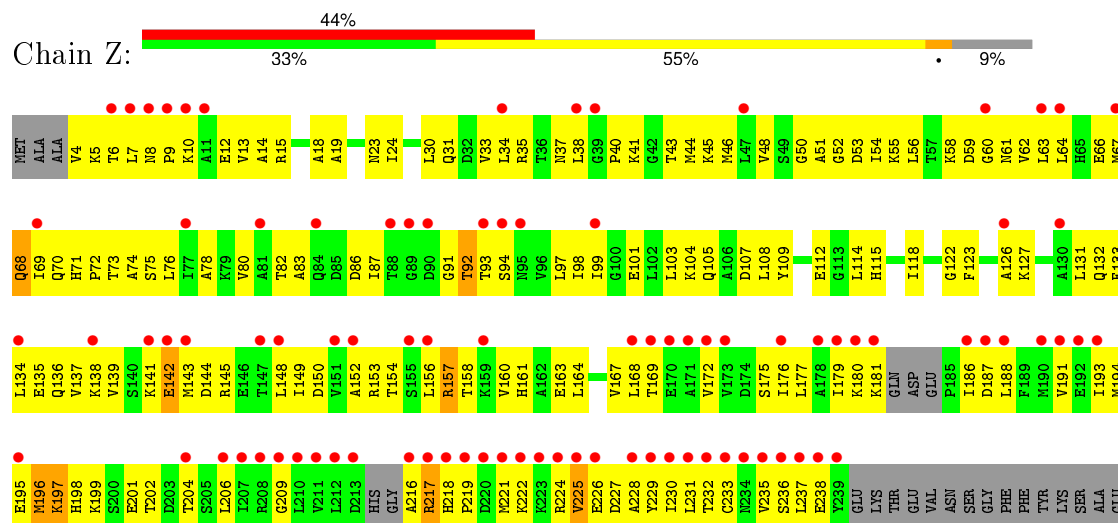


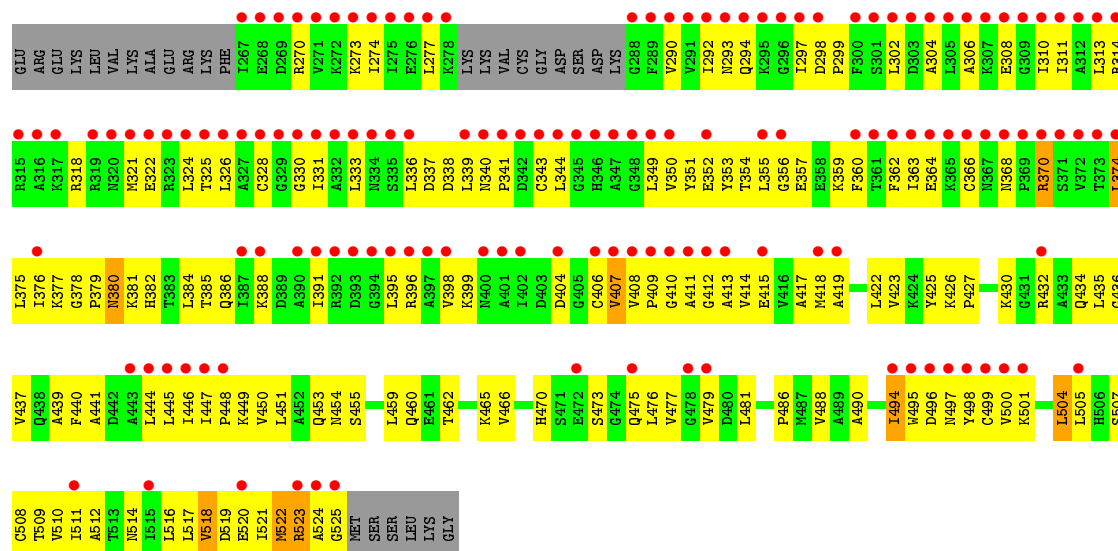


• Molecule 7: T-COMPLEX PROTEIN 1 SUBUNIT THETA

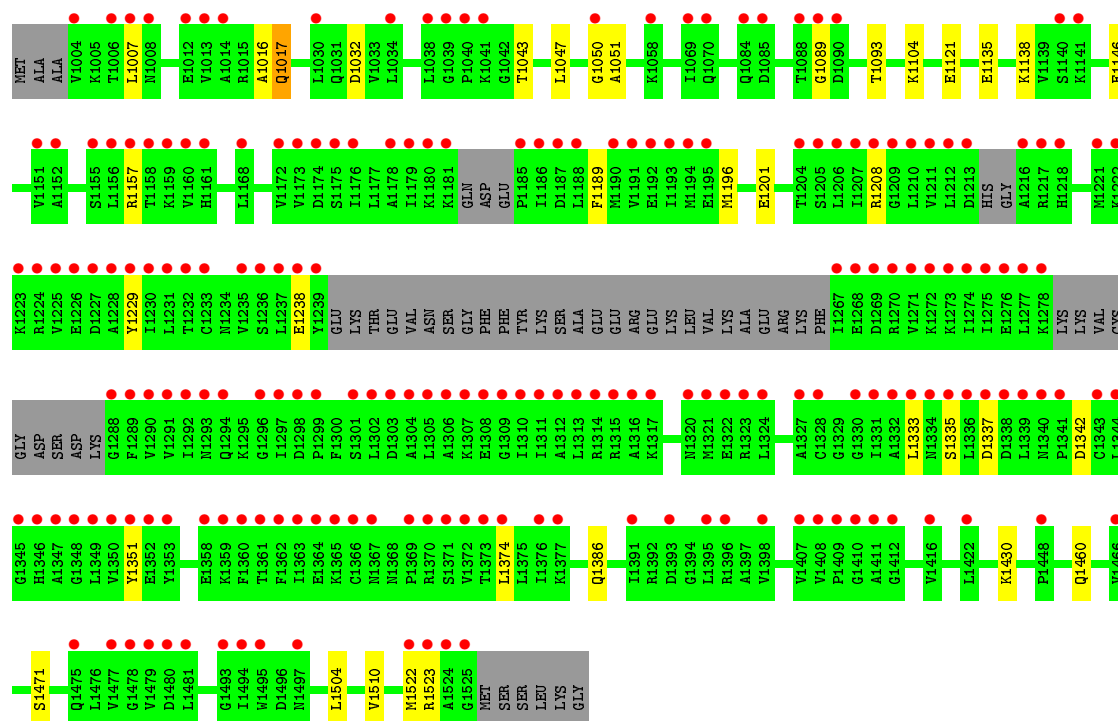
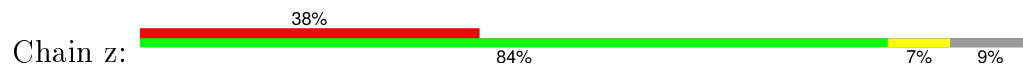


• Molecule 8: T-COMPLEX PROTEIN 1 SUBUNIT ZETA





● Molecule 8: T-COMPLEX PROTEIN 1 SUBUNIT ZETA



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	272.70 Å 313.50 Å 158.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	200.00 – 5.50 97.58 – 5.44	Depositor EDS
% Data completeness (in resolution range)	99.1 (200.00-5.50) 98.4 (97.58-5.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 5.41 Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.340 , 0.399 0.328 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	257.8	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 427.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.16$	Xtriage
Outliers	0 of 45495 reflections	Xtriage
F_o, F_c correlation	0.75	EDS
Total number of atoms	51877	wwPDB-VP
Average B, all atoms (Å ²)	277.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.22	0/3657	0.44	0/4934
1	a	0.22	0/2733	0.46	0/3695
2	B	0.22	0/3638	0.43	0/4903
2	b	0.21	0/2680	0.44	0/3615
3	D	0.21	0/3632	0.46	0/4891
3	d	0.21	0/2707	0.45	0/3650
4	E	0.22	0/3712	0.44	0/4997
4	e	0.21	0/2743	0.44	0/3687
5	G	0.21	0/3758	0.45	0/5073
5	g	0.21	0/2763	0.46	0/3733
6	H	0.23	0/3716	0.43	0/5008
6	h	0.22	0/2751	0.45	0/3711
7	Q	0.23	0/3724	0.44	0/5032
7	q	0.23	0/2774	0.43	0/3746
8	Z	0.22	0/3702	0.44	0/4995
8	z	0.21	0/3702	0.45	0/4995
All	All	0.22	0/52392	0.44	0/70665

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3625	0	3783	380	0
1	a	2705	0	2799	0	0
2	B	3602	0	3705	353	0
2	b	2658	0	2733	0	0
3	D	3610	0	3810	456	0
3	d	2690	0	2818	0	0
4	E	3674	0	3781	382	0
4	e	2724	0	2822	0	0
5	G	3719	0	3870	398	0
5	g	2735	0	2851	0	0
6	H	3671	0	3783	366	0
6	h	2724	0	2842	0	0
7	Q	3673	0	3719	383	0
7	q	2739	0	2777	0	0
8	Z	3664	0	3820	413	0
8	z	3664	0	3820	0	0
All	All	51877	0	53733	2912	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 52.

All (2912) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:456:GLY:HA3	8:Z:118:ILE:HD11	1.37	1.06
1:A:211:ILE:HG22	1:A:213:GLY:H	1.21	1.04
3:D:540:ASN:HB3	3:D:542:ARG:HD3	1.36	1.03
4:E:94:LEU:HD21	4:E:523:MET:HB2	1.39	1.03
7:Q:525:ILE:HG23	7:Q:526:MET:H	1.22	1.03
3:D:31:ASP:HB3	3:D:36:ILE:HB	1.39	1.03
6:H:8:LEU:HA	7:Q:80:HIS:HB2	1.38	1.02
1:A:140:THR:HB	1:A:144:GLY:HA3	1.39	1.01
8:Z:206:LEU:HD13	8:Z:374:LEU:HD12	1.43	1.01
7:Q:225:LYS:HE3	7:Q:361:VAL:HG22	1.42	1.00
7:Q:33:ILE:HG13	7:Q:112:LEU:HB3	1.41	1.00
1:A:532:LYS:HD2	3:D:63:MET:HG2	1.39	0.99
4:E:31:LEU:HA	4:E:34:LEU:HD23	1.45	0.99
3:D:126:LEU:HB3	3:D:131:ILE:HD12	1.46	0.97
4:E:55:ASN:HD22	4:E:466:SER:HA	1.24	0.97
8:Z:231:LEU:HD11	8:Z:339:LEU:HB3	1.43	0.97
3:D:211:ILE:HG23	3:D:389:VAL:HG23	1.46	0.97
4:E:87:ILE:HD13	4:E:527:ILE:HG21	1.43	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:352:LEU:HD11	7:Q:359:GLN:HB3	1.42	0.97
4:E:228:VAL:HG23	4:E:374:ILE:HB	1.44	0.96
5:G:51:LEU:HG	5:G:57:ILE:HG12	1.48	0.96
6:H:19:ILE:H	6:H:20:PRO:HD2	1.27	0.96
1:A:12:SER:HB2	1:A:17:ILE:HB	1.47	0.96
6:H:25:ASN:HD22	6:H:75:ALA:HB2	1.28	0.95
7:Q:428:GLU:HA	7:Q:435:GLN:HE21	1.28	0.95
6:H:30:GLN:HA	6:H:102:ALA:HB1	1.48	0.95
7:Q:104:VAL:HG23	7:Q:511:ALA:HB2	1.49	0.95
6:H:329:SER:HB3	6:H:341:VAL:HG13	1.49	0.95
2:B:326:VAL:HG12	2:B:365:VAL:HG11	1.49	0.94
2:B:218:PHE:HB2	2:B:326:VAL:HG11	1.48	0.94
2:B:33:ILE:HA	2:B:107:ALA:HB1	1.50	0.94
8:Z:225:VAL:HB	8:Z:228:ALA:HB2	1.50	0.94
5:G:466:LEU:HA	5:G:487:LEU:HD22	1.48	0.93
5:G:72:VAL:HG13	8:Z:6:THR:HA	1.50	0.93
3:D:315:LEU:H	3:D:315:LEU:HD22	1.32	0.92
5:G:23:GLN:HE21	5:G:113:LEU:HD13	1.34	0.92
8:Z:41:LYS:HD2	8:Z:455:SER:HA	1.49	0.92
3:D:245:GLU:HG3	3:D:246:LYS:HD2	1.52	0.92
3:D:197:VAL:HG12	3:D:387:LYS:HA	1.51	0.92
8:Z:101:GLU:HB2	8:Z:446:ILE:HD12	1.52	0.91
2:B:121:ILE:HG23	2:B:431:LYS:HD2	1.49	0.91
5:G:204:ILE:HD13	5:G:355:ILE:HG21	1.50	0.91
1:A:106:GLU:HA	1:A:109:LYS:HD2	1.50	0.90
3:D:210:ASP:O	3:D:388:THR:HA	1.70	0.90
4:E:204:VAL:HB	4:E:410:ARG:HG3	1.51	0.90
1:A:351:VAL:HG13	1:A:364:ILE:HG12	1.54	0.90
1:A:408:VAL:HG21	1:A:504:PHE:HB3	1.50	0.90
7:Q:241:VAL:HG13	7:Q:321:LEU:HD22	1.54	0.90
1:A:220:VAL:HG13	1:A:306:MET:HG3	1.52	0.90
7:Q:90:SER:HB3	7:Q:105:LEU:HD21	1.54	0.90
6:H:190:LEU:HD11	6:H:195:ILE:HD11	1.52	0.90
5:G:152:MET:SD	5:G:402:LEU:HD11	2.11	0.90
5:G:241:LEU:HD13	5:G:338:LEU:HD11	1.54	0.90
5:G:239:VAL:HG22	5:G:343:VAL:HG22	1.53	0.89
6:H:215:ALA:HB3	6:H:373:ILE:HD11	1.53	0.89
4:E:50:THR:HB	4:E:57:LEU:HD12	1.54	0.89
5:G:74:HIS:HB2	8:Z:5:LYS:HB2	1.55	0.89
6:H:17:GLN:HB3	6:H:518:GLU:HG3	1.54	0.89
7:Q:247:ASP:HA	7:Q:298:ALA:HB2	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:26:ASN:HD21	5:G:519:ILE:HD12	1.37	0.89
7:Q:199:VAL:HG12	7:Q:396:VAL:HG12	1.53	0.89
1:A:349:GLU:HB3	1:A:366:ASN:HB3	1.54	0.89
1:A:31:ILE:HG22	1:A:43:LYS:HE2	1.54	0.89
5:G:203:LYS:HD2	5:G:384:LEU:HG	1.54	0.88
8:Z:230:ILE:HG21	8:Z:324:LEU:HD21	1.54	0.88
1:A:10:ASP:O	1:A:531:ILE:HA	1.72	0.88
3:D:178:VAL:HB	3:D:403:GLU:HG2	1.55	0.88
8:Z:237:LEU:HG	8:Z:336:LEU:HD11	1.56	0.88
2:B:144:SER:HB2	2:B:474:THR:HG21	1.55	0.88
6:H:183:VAL:HG13	6:H:190:LEU:HD22	1.56	0.88
3:D:119:LEU:HD12	3:D:529:VAL:HG21	1.56	0.88
7:Q:199:VAL:HG13	7:Q:400:LYS:HD2	1.53	0.87
2:B:229:PRO:HG2	2:B:310:MET:HB2	1.56	0.87
6:H:23:VAL:HG22	6:H:109:LYS:HE3	1.54	0.87
8:Z:466:VAL:HG22	8:Z:486:PRO:HB3	1.55	0.87
3:D:208:LEU:HG	3:D:416:ARG:HD3	1.56	0.87
3:D:152:THR:HG22	3:D:515:LEU:HD21	1.53	0.87
3:D:101:GLN:HE22	3:D:105:ALA:HB3	1.37	0.86
4:E:99:ASP:HA	4:E:103:GLY:HA2	1.56	0.86
8:Z:224:ARG:HH11	8:Z:351:TYR:HB3	1.38	0.86
1:A:530:LEU:HD12	1:A:531:ILE:N	1.90	0.86
1:A:2:GLU:HG3	3:D:43:ALA:HB3	1.56	0.86
7:Q:142:ILE:HG22	7:Q:146:LEU:HD23	1.57	0.86
2:B:158:ASP:HA	2:B:161:ASN:HD22	1.41	0.85
3:D:239:SER:HB2	3:D:321:ASN:HB3	1.57	0.85
6:H:33:ALA:HB1	6:H:99:LEU:HA	1.58	0.85
4:E:156:LEU:HB3	4:E:161:ASN:HB3	1.56	0.85
1:A:180:LYS:HD3	1:A:403:LEU:HD23	1.58	0.85
7:Q:112:LEU:HD22	7:Q:519:LEU:HD21	1.55	0.85
6:H:120:ILE:HD11	7:Q:457:GLY:HA3	1.57	0.85
6:H:26:ILE:HG23	6:H:105:LEU:HB3	1.58	0.85
4:E:188:ILE:HG23	4:E:224:LEU:HB2	1.59	0.85
8:Z:199:LYS:HZ1	8:Z:377:LYS:HD3	1.41	0.85
8:Z:277:LEU:HD22	8:Z:340:ASN:HA	1.58	0.84
6:H:48:LEU:HG	6:H:58:ILE:HG12	1.59	0.84
4:E:247:LYS:HB3	4:E:353:LEU:HD13	1.57	0.84
1:A:137:ILE:HD12	1:A:410:PRO:HD3	1.57	0.84
6:H:154:LEU:HD23	6:H:157:LYS:HZ3	1.41	0.84
3:D:167:LEU:HD23	3:D:191:VAL:HG21	1.56	0.84
8:Z:103:LEU:HD22	8:Z:516:LEU:HD21	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:247:ALA:HA	3:D:299:ASN:HD21	1.43	0.84
7:Q:183:ILE:HG23	7:Q:217:VAL:HG22	1.58	0.84
4:E:209:ILE:HA	4:E:383:VAL:HG22	1.59	0.84
3:D:421:LYS:HE2	3:D:515:LEU:HD23	1.60	0.83
4:E:458:ILE:HB	4:E:459:PRO:HD3	1.61	0.83
1:A:506:PRO:HB2	1:A:509:VAL:HG23	1.59	0.83
5:G:238:ILE:HD13	5:G:323:ILE:HG21	1.59	0.83
4:E:163:GLU:HB3	4:E:164:PRO:HD3	1.60	0.83
6:H:227:MET:HA	6:H:230:LYS:NZ	1.93	0.83
1:A:112:ILE:HG23	1:A:433:ARG:HD3	1.58	0.83
4:E:98:GLN:HE21	4:E:102:ILE:HD11	1.41	0.83
1:A:237:LEU:HD13	1:A:331:LEU:HG	1.61	0.83
2:B:239:ILE:HG21	2:B:331:ILE:HG12	1.61	0.82
4:E:25:LYS:HG2	4:E:536:PRO:HA	1.60	0.82
7:Q:205:CYS:SG	7:Q:376:VAL:HA	2.19	0.82
5:G:407:LEU:HD13	5:G:496:TRP:HB3	1.61	0.82
1:A:356:ILE:HD13	1:A:361:LEU:HD22	1.61	0.82
7:Q:390:ARG:HH11	7:Q:390:ARG:HG2	1.45	0.82
1:A:351:VAL:HG22	1:A:364:ILE:HG23	1.62	0.82
1:A:199:LYS:HB2	1:A:385:CYS:HB3	1.61	0.82
7:Q:297:VAL:HG21	7:Q:312:LEU:HD21	1.61	0.82
8:Z:201:GLU:HA	8:Z:377:LYS:O	1.80	0.82
5:G:130:LEU:HD23	5:G:510:VAL:HG21	1.61	0.82
8:Z:448:PRO:HA	8:Z:451:LEU:HD12	1.61	0.82
6:H:313:ARG:HG3	6:H:313:ARG:HH11	1.42	0.82
1:A:85:GLU:HB3	1:A:512:LYS:HE2	1.62	0.82
1:A:532:LYS:HG3	3:D:63:MET:O	1.80	0.81
5:G:491:LYS:HA	5:G:496:TRP:HE1	1.45	0.81
4:E:20:LYS:NZ	6:H:31:VAL:HB	1.94	0.81
2:B:421:VAL:HA	2:B:424:LEU:HD12	1.61	0.81
5:G:156:ILE:HG23	5:G:394:ALA:HB1	1.62	0.81
2:B:95:VAL:HG23	2:B:96:GLY:H	1.44	0.81
7:Q:151:ALA:HB3	7:Q:159:GLU:HG3	1.60	0.81
7:Q:238:LYS:NZ	7:Q:341:LEU:HD11	1.96	0.81
7:Q:240:ALA:HB2	7:Q:344:MET:SD	2.20	0.81
6:H:346:GLN:HB3	6:H:363:GLY:HA3	1.62	0.81
4:E:510:LEU:HG	4:E:514:LYS:NZ	1.94	0.81
3:D:443:SER:OG	3:D:454:ILE:HB	1.80	0.81
2:B:209:LEU:HD21	2:B:382:ILE:HG22	1.63	0.81
8:Z:168:LEU:HD21	8:Z:391:ILE:HG12	1.61	0.81
8:Z:406:CYS:HB3	8:Z:498:TYR:HB2	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:454:ALA:HB2	2:B:480:MET:SD	2.20	0.81
2:B:520:ILE:HD12	4:E:60:MET:HB3	1.60	0.81
5:G:238:ILE:HD11	5:G:291:ILE:HG13	1.62	0.81
4:E:161:ASN:HD22	4:E:164:PRO:HB2	1.46	0.80
7:Q:276:MET:SD	7:Q:300:MET:HB2	2.20	0.80
4:E:527:ILE:HA	4:E:530:ILE:HD12	1.63	0.80
2:B:354:ILE:HD12	2:B:359:LEU:HD22	1.63	0.80
2:B:53:LEU:HA	2:B:60:SER:O	1.81	0.80
8:Z:231:LEU:HG	8:Z:339:LEU:HD13	1.61	0.80
4:E:234:PHE:HE1	4:E:372:LEU:HD13	1.47	0.80
3:D:236:VAL:HG21	3:D:329:LYS:HG2	1.64	0.80
6:H:6:VAL:HG12	6:H:7:ILE:HG13	1.62	0.80
1:A:530:LEU:HD12	1:A:531:ILE:H	1.46	0.80
4:E:489:LEU:HD21	4:E:498:THR:HB	1.64	0.80
6:H:25:ASN:ND2	6:H:75:ALA:HB2	1.95	0.80
6:H:190:LEU:HD23	6:H:397:ARG:HB2	1.63	0.80
2:B:214:LEU:HG	2:B:373:ILE:HG12	1.62	0.80
4:E:21:ASP:HB3	4:E:25:LYS:HD2	1.61	0.79
4:E:97:SER:O	4:E:101:GLU:HG2	1.82	0.79
8:Z:228:ALA:HB1	8:Z:290:VAL:HG21	1.65	0.79
2:B:465:LEU:HA	2:B:485:ILE:HD12	1.64	0.79
1:A:27:SER:HB2	5:G:9:VAL:HG11	1.65	0.79
1:A:27:SER:O	1:A:31:ILE:HG13	1.83	0.79
6:H:522:ASN:HB3	7:Q:77:GLU:HB2	1.63	0.79
6:H:49:ILE:HD11	6:H:65:ILE:HG23	1.65	0.79
4:E:298:ASN:HA	4:E:319:LEU:HG	1.63	0.79
6:H:23:VAL:HG13	6:H:109:LYS:HZ1	1.47	0.79
1:A:237:LEU:HD21	1:A:334:LEU:HD22	1.62	0.79
4:E:251:LEU:HD21	4:E:348:LEU:HD22	1.65	0.78
5:G:347:ALA:HB3	5:G:365:GLU:HB3	1.65	0.78
3:D:93:MET:HA	3:D:96:GLU:OE1	1.83	0.78
3:D:64:ILE:HD11	3:D:80:ILE:HG23	1.65	0.78
1:A:418:ALA:HB2	1:A:471:HIS:NE2	1.98	0.78
2:B:136:ALA:HB1	2:B:424:LEU:HD13	1.65	0.78
2:B:97:ASP:CG	2:B:98:GLY:H	1.87	0.78
6:H:211:VAL:HG13	6:H:362:THR:HB	1.64	0.78
1:A:190:TYR:HD2	1:A:400:LYS:HB2	1.48	0.77
6:H:239:LEU:HD22	6:H:319:LEU:HD12	1.65	0.77
4:E:177:VAL:HB	4:E:397:GLU:HG2	1.65	0.77
5:G:49:MET:HE2	5:G:51:LEU:HD11	1.65	0.77
3:D:33:PRO:HA	3:D:536:ASP:CG	2.04	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:HG21	1:A:319:ILE:HG21	1.66	0.77
7:Q:524:ILE:HG21	8:Z:46:MET:H	1.50	0.77
1:A:408:VAL:CG2	1:A:504:PHE:HB3	2.14	0.77
4:E:98:GLN:NE2	4:E:102:ILE:HD11	1.98	0.77
7:Q:333:LEU:HD13	7:Q:339:PRO:HB3	1.65	0.77
8:Z:118:ILE:H	8:Z:118:ILE:HD12	1.50	0.77
6:H:231:LYS:HA	6:H:348:PHE:O	1.84	0.77
2:B:196:LEU:HD22	2:B:394:LEU:HB3	1.67	0.77
7:Q:225:LYS:HA	7:Q:313:VAL:HG22	1.66	0.77
1:A:530:LEU:HD13	3:D:62:LYS:HB3	1.65	0.77
2:B:513:VAL:HA	2:B:516:ARG:NH1	1.99	0.77
8:Z:48:VAL:HG22	8:Z:54:ILE:HG12	1.65	0.76
4:E:404:ASP:HA	4:E:407:CYS:SG	2.25	0.76
4:E:20:LYS:HZ2	6:H:31:VAL:HB	1.51	0.76
6:H:97:VAL:HG23	6:H:506:ALA:HB2	1.68	0.76
4:E:193:VAL:HG13	4:E:204:VAL:HG11	1.65	0.76
6:H:238:ALA:HB3	6:H:289:VAL:HG22	1.68	0.76
2:B:50:LYS:HA	3:D:538:VAL:HG22	1.66	0.76
5:G:130:LEU:HD11	5:G:507:LYS:HD3	1.65	0.76
2:B:11:ILE:HA	4:E:85:HIS:H	1.51	0.76
5:G:388:GLU:O	5:G:392:GLN:HG3	1.86	0.76
2:B:299:TYR:HB3	2:B:300:PRO:HD3	1.67	0.76
8:Z:440:PHE:O	8:Z:444:LEU:HG	1.86	0.76
6:H:238:ALA:HB2	6:H:286:ALA:HB1	1.66	0.76
6:H:235:PRO:HD2	6:H:345:CYS:O	1.86	0.76
1:A:68:GLU:HB2	5:G:11:SER:HA	1.68	0.76
3:D:24:LYS:HD3	3:D:28:GLN:HE22	1.50	0.76
4:E:35:LYS:HA	4:E:38:ILE:HD12	1.68	0.76
5:G:416:MET:HG2	5:G:466:LEU:HD22	1.66	0.76
8:Z:46:MET:HB2	8:Z:56:LEU:HD13	1.68	0.76
1:A:356:ILE:HG23	1:A:378:ARG:NH2	2.00	0.76
5:G:86:THR:O	5:G:90:GLU:HG2	1.86	0.76
5:G:466:LEU:HG	5:G:487:LEU:HD13	1.67	0.75
6:H:157:LYS:O	6:H:161:THR:HG23	1.86	0.75
8:Z:118:ILE:HG21	8:Z:432:ARG:HB2	1.68	0.75
8:Z:228:ALA:HB1	8:Z:290:VAL:CG2	2.17	0.75
8:Z:293:ASN:HD22	8:Z:297:ILE:HD11	1.51	0.75
1:A:17:ILE:HG23	1:A:18:ARG:H	1.52	0.75
3:D:237:ALA:HB1	3:D:321:ASN:OD1	1.86	0.75
3:D:433:ILE:HD11	3:D:465:PRO:HG3	1.68	0.75
4:E:236:HIS:HB3	4:E:239:MET:HG3	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:29:CYS:HA	6:H:79:LEU:HD11	1.66	0.75
8:Z:114:LEU:HD23	8:Z:432:ARG:HD3	1.68	0.75
7:Q:20:LYS:NZ	8:Z:68:GLN:HB3	2.02	0.75
5:G:70:ILE:HG23	8:Z:7:LEU:HD23	1.68	0.75
6:H:19:ILE:N	6:H:20:PRO:HD2	2.01	0.75
7:Q:521:VAL:HG13	8:Z:45:LYS:HA	1.69	0.74
4:E:466:SER:HB3	4:E:493:CYS:SG	2.26	0.74
8:Z:466:VAL:HG21	8:Z:479:VAL:HG22	1.68	0.74
8:Z:216:ALA:HB1	8:Z:221:MET:HB2	1.69	0.74
3:D:477:ILE:H	3:D:477:ILE:HD12	1.52	0.74
6:H:51:ASP:OD2	6:H:55:LYS:HB3	1.88	0.74
2:B:407:VAL:HG23	2:B:495:GLU:HB2	1.70	0.74
5:G:73:GLN:HB2	8:Z:5:LYS:HB3	1.67	0.74
6:H:394:MET:HE3	6:H:397:ARG:HH21	1.51	0.74
3:D:529:VAL:O	3:D:533:LEU:HG	1.87	0.74
7:Q:58:ASN:HD21	7:Q:62:LYS:HB2	1.53	0.74
7:Q:129:ILE:HD12	7:Q:516:VAL:HG13	1.68	0.74
2:B:33:ILE:HG21	2:B:111:ARG:HD3	1.70	0.74
3:D:244:VAL:HG11	3:D:299:ASN:OD1	1.88	0.74
1:A:33:LYS:HA	1:A:95:ILE:HD11	1.68	0.74
6:H:200:VAL:HG11	6:H:358:TYR:HE2	1.50	0.74
6:H:414:MET:HG2	6:H:464:LEU:HG	1.67	0.74
3:D:101:GLN:NE2	3:D:105:ALA:HB3	2.02	0.74
7:Q:234:VAL:HG11	7:Q:289:ASN:OD1	1.87	0.74
3:D:32:LYS:O	3:D:36:ILE:HG22	1.87	0.74
7:Q:104:VAL:HG13	7:Q:105:LEU:HD23	1.70	0.74
4:E:306:PHE:HB2	4:E:323:ARG:HB3	1.69	0.74
2:B:51:ILE:HD12	2:B:63:VAL:HG22	1.69	0.74
7:Q:49:PRO:HA	7:Q:170:SER:HA	1.70	0.74
4:E:413:ILE:HG23	4:E:414:ARG:HG3	1.69	0.74
2:B:190:LEU:HD11	2:B:371:CYS:SG	2.28	0.74
5:G:238:ILE:HA	5:G:289:VAL:HG23	1.69	0.73
5:G:64:ASN:HB2	5:G:95:THR:HG21	1.68	0.73
1:A:180:LYS:HZ1	1:A:403:LEU:HB3	1.53	0.73
4:E:511:ILE:H	4:E:511:ILE:HD12	1.53	0.73
6:H:135:LYS:O	6:H:139:ILE:HG12	1.87	0.73
4:E:236:HIS:CD2	4:E:315:LEU:HD12	2.24	0.73
5:G:240:LEU:HD12	5:G:331:ILE:HG12	1.69	0.73
5:G:74:HIS:H	8:Z:5:LYS:HB2	1.52	0.73
3:D:193:ALA:HB1	3:D:389:VAL:HG21	1.69	0.73
3:D:94:LEU:HD22	3:D:113:VAL:HG13	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:17:GLU:HA	8:Z:70:GLN:CD	2.09	0.73
6:H:227:MET:HA	6:H:230:LYS:HZ1	1.53	0.73
1:A:238:ASP:HB3	1:A:329:SER:HA	1.69	0.73
5:G:89:GLU:HA	5:G:389:ARG:NH2	2.03	0.73
8:Z:115:HIS:HB3	8:Z:118:ILE:HD13	1.68	0.73
1:A:43:LYS:HG2	5:G:520:ASP:OD1	1.88	0.73
3:D:256:LEU:N	3:D:256:LEU:HD12	2.03	0.73
7:Q:402:LEU:HD12	7:Q:406:LYS:HA	1.70	0.73
2:B:43:LEU:HD12	2:B:44:GLY:H	1.54	0.73
8:Z:131:LEU:HD23	8:Z:505:LEU:HD12	1.69	0.73
3:D:217:LEU:HD11	3:D:398:LYS:HG3	1.71	0.72
2:B:12:PHE:HB3	2:B:16:ALA:HB3	1.70	0.72
3:D:235:LYS:HE3	3:D:367:GLU:HB2	1.69	0.72
8:Z:176:ILE:HD13	8:Z:179:ILE:HD11	1.71	0.72
3:D:32:LYS:NZ	3:D:33:PRO:HD2	2.03	0.72
6:H:188:ASP:O	6:H:189:LEU:HB2	1.88	0.72
1:A:136:LEU:HD22	1:A:407:SER:HB3	1.69	0.72
4:E:331:GLU:OE1	6:H:297:ASP:HB3	1.89	0.72
3:D:290:VAL:HG21	3:D:319:PHE:HB2	1.70	0.72
5:G:220:ILE:HD11	5:G:323:ILE:HD11	1.72	0.72
2:B:79:PRO:HD3	2:B:522:LYS:HD2	1.70	0.72
6:H:19:ILE:H	6:H:20:PRO:CD	2.02	0.72
1:A:121:TYR:HB3	1:A:518:THR:HG23	1.71	0.72
1:A:135:ASN:HB3	1:A:484:LYS:HD3	1.70	0.72
5:G:49:MET:HG3	5:G:59:MET:HG2	1.72	0.71
3:D:421:LYS:HG2	3:D:515:LEU:HB3	1.71	0.71
7:Q:233:SER:HA	7:Q:351:TYR:HA	1.72	0.71
3:D:78:ALA:HB2	3:D:109:THR:HG21	1.72	0.71
7:Q:230:ASP:HB3	7:Q:311:MET:HA	1.71	0.71
8:Z:97:LEU:HD23	8:Z:450:VAL:HG21	1.72	0.71
1:A:2:GLU:CG	3:D:43:ALA:HB3	2.20	0.71
4:E:55:ASN:ND2	4:E:466:SER:HA	2.02	0.71
8:Z:222:LYS:HB2	8:Z:311:ILE:HD11	1.71	0.71
4:E:510:LEU:HG	4:E:514:LYS:HZ2	1.52	0.71
7:Q:289:ASN:OD1	7:Q:290:VAL:HG23	1.89	0.71
4:E:534:ARG:HH21	6:H:35:ALA:CB	2.03	0.71
5:G:399:ARG:O	5:G:403:LEU:HD13	1.91	0.71
7:Q:526:MET:HG2	8:Z:48:VAL:O	1.90	0.71
1:A:8:PHE:O	1:A:533:LEU:HD22	1.91	0.71
2:B:124:GLN:HG2	4:E:55:ASN:ND2	2.06	0.71
8:Z:414:VAL:HA	8:Z:475:GLN:HE22	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:43:ARG:NH2	6:H:480:ASN:HA	2.05	0.71
6:H:167:LEU:HB3	6:H:384:GLU:HG2	1.72	0.71
5:G:407:LEU:HB3	5:G:498:PRO:HA	1.72	0.71
3:D:187:SER:HB2	3:D:188:PRO:HD3	1.73	0.71
3:D:252:ILE:HB	3:D:303:ILE:HD13	1.71	0.71
7:Q:176:GLU:HG3	7:Q:212:VAL:HG13	1.73	0.71
2:B:231:ARG:HH21	2:B:348:LEU:HD11	1.55	0.71
6:H:19:ILE:HA	6:H:22:LEU:HD23	1.73	0.71
6:H:366:LYS:HD3	6:H:368:LYS:NZ	2.06	0.71
8:Z:193:ILE:HG21	8:Z:388:LYS:HG3	1.71	0.71
7:Q:524:ILE:CG2	8:Z:46:MET:H	2.03	0.70
7:Q:113:GLU:O	7:Q:116:GLU:HG2	1.91	0.70
5:G:27:ILE:HG23	5:G:106:LEU:HB3	1.73	0.70
2:B:518:ASP:CG	4:E:59:LYS:HZ3	1.94	0.70
7:Q:452:LEU:HG	7:Q:482:ILE:HD11	1.73	0.70
3:D:210:ASP:HB3	3:D:387:LYS:O	1.92	0.70
5:G:401:VAL:HA	5:G:405:PRO:HB3	1.72	0.70
4:E:222:THR:HG22	4:E:387:ILE:HA	1.73	0.70
6:H:313:ARG:HG3	6:H:313:ARG:NH1	2.04	0.70
2:B:187:VAL:HG21	2:B:397:LEU:HD13	1.72	0.70
7:Q:232:THR:O	7:Q:351:TYR:HA	1.91	0.70
6:H:278:LEU:HD23	6:H:302:TYR:HB2	1.73	0.70
7:Q:525:ILE:HG23	7:Q:526:MET:N	2.01	0.70
1:A:532:LYS:HG2	3:D:65:GLN:CB	2.20	0.70
5:G:47:MET:O	8:Z:518:VAL:HG22	1.91	0.70
3:D:299:ASN:OD1	3:D:300:VAL:HG23	1.91	0.70
4:E:209:ILE:HA	4:E:383:VAL:CG2	2.21	0.70
8:Z:138:LYS:HA	8:Z:408:VAL:HG12	1.74	0.70
8:Z:455:SER:HB3	8:Z:481:LEU:HD13	1.73	0.70
3:D:192:ASP:O	3:D:195:MET:HG3	1.91	0.70
4:E:362:ILE:HB	4:E:364:PHE:CE1	2.27	0.70
2:B:279:VAL:HG11	2:B:303:LEU:HB3	1.73	0.70
8:Z:105:GLN:HA	8:Z:108:LEU:HD12	1.72	0.70
4:E:247:LYS:O	4:E:353:LEU:HD22	1.91	0.70
1:A:458:GLN:HB3	1:A:463:LEU:HD11	1.72	0.70
7:Q:523:GLN:HB3	8:Z:45:LYS:NZ	2.07	0.70
6:H:161:THR:HG21	6:H:491:PHE:HB3	1.72	0.70
8:Z:135:GLU:HA	8:Z:138:LYS:HD3	1.74	0.70
7:Q:70:ALA:H	7:Q:101:THR:HG21	1.56	0.70
4:E:468:MET:SD	4:E:496:LYS:HB3	2.31	0.70
4:E:87:ILE:CD1	4:E:527:ILE:HG21	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:337:ASN:H	7:Q:338:PRO:HD2	1.55	0.70
7:Q:417:ILE:HD11	7:Q:449:PRO:HG3	1.73	0.70
5:G:200:ARG:HE	5:G:322:ARG:HH11	1.40	0.70
2:B:416:LEU:HD22	2:B:474:THR:HG23	1.74	0.70
5:G:238:ILE:HD11	5:G:291:ILE:CG1	2.22	0.70
2:B:427:ARG:O	2:B:429:PRO:HD3	1.91	0.70
3:D:144:LEU:HB2	3:D:526:THR:HG21	1.71	0.70
4:E:85:HIS:O	4:E:89:LYS:HG3	1.92	0.69
5:G:73:GLN:NE2	8:Z:9:PRO:HD3	2.07	0.69
7:Q:17:GLU:HA	8:Z:70:GLN:OE1	1.92	0.69
8:Z:222:LYS:HD2	8:Z:311:ILE:HD11	1.74	0.69
6:H:239:LEU:HD23	6:H:290:LEU:HB2	1.74	0.69
7:Q:221:MET:HA	7:Q:374:THR:OG1	1.92	0.69
3:D:178:VAL:CB	3:D:403:GLU:HG2	2.22	0.69
7:Q:103:PHE:HE1	7:Q:448:ILE:HG12	1.57	0.69
8:Z:30:LEU:HD22	8:Z:74:ALA:HB1	1.74	0.69
7:Q:80:HIS:HB3	7:Q:83:ALA:HB3	1.72	0.69
5:G:156:ILE:HD11	5:G:398:CYS:SG	2.33	0.69
1:A:2:GLU:HA	3:D:88:HIS:HB3	1.74	0.69
6:H:154:LEU:HD23	6:H:157:LYS:NZ	2.07	0.69
5:G:14:THR:HG23	5:G:525:GLY:HA3	1.74	0.69
4:E:286:GLU:HA	4:E:313:LEU:HD13	1.74	0.69
1:A:172:VAL:O	1:A:176:VAL:HG23	1.92	0.69
2:B:187:VAL:O	2:B:191:LYS:HB2	1.93	0.69
5:G:397:VAL:HA	5:G:400:ASN:HD22	1.57	0.69
6:H:200:VAL:HG11	6:H:358:TYR:CE2	2.27	0.69
7:Q:161:SER:HB2	7:Q:181:LYS:HD2	1.74	0.69
3:D:146:LYS:O	3:D:149:GLU:HG2	1.93	0.69
8:Z:224:ARG:CZ	8:Z:349:LEU:HD11	2.23	0.69
4:E:161:ASN:HB2	4:E:164:PRO:HD2	1.73	0.69
8:Z:197:LYS:HE2	8:Z:381:LYS:HG3	1.75	0.69
2:B:186:ALA:HA	2:B:189:ARG:HH12	1.57	0.69
7:Q:237:ALA:HA	7:Q:289:ASN:HD21	1.55	0.69
1:A:348:ALA:HA	1:A:367:THR:HA	1.74	0.69
2:B:280:GLU:HG2	2:B:284:LYS:HE3	1.75	0.69
4:E:166:ILE:HG22	4:E:170:LYS:HE2	1.75	0.69
3:D:193:ALA:CB	3:D:389:VAL:HG21	2.23	0.69
3:D:237:ALA:HB2	3:D:327:VAL:HG12	1.75	0.69
1:A:328:LEU:HD21	1:A:344:MET:HB3	1.73	0.69
7:Q:410:PRO:O	7:Q:414:ALA:HB3	1.93	0.69
2:B:398:ALA:O	2:B:402:LYS:HD2	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:409:PRO:O	8:Z:413:ALA:HB3	1.93	0.69
8:Z:294:GLN:NE2	8:Z:318:ARG:HD3	2.08	0.69
2:B:30:ILE:HA	2:B:33:ILE:HD12	1.74	0.68
1:A:31:ILE:HG12	5:G:16:ARG:HH12	1.58	0.68
7:Q:337:ASN:C	7:Q:339:PRO:HD2	2.13	0.68
6:H:406:VAL:HB	6:H:412:ILE:HD11	1.75	0.68
7:Q:85:MET:HA	7:Q:88:MET:SD	2.33	0.68
3:D:256:LEU:HD21	3:D:301:LEU:HD21	1.74	0.68
3:D:416:ARG:HH11	3:D:420:LYS:NZ	1.91	0.68
6:H:133:VAL:HG12	6:H:137:LYS:NZ	2.09	0.68
1:A:211:ILE:HG12	1:A:376:ILE:HG12	1.76	0.68
6:H:412:ILE:O	6:H:416:LEU:HG	1.94	0.68
1:A:145:ARG:HG2	1:A:149:ILE:HD11	1.76	0.68
4:E:218:ARG:HA	4:E:389:GLY:HA2	1.76	0.68
3:D:415:ILE:O	3:D:419:VAL:HG13	1.94	0.68
2:B:516:ARG:HG2	4:E:58:ASP:H	1.57	0.68
8:Z:414:VAL:HA	8:Z:475:GLN:NE2	2.08	0.68
7:Q:53:ASN:HB3	7:Q:67:ASN:OD1	1.94	0.68
1:A:69:HIS:HB2	5:G:8:LEU:O	1.94	0.68
7:Q:239:ILE:HD12	7:Q:328:VAL:HG11	1.76	0.68
3:D:41:ILE:HG23	3:D:120:LEU:HB3	1.75	0.68
2:B:25:ARG:HD2	2:B:117:ILE:HD13	1.76	0.68
3:D:52:ARG:HA	3:D:114:ILE:HD11	1.76	0.68
5:G:112:PHE:HE2	5:G:436:PRO:HA	1.59	0.68
3:D:505:ASN:O	3:D:509:GLU:HG2	1.94	0.68
8:Z:44:MET:SD	8:Z:56:LEU:HG	2.34	0.68
7:Q:225:LYS:NZ	7:Q:352:LEU:HB2	2.09	0.68
3:D:177:LYS:HD3	3:D:407:SER:HB3	1.76	0.68
7:Q:203:ARG:HH22	7:Q:223:PHE:HD1	1.41	0.67
6:H:21:GLN:NE2	6:H:22:LEU:HD13	2.09	0.67
7:Q:174:GLY:HA2	7:Q:177:VAL:HG13	1.76	0.67
6:H:30:GLN:O	6:H:34:GLU:HG2	1.94	0.67
5:G:23:GLN:NE2	5:G:113:LEU:HB3	2.10	0.67
1:A:234:ILE:HG21	1:A:319:ILE:CG2	2.24	0.67
4:E:27:ARG:HH22	4:E:534:ARG:NH2	1.92	0.67
5:G:246:GLU:HA	5:G:297:SER:HB3	1.75	0.67
5:G:29:ALA:HA	8:Z:4:VAL:HG13	1.76	0.67
6:H:198:LYS:HZ3	6:H:217:LYS:HG3	1.59	0.67
5:G:140:ILE:HG13	5:G:476:GLU:OE1	1.93	0.67
8:Z:12:GLU:O	8:Z:522:MET:HA	1.94	0.67
4:E:204:VAL:CG2	4:E:413:ILE:HG21	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:181:LYS:HE2	8:Z:370:ARG:HH12	1.57	0.67
4:E:94:LEU:HD11	4:E:523:MET:HB3	1.76	0.67
1:A:530:LEU:HD21	3:D:63:MET:H	1.59	0.67
6:H:153:LYS:HG2	6:H:157:LYS:HZ2	1.59	0.67
5:G:33:ILE:HD11	5:G:67:LEU:HD22	1.76	0.67
5:G:64:ASN:ND2	5:G:68:ARG:HD2	2.10	0.67
6:H:22:LEU:HD22	6:H:22:LEU:H	1.60	0.67
1:A:2:GLU:CA	3:D:88:HIS:HB3	2.25	0.67
1:A:241:LEU:HG	1:A:331:LEU:HD21	1.77	0.67
3:D:256:LEU:HD11	3:D:303:ILE:CD1	2.25	0.67
8:Z:504:LEU:HD23	8:Z:505:LEU:N	2.10	0.67
3:D:249:ILE:HG21	3:D:345:THR:HG21	1.76	0.67
5:G:70:ILE:HG22	8:Z:6:THR:O	1.95	0.67
5:G:498:PRO:HB2	5:G:501:VAL:HG23	1.77	0.67
4:E:536:PRO:HD2	6:H:50:VAL:O	1.94	0.67
5:G:129:ALA:HA	5:G:132:ASP:OD2	1.95	0.67
5:G:359:TYR:HD1	5:G:359:TYR:H	1.42	0.67
4:E:344:ARG:HE	4:E:345:PHE:H	1.40	0.67
8:Z:197:LYS:O	8:Z:198:HIS:HB2	1.95	0.67
6:H:417:SER:HA	6:H:439:ALA:HB1	1.77	0.67
6:H:198:LYS:NZ	6:H:217:LYS:HG3	2.10	0.67
6:H:450:CYS:SG	6:H:460:ILE:HG21	2.35	0.67
1:A:20:GLN:HB2	5:G:7:VAL:N	2.10	0.67
2:B:279:VAL:HG21	2:B:303:LEU:HB2	1.75	0.67
2:B:461:LEU:HD21	2:B:478:LEU:HD13	1.76	0.67
6:H:118:PRO:HA	6:H:121:ILE:HD12	1.77	0.66
5:G:19:GLY:O	5:G:23:GLN:HG2	1.94	0.66
8:Z:199:LYS:NZ	8:Z:377:LYS:HD3	2.11	0.66
3:D:241:ILE:O	3:D:326:MET:HB2	1.95	0.66
6:H:237:ILE:O	6:H:342:LEU:HA	1.95	0.66
3:D:256:LEU:HD11	3:D:303:ILE:HG13	1.76	0.66
4:E:227:GLY:HA3	4:E:375:GLU:HA	1.77	0.66
7:Q:397:ASN:O	7:Q:401:VAL:HG23	1.94	0.66
7:Q:523:GLN:O	8:Z:45:LYS:HD2	1.95	0.66
8:Z:230:ILE:HD13	8:Z:290:VAL:HB	1.77	0.66
5:G:144:VAL:O	5:G:405:PRO:HB2	1.95	0.66
2:B:194:GLY:HA3	2:B:401:VAL:HG21	1.77	0.66
1:A:313:LYS:HE2	1:A:317:LYS:HE3	1.76	0.66
3:D:175:ASN:HA	3:D:180:SER:HB3	1.78	0.66
4:E:118:GLU:O	4:E:121:GLU:HG2	1.96	0.66
2:B:111:ARG:HH11	2:B:111:ARG:HG2	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:72:ILE:O	7:Q:76:LEU:HG	1.94	0.66
8:Z:417:ALA:HB2	8:Z:470:HIS:HE2	1.61	0.66
5:G:469:LYS:HA	5:G:472:GLN:OE1	1.96	0.66
5:G:379:ALA:HB3	5:G:383:ILE:HD12	1.76	0.66
8:Z:118:ILE:CG2	8:Z:432:ARG:HB2	2.26	0.66
7:Q:239:ILE:HD13	7:Q:324:LEU:HD11	1.78	0.66
7:Q:328:VAL:HG12	7:Q:366:GLU:HG2	1.75	0.66
3:D:137:SER:HB3	3:D:530:ARG:HG3	1.78	0.66
3:D:232:LEU:HD21	3:D:339:ILE:HD11	1.76	0.66
3:D:474:LEU:HD11	3:D:501:GLY:HA2	1.78	0.66
4:E:156:LEU:HD23	4:E:161:ASN:HB3	1.77	0.66
5:G:104:GLU:HG2	5:G:446:VAL:HG11	1.78	0.66
7:Q:206:LYS:HB3	7:Q:385:MET:HG2	1.76	0.66
6:H:453:ALA:HB3	6:H:479:ILE:HD11	1.78	0.66
2:B:72:LYS:NZ	2:B:89:ARG:HG3	2.10	0.66
5:G:10:LEU:H	5:G:10:LEU:HD12	1.60	0.66
7:Q:44:ARG:NE	7:Q:451:ALA:HB2	2.11	0.66
2:B:51:ILE:HG23	2:B:63:VAL:HG22	1.78	0.66
7:Q:55:MET:SD	7:Q:63:LEU:HD11	2.36	0.66
6:H:141:VAL:HG21	6:H:474:TRP:HE1	1.60	0.66
8:Z:7:LEU:HD11	8:Z:522:MET:SD	2.35	0.66
5:G:240:LEU:HD12	5:G:324:ALA:HB2	1.77	0.66
3:D:126:LEU:HD11	3:D:453:CYS:HA	1.78	0.65
8:Z:13:VAL:HG22	8:Z:522:MET:HG2	1.78	0.65
8:Z:270:ARG:HB3	8:Z:336:LEU:HD13	1.78	0.65
1:A:86:VAL:HG13	1:A:512:LYS:NZ	2.10	0.65
4:E:170:LYS:NZ	4:E:183:ARG:HA	2.11	0.65
4:E:437:ALA:O	4:E:445:GLN:HG3	1.96	0.65
5:G:422:LEU:HD23	5:G:441:ALA:HB2	1.77	0.65
8:Z:218:HIS:ND1	8:Z:219:PRO:HD2	2.11	0.65
4:E:435:GLN:O	4:E:439:LYS:HG3	1.95	0.65
8:Z:94:SER:O	8:Z:98:ILE:HG12	1.95	0.65
3:D:105:ALA:HA	3:D:417:CYS:SG	2.37	0.65
4:E:248:ILE:O	4:E:353:LEU:HA	1.97	0.65
2:B:337:HIS:H	2:B:338:PRO:HD2	1.60	0.65
5:G:376:LEU:HD21	5:G:391:LEU:HD22	1.78	0.65
5:G:137:LEU:HD11	5:G:506:TYR:CE2	2.31	0.65
7:Q:411:GLY:HA3	7:Q:499:ASP:OD2	1.97	0.65
2:B:141:LEU:HG	2:B:417:MET:SD	2.36	0.65
2:B:411:GLY:HA2	2:B:446:LEU:HD23	1.77	0.65
5:G:72:VAL:HG21	5:G:81:ILE:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:152:ALA:HB3	8:Z:169:THR:HG23	1.77	0.65
6:H:197:ILE:HG21	6:H:386:GLU:HG3	1.78	0.65
7:Q:24:GLY:HA2	7:Q:522:ASP:O	1.97	0.65
3:D:30:ARG:HG3	3:D:539:VAL:HG22	1.78	0.65
4:E:90:LEU:O	4:E:523:MET:HE3	1.96	0.65
7:Q:44:ARG:HA	7:Q:102:ASN:HD21	1.61	0.65
6:H:23:VAL:HA	6:H:109:LYS:NZ	2.11	0.65
4:E:20:LYS:HZ3	6:H:32:ILE:CD1	2.09	0.65
3:D:248:LYS:HD2	3:D:359:LEU:HD13	1.78	0.65
4:E:437:ALA:HA	4:E:448:MET:SD	2.37	0.65
4:E:221:ASP:HB3	4:E:388:ARG:HD2	1.78	0.65
2:B:221:ASP:OD1	2:B:359:LEU:HG	1.97	0.65
3:D:251:LEU:HD12	3:D:336:ILE:HG23	1.78	0.65
1:A:445:LEU:N	1:A:446:PRO:HD2	2.12	0.65
1:A:233:LYS:HA	1:A:346:GLY:O	1.96	0.65
7:Q:238:LYS:HZ2	7:Q:341:LEU:HD11	1.61	0.65
1:A:192:VAL:HG13	1:A:400:LYS:HD2	1.77	0.65
3:D:235:LYS:HZ2	3:D:242:THR:HA	1.61	0.65
3:D:194:VAL:HA	3:D:197:VAL:HG22	1.78	0.65
5:G:221:ASN:HD22	5:G:316:ARG:HH22	1.44	0.65
3:D:232:LEU:HD22	3:D:335:ASP:HB3	1.78	0.65
8:Z:145:ARG:O	8:Z:149:ILE:HG13	1.96	0.65
6:H:364:CYS:HB2	6:H:367:ALA:HB2	1.79	0.65
4:E:161:ASN:ND2	4:E:164:PRO:HB2	2.11	0.65
3:D:293:ILE:HD13	3:D:301:LEU:HD22	1.80	0.65
6:H:6:VAL:CG2	7:Q:21:HIS:HB2	2.27	0.65
3:D:232:LEU:HD11	3:D:339:ILE:HD11	1.79	0.65
5:G:46:MET:HG2	8:Z:517:LEU:HD22	1.77	0.64
3:D:446:LEU:HD23	3:D:454:ILE:HD11	1.79	0.64
8:Z:374:LEU:HD23	8:Z:391:ILE:HD13	1.77	0.64
8:Z:273:LYS:O	8:Z:277:LEU:HG	1.97	0.64
5:G:130:LEU:HD23	5:G:510:VAL:CG2	2.28	0.64
7:Q:226:GLU:HG3	7:Q:314:ARG:HG2	1.78	0.64
3:D:179:VAL:CG1	3:D:404:ALA:HA	2.26	0.64
4:E:224:LEU:HD13	4:E:385:ILE:HG12	1.78	0.64
1:A:487:GLY:HA3	1:A:498:ASN:HD21	1.63	0.64
5:G:149:ARG:HG3	5:G:177:LEU:HD11	1.78	0.64
8:Z:176:ILE:HD11	8:Z:395:LEU:HB3	1.79	0.64
3:D:154:MET:HB3	3:D:492:LYS:HD3	1.79	0.64
8:Z:154:THR:HA	8:Z:157:ARG:HD2	1.79	0.64
7:Q:173:TYR:HB3	7:Q:388:ILE:HG12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:31:GLN:CG	8:Z:97:LEU:HA	2.27	0.64
8:Z:415:GLU:HG2	8:Z:447:ILE:HB	1.79	0.64
4:E:90:LEU:HA	4:E:93:GLU:OE1	1.97	0.64
3:D:227:VAL:HG11	3:D:378:LYS:HE3	1.79	0.64
2:B:236:LYS:NZ	2:B:288:ASN:HD21	1.96	0.64
2:B:97:ASP:CG	2:B:98:GLY:N	2.48	0.64
1:A:29:ALA:HB1	1:A:95:ILE:HA	1.80	0.64
1:A:112:ILE:HA	1:A:433:ARG:CZ	2.27	0.64
8:Z:426:LYS:N	8:Z:427:PRO:HD2	2.13	0.64
4:E:204:VAL:HG21	4:E:413:ILE:HG21	1.80	0.64
4:E:410:ARG:HA	4:E:413:ILE:HG22	1.79	0.64
3:D:213:ILE:HD11	3:D:412:LEU:HD11	1.78	0.64
4:E:460:MET:HG2	4:E:470:PRO:HB3	1.77	0.64
2:B:287:ILE:HG22	2:B:343:LEU:HD21	1.79	0.64
6:H:128:ALA:HB1	6:H:438:TYR:CD2	2.33	0.64
5:G:240:LEU:CD1	5:G:324:ALA:HB2	2.28	0.64
1:A:117:VAL:HG12	1:A:121:TYR:CE2	2.33	0.64
8:Z:417:ALA:CB	8:Z:470:HIS:HE2	2.11	0.64
6:H:119:GLN:HB2	7:Q:52:MET:HE2	1.79	0.64
1:A:2:GLU:HB3	3:D:90:ALA:HB3	1.79	0.64
1:A:148:LEU:HD13	1:A:399:VAL:HG13	1.79	0.64
4:E:31:LEU:HD12	4:E:34:LEU:HB2	1.80	0.63
5:G:49:MET:O	8:Z:521:ILE:HG23	1.98	0.63
5:G:33:ILE:HG21	5:G:80:MET:HG3	1.79	0.63
5:G:225:THR:HG21	5:G:301:GLN:HG2	1.80	0.63
3:D:41:ILE:HD12	3:D:120:LEU:HB3	1.80	0.63
1:A:190:TYR:OH	1:A:396:LEU:HD22	1.98	0.63
1:A:356:ILE:HG23	1:A:378:ARG:HH21	1.64	0.63
1:A:85:GLU:HB3	1:A:512:LYS:CE	2.27	0.63
6:H:407:ALA:HB1	6:H:487:ASN:HD22	1.60	0.63
5:G:160:ILE:HG23	5:G:165:ILE:HG23	1.80	0.63
7:Q:20:LYS:HZ3	8:Z:68:GLN:HB3	1.60	0.63
5:G:62:ASP:O	5:G:66:ILE:HG13	1.98	0.63
7:Q:138:LYS:HE3	7:Q:142:ILE:HD11	1.80	0.63
1:A:448:ILE:O	1:A:452:LEU:HG	1.98	0.63
4:E:481:GLN:HE21	4:E:487:PRO:CA	2.11	0.63
1:A:210:LEU:CD1	1:A:375:VAL:HG22	2.28	0.63
8:Z:476:LEU:HB3	8:Z:488:VAL:HG13	1.81	0.63
5:G:46:MET:HA	8:Z:517:LEU:HB3	1.80	0.63
2:B:219:LEU:HB3	2:B:372:THR:HG21	1.81	0.63
5:G:221:ASN:HD22	5:G:316:ARG:NH2	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ASP:CB	1:A:329:SER:HA	2.27	0.63
5:G:435:TRP:HB2	5:G:436:PRO:HD3	1.80	0.63
4:E:223:LYS:HD3	4:E:388:ARG:NH2	2.14	0.63
6:H:23:VAL:HA	6:H:109:LYS:HZ1	1.64	0.63
3:D:417:CYS:HA	3:D:516:LEU:HD12	1.80	0.63
3:D:515:LEU:HG	3:D:519:VAL:CG2	2.28	0.63
4:E:234:PHE:HA	4:E:322:VAL:HG22	1.79	0.63
7:Q:338:PRO:N	7:Q:339:PRO:HD2	2.13	0.63
6:H:73:HIS:CD2	6:H:74:PRO:HD2	2.34	0.63
1:A:118:ILE:HG23	1:A:522:ILE:HG12	1.80	0.63
7:Q:17:GLU:HB2	8:Z:68:GLN:HG2	1.80	0.63
8:Z:224:ARG:NH2	8:Z:349:LEU:HD11	2.12	0.63
6:H:522:ASN:CB	7:Q:77:GLU:HB2	2.27	0.63
2:B:497:PHE:CE2	2:B:501:ARG:HD3	2.33	0.63
4:E:41:ALA:O	4:E:44:VAL:HG12	1.98	0.63
4:E:291:GLN:HA	4:E:294:GLU:OE1	1.98	0.63
5:G:237:ARG:HB3	5:G:343:VAL:CG1	2.29	0.63
6:H:453:ALA:CB	6:H:479:ILE:HD11	2.29	0.63
2:B:238:LEU:HB2	2:B:343:LEU:CD2	2.29	0.63
7:Q:171:LYS:HB2	7:Q:173:TYR:CE1	2.34	0.63
6:H:226:GLU:O	6:H:227:MET:HB2	1.99	0.63
4:E:118:GLU:HA	4:E:121:GLU:OE2	1.98	0.63
5:G:424:GLU:HA	5:G:427:LYS:NZ	2.14	0.63
8:Z:376:ILE:HD11	8:Z:391:ILE:HD12	1.81	0.63
7:Q:324:LEU:O	7:Q:328:VAL:HG22	1.99	0.63
3:D:218:GLY:O	3:D:394:ARG:HB3	1.99	0.63
3:D:514:PRO:HG2	3:D:517:VAL:HG23	1.81	0.63
7:Q:91:HIS:O	7:Q:95:GLN:HG2	1.98	0.63
7:Q:191:PHE:N	7:Q:192:PRO:CD	2.62	0.63
8:Z:105:GLN:HB3	8:Z:439:ALA:HB1	1.81	0.62
1:A:137:ILE:HD13	1:A:499:LYS:HG3	1.80	0.62
6:H:133:VAL:HA	6:H:136:ILE:HD12	1.81	0.62
3:D:63:MET:HG3	3:D:71:VAL:HG13	1.80	0.62
4:E:145:ILE:HD11	4:E:514:LYS:HA	1.81	0.62
4:E:424:ALA:HB1	4:E:487:PRO:O	1.98	0.62
8:Z:224:ARG:NH1	8:Z:351:TYR:HB3	2.10	0.62
1:A:467:LEU:HD22	1:A:488:LEU:HG	1.80	0.62
1:A:103:ASN:HB3	1:A:440:GLU:HB3	1.81	0.62
6:H:100:LEU:HD21	6:H:445:ILE:HD11	1.80	0.62
5:G:285:LEU:O	5:G:340:GLU:HG3	1.99	0.62
2:B:513:VAL:HA	2:B:516:ARG:HH12	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:130:LEU:HB2	5:G:510:VAL:HG11	1.80	0.62
3:D:72:THR:HG21	3:D:83:GLN:HE21	1.64	0.62
1:A:68:GLU:HB2	5:G:11:SER:CA	2.29	0.62
8:Z:470:HIS:HA	8:Z:477:VAL:HG21	1.82	0.62
5:G:53:PRO:HD2	8:Z:525:GLY:HA2	1.81	0.62
3:D:540:ASN:O	3:D:541:THR:HG22	1.99	0.62
4:E:360:LYS:HE2	4:E:362:ILE:HG12	1.82	0.62
1:A:46:VAL:HA	1:A:51:ASP:O	1.99	0.62
7:Q:20:LYS:HD3	7:Q:527:ALA:N	2.15	0.62
8:Z:230:ILE:HA	8:Z:290:VAL:O	2.00	0.62
8:Z:233:CYS:HB3	8:Z:293:ASN:OD1	1.99	0.62
3:D:119:LEU:HB2	3:D:529:VAL:HG11	1.80	0.62
1:A:138:ILE:HB	1:A:406:LYS:HE2	1.81	0.62
2:B:468:ALA:HB3	2:B:485:ILE:HD13	1.82	0.62
1:A:206:MET:HA	1:A:206:MET:CE	2.30	0.62
1:A:225:MET:SD	1:A:306:MET:HA	2.40	0.62
5:G:10:LEU:HD22	5:G:523:VAL:HG11	1.81	0.62
8:Z:122:GLY:HA3	8:Z:436:GLY:HA3	1.81	0.62
7:Q:198:ASN:ND2	7:Q:200:ASP:HB2	2.13	0.62
5:G:245:LEU:HB2	5:G:296:ILE:HG23	1.82	0.62
2:B:232:ILE:CG2	2:B:235:ALA:HB2	2.29	0.62
6:H:78:THR:O	6:H:82:ILE:HG13	2.00	0.62
5:G:433:GLU:C	5:G:436:PRO:HD2	2.20	0.62
7:Q:166:THR:HG21	7:Q:496:GLY:O	1.99	0.62
3:D:82:LYS:NZ	3:D:99:LYS:HZ3	1.97	0.62
8:Z:447:ILE:O	8:Z:451:LEU:HG	2.00	0.62
8:Z:156:LEU:HD21	8:Z:168:LEU:HD22	1.81	0.62
1:A:180:LYS:HZ2	1:A:403:LEU:HG	1.65	0.62
7:Q:390:ARG:NH1	7:Q:390:ARG:HG2	2.13	0.62
2:B:38:LEU:HG	2:B:50:LYS:HE2	1.81	0.62
7:Q:230:ASP:OD1	7:Q:306:ASN:HA	2.00	0.62
1:A:211:ILE:HG22	1:A:213:GLY:N	2.04	0.62
7:Q:388:ILE:O	7:Q:392:VAL:HG23	2.00	0.62
3:D:416:ARG:O	3:D:419:VAL:HG22	1.99	0.62
7:Q:45:THR:O	7:Q:51:GLY:HA2	2.00	0.62
3:D:244:VAL:HG11	3:D:299:ASN:CG	2.20	0.61
5:G:218:VAL:HG21	5:G:323:ILE:HG12	1.82	0.61
3:D:256:LEU:HD11	3:D:303:ILE:CG1	2.29	0.61
7:Q:337:ASN:N	7:Q:338:PRO:HD2	2.15	0.61
2:B:244:MET:HB2	2:B:296:ILE:HG23	1.81	0.61
5:G:200:ARG:NE	5:G:322:ARG:HH11	1.97	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:218:HIS:HB3	8:Z:221:MET:HG3	1.82	0.61
3:D:112:VAL:HG13	3:D:113:VAL:N	2.15	0.61
8:Z:61:ASN:HB2	8:Z:92:THR:HG21	1.81	0.61
1:A:284:ASN:OD1	1:A:285:VAL:HG23	2.00	0.61
2:B:520:ILE:HD12	4:E:60:MET:H	1.65	0.61
3:D:348:VAL:HG21	3:D:354:PHE:HD1	1.65	0.61
3:D:147:GLY:HA2	3:D:150:ILE:HD12	1.81	0.61
2:B:337:HIS:N	2:B:338:PRO:HD2	2.15	0.61
3:D:215:LYS:HB3	3:D:405:GLU:OE2	2.01	0.61
5:G:74:HIS:N	8:Z:5:LYS:HB2	2.16	0.61
6:H:166:LYS:HD2	6:H:388:SER:OG	2.00	0.61
1:A:2:GLU:OE1	3:D:44:ALA:HB2	2.00	0.61
4:E:385:ILE:HG21	4:E:402:LEU:HD21	1.82	0.61
6:H:136:ILE:HD11	6:H:503:LEU:HD12	1.81	0.61
7:Q:40:ALA:HB1	7:Q:106:VAL:HA	1.82	0.61
7:Q:33:ILE:O	7:Q:37:LYS:HG3	2.00	0.61
6:H:366:LYS:HD3	6:H:368:LYS:HZ1	1.65	0.61
6:H:175:PHE:HB3	6:H:389:LEU:HD21	1.82	0.61
3:D:112:VAL:HG13	3:D:113:VAL:H	1.65	0.61
4:E:534:ARG:HH21	6:H:35:ALA:HB2	1.66	0.61
2:B:281:ARG:HH11	2:B:281:ARG:HG2	1.65	0.61
3:D:434:GLU:HG3	3:D:492:LYS:HD2	1.81	0.61
1:A:216:LEU:HB3	1:A:362:ILE:HB	1.82	0.61
6:H:201:GLN:OE1	6:H:379:GLU:HG2	2.00	0.61
4:E:94:LEU:HD21	4:E:523:MET:CB	2.24	0.61
3:D:348:VAL:HG11	3:D:354:PHE:N	2.16	0.61
3:D:80:ILE:O	3:D:84:MET:HG2	2.01	0.61
3:D:55:LEU:HD22	3:D:114:ILE:HD12	1.83	0.61
2:B:520:ILE:CD1	4:E:60:MET:H	2.14	0.61
5:G:229:MET:SD	5:G:310:THR:HA	2.41	0.61
6:H:278:LEU:HG	6:H:303:PHE:CE1	2.35	0.61
6:H:515:SER:O	7:Q:52:MET:HB3	2.00	0.61
4:E:481:GLN:HE21	4:E:487:PRO:HA	1.65	0.61
5:G:48:LYS:HD2	8:Z:520:GLU:HG3	1.82	0.61
1:A:489:ASP:OD1	1:A:491:VAL:HB	2.00	0.61
8:Z:101:GLU:OE2	8:Z:104:LYS:HD3	2.00	0.60
2:B:158:ASP:HA	2:B:161:ASN:ND2	2.15	0.60
7:Q:29:VAL:O	7:Q:33:ILE:HD13	2.01	0.60
5:G:134:ILE:HD11	5:G:507:LYS:HE2	1.82	0.60
6:H:352:GLN:HG2	6:H:357:ARG:HG2	1.83	0.60
4:E:437:ALA:HB2	4:E:448:MET:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:432:GLU:HG2	3:D:464:ILE:HB	1.83	0.60
8:Z:426:LYS:HD2	8:Z:434:GLN:HG2	1.83	0.60
4:E:486:ASN:HB3	4:E:487:PRO:HD2	1.83	0.60
8:Z:238:GLU:HA	8:Z:298:ASP:HB2	1.82	0.60
1:A:222:SER:OG	1:A:301:VAL:HG22	2.00	0.60
1:A:28:ILE:HA	1:A:31:ILE:HD12	1.83	0.60
4:E:20:LYS:HZ3	6:H:32:ILE:HD13	1.66	0.60
7:Q:477:ASN:HB3	7:Q:491:ASP:CG	2.22	0.60
3:D:509:GLU:O	3:D:510:LEU:HB2	2.01	0.60
5:G:165:ILE:HD12	5:G:387:VAL:HG13	1.83	0.60
8:Z:34:LEU:HD12	8:Z:37:ASN:HD21	1.67	0.60
1:A:20:GLN:NE2	5:G:7:VAL:HG23	2.16	0.60
5:G:49:MET:O	8:Z:521:ILE:HG13	2.01	0.60
5:G:23:GLN:O	5:G:27:ILE:HD13	2.02	0.60
2:B:236:LYS:HZ3	2:B:288:ASN:HD21	1.47	0.60
5:G:134:ILE:CD1	5:G:507:LYS:HE2	2.30	0.60
3:D:235:LYS:NZ	3:D:242:THR:HA	2.17	0.60
1:A:458:GLN:HB3	1:A:463:LEU:CD1	2.31	0.60
3:D:146:LYS:O	3:D:150:ILE:HG13	2.01	0.60
4:E:85:HIS:ND1	4:E:87:ILE:HG22	2.16	0.60
4:E:88:ALA:O	4:E:92:VAL:HG23	2.02	0.60
7:Q:147:VAL:HG21	7:Q:407:ARG:HB3	1.84	0.60
6:H:352:GLN:CG	6:H:357:ARG:HG2	2.32	0.60
6:H:407:ALA:O	6:H:411:ALA:HB3	2.00	0.60
4:E:41:ALA:HA	4:E:44:VAL:HG12	1.84	0.60
8:Z:419:ALA:O	8:Z:423:VAL:HG23	2.02	0.60
1:A:175:ALA:HB1	1:A:195:ILE:HD12	1.83	0.60
5:G:452:ILE:HD11	5:G:457:ALA:HB3	1.84	0.60
3:D:24:LYS:NZ	3:D:539:VAL:HG11	2.16	0.60
7:Q:17:GLU:HB2	8:Z:68:GLN:CG	2.32	0.60
5:G:72:VAL:HG22	8:Z:6:THR:HG23	1.83	0.60
1:A:351:VAL:CG1	1:A:364:ILE:HG12	2.31	0.60
4:E:458:ILE:O	4:E:462:LEU:HG	2.01	0.60
6:H:392:ALA:O	6:H:396:VAL:HG23	2.01	0.60
8:Z:48:VAL:HA	8:Z:53:ASP:O	2.01	0.60
5:G:500:ALA:HA	5:G:503:LEU:HB3	1.83	0.60
1:A:24:ALA:O	1:A:28:ILE:HG12	2.01	0.60
1:A:401:ARG:HH21	1:A:506:PRO:HG2	1.65	0.60
4:E:98:GLN:HE21	4:E:102:ILE:CD1	2.13	0.60
8:Z:118:ILE:HG21	8:Z:432:ARG:HD2	1.83	0.60
5:G:51:LEU:O	8:Z:523:ARG:HG3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:190:LEU:HD23	6:H:397:ARG:CB	2.32	0.60
5:G:137:LEU:HB3	5:G:499:LEU:HD11	1.84	0.60
5:G:156:ILE:CG2	5:G:394:ALA:HB1	2.29	0.60
8:Z:354:THR:HG22	8:Z:359:LYS:HG3	1.82	0.60
4:E:210:LYS:HB3	4:E:383:VAL:O	2.01	0.60
8:Z:109:TYR:CE2	8:Z:435:LEU:HB3	2.36	0.60
5:G:50:LEU:O	5:G:51:LEU:HD12	2.02	0.60
2:B:229:PRO:HG2	2:B:232:ILE:HD11	1.84	0.60
1:A:180:LYS:NZ	1:A:403:LEU:HB3	2.17	0.60
6:H:347:VAL:HB	6:H:362:THR:HG23	1.83	0.60
7:Q:57:ILE:HA	7:Q:62:LYS:O	2.02	0.60
1:A:145:ARG:O	1:A:147:CYS:N	2.35	0.60
8:Z:153:ARG:O	8:Z:157:ARG:HG3	2.02	0.60
6:H:21:GLN:HE22	6:H:22:LEU:HD13	1.67	0.59
2:B:416:LEU:HD22	2:B:474:THR:CG2	2.32	0.59
6:H:6:VAL:HG21	7:Q:21:HIS:HB2	1.84	0.59
8:Z:411:ALA:HB2	8:Z:494:ILE:HG21	1.82	0.59
3:D:63:MET:SD	3:D:73:ILE:HD11	2.42	0.59
6:H:23:VAL:HG13	6:H:109:LYS:NZ	2.17	0.59
3:D:120:LEU:HD23	3:D:529:VAL:HG13	1.83	0.59
2:B:86:ASP:O	2:B:90:VAL:HG23	2.02	0.59
3:D:433:ILE:HG13	3:D:483:LEU:HD23	1.84	0.59
5:G:374:ILE:HG21	5:G:391:LEU:HD21	1.83	0.59
1:A:450:ASN:OD1	1:A:460:SER:HB2	2.02	0.59
1:A:12:SER:O	1:A:529:ASP:HA	2.02	0.59
2:B:327:THR:HG22	2:B:365:VAL:HG12	1.82	0.59
5:G:137:LEU:O	5:G:140:ILE:HD13	2.02	0.59
3:D:408:ILE:O	3:D:412:LEU:HG	2.03	0.59
6:H:37:ARG:HG3	6:H:99:LEU:HD22	1.84	0.59
4:E:234:PHE:CE1	4:E:372:LEU:HD13	2.34	0.59
6:H:495:PRO:HB2	6:H:498:VAL:HG23	1.83	0.59
5:G:275:ILE:HG21	5:G:299:LEU:HB2	1.85	0.59
4:E:28:LEU:O	4:E:532:ASP:HA	2.02	0.59
1:A:532:LYS:HG2	3:D:65:GLN:HB2	1.82	0.59
5:G:398:CYS:HA	5:G:401:VAL:HG12	1.85	0.59
5:G:26:ASN:ND2	5:G:519:ILE:HD12	2.14	0.59
3:D:256:LEU:HD11	3:D:303:ILE:HD12	1.83	0.59
7:Q:402:LEU:HA	7:Q:405:ASP:O	2.02	0.59
7:Q:416:GLU:OE1	7:Q:448:ILE:HG21	2.02	0.59
1:A:232:ALA:HB3	1:A:348:ALA:HB3	1.84	0.59
5:G:469:LYS:HD2	5:G:472:GLN:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:126:ARG:O	6:H:130:GLN:HG3	2.02	0.59
2:B:408:TYR:CE1	2:B:494:THR:HG22	2.38	0.59
6:H:415:GLU:HB2	6:H:468:HIS:NE2	2.18	0.59
1:A:243:LYS:HE2	1:A:271:THR:OG1	2.01	0.59
2:B:49:ASP:HB3	2:B:65:ASN:OD1	2.02	0.59
8:Z:108:LEU:O	8:Z:112:GLU:HG3	2.03	0.59
8:Z:181:LYS:CE	8:Z:370:ARG:HH12	2.15	0.59
6:H:108:VAL:HG21	6:H:121:ILE:HG21	1.85	0.59
4:E:308:ASP:HA	4:E:311:ASN:HD22	1.66	0.59
2:B:399:GLN:OE1	2:B:498:GLN:HG3	2.03	0.59
7:Q:238:LYS:HE2	7:Q:346:HIS:HE1	1.67	0.59
2:B:519:ASN:O	2:B:520:ILE:HD13	2.03	0.59
5:G:22:VAL:HG11	5:G:520:ASP:O	2.03	0.59
3:D:252:ILE:HG21	3:D:351:VAL:HG22	1.84	0.59
4:E:223:LYS:HD3	4:E:388:ARG:HH21	1.67	0.59
3:D:436:ALA:HA	3:D:458:ALA:HB1	1.84	0.59
1:A:115:THR:HG23	3:D:58:LYS:HE3	1.85	0.59
2:B:403:ASP:OD2	2:B:498:GLN:HG2	2.02	0.59
7:Q:356:GLY:O	7:Q:357:ASP:HB2	2.02	0.59
5:G:23:GLN:HE22	5:G:113:LEU:HB3	1.67	0.59
2:B:409:GLY:HA2	2:B:495:GLU:OE2	2.03	0.59
2:B:338:PRO:HA	2:B:342:LYS:HG3	1.85	0.59
4:E:214:LYS:HD3	4:E:215:VAL:H	1.67	0.59
4:E:322:VAL:HG21	4:E:372:LEU:HD22	1.84	0.59
6:H:153:LYS:HG2	6:H:157:LYS:NZ	2.17	0.59
5:G:226:HIS:HB3	5:G:229:MET:HG3	1.84	0.59
2:B:476:ALA:HB1	2:B:485:ILE:HD11	1.84	0.59
2:B:445:MET:O	2:B:449:ILE:HG12	2.03	0.59
5:G:359:TYR:N	5:G:359:TYR:CD1	2.71	0.59
2:B:446:LEU:O	2:B:450:ILE:HG13	2.02	0.59
8:Z:476:LEU:O	8:Z:488:VAL:HA	2.03	0.59
3:D:223:ASP:HB2	3:D:394:ARG:HD2	1.85	0.59
3:D:122:SER:HA	3:D:125:LYS:HE3	1.85	0.59
2:B:223:LYS:NZ	2:B:351:GLU:HB2	2.18	0.59
1:A:242:GLN:HA	1:A:293:ASP:HB2	1.84	0.59
7:Q:394:ASP:O	7:Q:398:THR:HG23	2.03	0.59
4:E:154:SER:HB3	4:E:416:ASN:ND2	2.18	0.59
3:D:178:VAL:CG2	3:D:403:GLU:HG2	2.32	0.59
6:H:37:ARG:HG2	6:H:448:GLN:HG2	1.84	0.59
3:D:33:PRO:HA	3:D:536:ASP:OD1	2.02	0.58
1:A:172:VAL:HG13	1:A:396:LEU:HD23	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:165:SER:HB3	6:H:480:ASN:HB3	1.85	0.58
3:D:343:ILE:HD11	3:D:379:ILE:HG21	1.85	0.58
4:E:221:ASP:CB	4:E:388:ARG:HD2	2.33	0.58
3:D:227:VAL:O	3:D:389:VAL:HA	2.04	0.58
4:E:387:ILE:HG22	4:E:395:ILE:HG23	1.85	0.58
3:D:230:LEU:HD23	3:D:339:ILE:HG12	1.85	0.58
4:E:86:GLN:OE1	4:E:86:GLN:N	2.36	0.58
8:Z:333:LEU:HD21	8:Z:343:CYS:SG	2.44	0.58
2:B:186:ALA:HA	2:B:189:ARG:NH1	2.17	0.58
8:Z:134:LEU:HA	8:Z:137:VAL:HG22	1.84	0.58
6:H:460:ILE:HG23	6:H:461:LEU:N	2.18	0.58
7:Q:37:LYS:O	7:Q:41:GLN:HG2	2.04	0.58
7:Q:47:TYR:HB2	7:Q:102:ASN:HD22	1.67	0.58
1:A:5:LEU:HD11	1:A:11:ARG:HB2	1.85	0.58
6:H:17:GLN:HB3	6:H:518:GLU:CG	2.30	0.58
6:H:278:LEU:HD21	6:H:299:ALA:HA	1.86	0.58
4:E:511:ILE:N	4:E:511:ILE:HD12	2.18	0.58
4:E:25:LYS:HZ3	4:E:536:PRO:HB3	1.68	0.58
2:B:418:ALA:HA	2:B:440:ALA:HB1	1.83	0.58
2:B:448:THR:HG23	2:B:458:SER:HB2	1.84	0.58
7:Q:523:GLN:HB3	8:Z:45:LYS:HZ1	1.68	0.58
5:G:237:ARG:HB3	5:G:343:VAL:HG11	1.84	0.58
6:H:521:LYS:CG	7:Q:57:ILE:HB	2.34	0.58
2:B:39:VAL:HA	2:B:50:LYS:NZ	2.19	0.58
6:H:233:HIS:O	6:H:235:PRO:HD3	2.03	0.58
7:Q:84:LYS:O	7:Q:88:MET:HG3	2.02	0.58
8:Z:142:GLU:C	8:Z:144:ASP:H	2.07	0.58
7:Q:143:LEU:HD21	7:Q:419:LEU:HD11	1.86	0.58
3:D:90:ALA:O	3:D:93:MET:HG3	2.04	0.58
4:E:535:LYS:HB2	6:H:50:VAL:HB	1.86	0.58
7:Q:411:GLY:O	7:Q:492:MET:HG3	2.03	0.58
6:H:497:MET:O	6:H:497:MET:HE2	2.03	0.58
1:A:115:THR:HG23	3:D:58:LYS:NZ	2.18	0.58
6:H:408:GLY:HA2	6:H:494:GLU:OE2	2.04	0.58
3:D:216:LYS:HE3	3:D:376:LEU:HD11	1.85	0.58
1:A:42:ASP:CG	5:G:518:ARG:HG2	2.24	0.58
1:A:530:LEU:HD11	3:D:63:MET:N	2.18	0.58
3:D:206:VAL:CG2	3:D:419:VAL:HG21	2.34	0.58
6:H:224:GLY:HA2	6:H:310:CYS:O	2.04	0.58
8:Z:322:GLU:O	8:Z:326:LEU:HG	2.03	0.58
2:B:155:PHE:CE2	2:B:157:GLN:HB3	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:186:ILE:CD1	8:Z:399:LYS:HA	2.34	0.58
6:H:186:LEU:HD12	6:H:186:LEU:N	2.19	0.58
8:Z:118:ILE:HD12	8:Z:118:ILE:N	2.18	0.58
8:Z:59:ASP:O	8:Z:63:LEU:HG	2.04	0.58
8:Z:406:CYS:CB	8:Z:498:TYR:HB2	2.34	0.58
1:A:467:LEU:O	1:A:471:HIS:HB2	2.03	0.58
8:Z:417:ALA:HB2	8:Z:470:HIS:NE2	2.18	0.58
2:B:499:VAL:O	2:B:503:VAL:HG23	2.04	0.58
8:Z:308:GLU:HB2	8:Z:310:ILE:HG12	1.86	0.58
4:E:144:ALA:O	4:E:148:LEU:HD12	2.03	0.58
3:D:346:LYS:HB2	3:D:358:MET:SD	2.44	0.58
3:D:32:LYS:HB3	3:D:33:PRO:HD2	1.86	0.58
4:E:25:LYS:HA	4:E:535:LYS:O	2.04	0.58
3:D:474:LEU:O	3:D:476:PRO:HD3	2.03	0.58
4:E:122:GLN:O	4:E:126:ARG:HG3	2.03	0.58
1:A:416:GLU:CD	1:A:416:GLU:H	2.06	0.58
3:D:364:LEU:HD21	3:D:366:GLU:OE1	2.04	0.58
7:Q:238:LYS:HZ3	7:Q:341:LEU:HD11	1.69	0.58
1:A:190:TYR:CD2	1:A:400:LYS:HB2	2.35	0.58
5:G:240:LEU:HB2	5:G:331:ILE:HA	1.84	0.58
4:E:166:ILE:O	4:E:170:LYS:HG3	2.04	0.58
4:E:438:ASP:HA	4:E:445:GLN:HE21	1.68	0.58
5:G:275:ILE:HG23	5:G:300:ALA:HB2	1.86	0.58
7:Q:460:ALA:HA	7:Q:463:VAL:HG12	1.86	0.58
3:D:486:ARG:O	3:D:494:THR:HG21	2.04	0.58
4:E:40:ALA:HB3	4:E:87:ILE:HG21	1.84	0.57
5:G:46:MET:HE2	8:Z:517:LEU:HD23	1.86	0.57
6:H:109:LYS:N	6:H:110:PRO:HD2	2.19	0.57
2:B:520:ILE:HG23	4:E:60:MET:O	2.04	0.57
8:Z:204:THR:HG22	8:Z:377:LYS:H	1.68	0.57
1:A:445:LEU:H	1:A:446:PRO:HD2	1.67	0.57
1:A:42:ASP:OD2	5:G:518:ARG:HG2	2.03	0.57
8:Z:186:ILE:HD12	8:Z:399:LYS:HA	1.86	0.57
6:H:455:PHE:HB2	6:H:482:GLU:OE2	2.04	0.57
3:D:81:LEU:HB3	3:D:95:VAL:HG22	1.84	0.57
8:Z:179:ILE:HD12	8:Z:187:ASP:O	2.04	0.57
1:A:533:LEU:HD23	1:A:533:LEU:N	2.19	0.57
1:A:46:VAL:HG22	1:A:52:VAL:HG22	1.85	0.57
1:A:277:LYS:HZ2	1:A:280:ALA:HB3	1.69	0.57
8:Z:101:GLU:HG2	8:Z:446:ILE:HB	1.86	0.57
2:B:516:ARG:O	4:E:57:LEU:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:ALA:HB3	2:B:349:ILE:HD12	1.86	0.57
6:H:37:ARG:HB2	6:H:99:LEU:HD13	1.87	0.57
8:Z:299:PRO:HA	8:Z:302:LEU:HD12	1.86	0.57
5:G:242:ASP:OD2	5:G:331:ILE:HG22	2.03	0.57
7:Q:53:ASN:O	7:Q:54:LYS:HD3	2.04	0.57
6:H:73:HIS:HD2	6:H:74:PRO:HD2	1.69	0.57
7:Q:186:ALA:O	7:Q:190:ILE:HG13	2.03	0.57
4:E:473:THR:O	4:E:477:VAL:HG23	2.05	0.57
5:G:38:ARG:HA	5:G:100:ILE:HD11	1.86	0.57
1:A:45:LEU:HD11	1:A:61:ILE:HA	1.86	0.57
5:G:479:GLY:C	5:G:487:LEU:HD12	2.24	0.57
2:B:516:ARG:HD2	4:E:58:ASP:OD2	2.04	0.57
7:Q:150:SER:HB2	7:Q:159:GLU:OE1	2.05	0.57
5:G:425:LYS:O	5:G:429:MET:HG2	2.03	0.57
1:A:526:ARG:O	3:D:60:MET:HB3	2.04	0.57
6:H:510:ALA:O	6:H:514:VAL:HG23	2.03	0.57
3:D:45:LYS:HD2	3:D:121:ASP:HB2	1.87	0.57
8:Z:446:ILE:O	8:Z:450:VAL:HG23	2.05	0.57
1:A:532:LYS:NZ	3:D:65:GLN:HB2	2.19	0.57
4:E:85:HIS:CG	4:E:87:ILE:HG22	2.39	0.57
1:A:176:VAL:HG13	1:A:190:TYR:CD1	2.39	0.57
6:H:226:GLU:HB3	6:H:227:MET:CE	2.34	0.57
3:D:256:LEU:HD13	3:D:312:LEU:CD1	2.33	0.57
6:H:522:ASN:HD21	7:Q:76:LEU:HA	1.69	0.57
4:E:218:ARG:CA	4:E:389:GLY:HA2	2.33	0.57
4:E:242:GLN:O	4:E:242:GLN:HG2	2.03	0.57
8:Z:407:VAL:O	8:Z:407:VAL:HG13	2.05	0.57
4:E:20:LYS:HZ2	6:H:31:VAL:CB	2.17	0.57
3:D:256:LEU:H	3:D:256:LEU:HD12	1.68	0.57
2:B:113:ALA:O	2:B:117:ILE:HG13	2.05	0.57
4:E:443:LEU:HD23	4:E:444:GLU:N	2.20	0.57
5:G:195:ILE:HG22	5:G:197:LYS:H	1.69	0.57
7:Q:420:ALA:HA	7:Q:442:ALA:HB1	1.87	0.57
7:Q:332:ALA:O	7:Q:334:PRO:HD3	2.04	0.57
5:G:108:VAL:O	5:G:111:HIS:HB3	2.04	0.57
1:A:140:THR:HB	1:A:144:GLY:CA	2.25	0.57
5:G:47:MET:HB3	5:G:61:ASN:ND2	2.20	0.57
1:A:220:VAL:HG22	1:A:306:MET:SD	2.44	0.57
7:Q:173:TYR:HD1	7:Q:173:TYR:H	1.50	0.57
4:E:20:LYS:NZ	6:H:32:ILE:HG12	2.20	0.57
2:B:172:LEU:HD21	2:B:386:ALA:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:50:LEU:HA	8:Z:521:ILE:O	2.03	0.57
4:E:457:VAL:HG23	4:E:458:ILE:N	2.20	0.57
5:G:240:LEU:HD23	5:G:240:LEU:N	2.18	0.57
6:H:450:CYS:HA	6:H:479:ILE:HD13	1.86	0.57
4:E:225:ILE:HG23	4:E:375:GLU:HB3	1.87	0.57
1:A:530:LEU:CD2	3:D:63:MET:H	2.17	0.57
1:A:137:ILE:HG23	1:A:499:LYS:HE3	1.87	0.57
2:B:349:ILE:HA	2:B:361:HIS:O	2.05	0.57
6:H:320:LYS:O	6:H:323:MET:HB3	2.05	0.57
3:D:217:LEU:HA	3:D:401:ILE:CD1	2.34	0.57
6:H:407:ALA:HB1	6:H:487:ASN:ND2	2.20	0.57
3:D:54:SER:HA	3:D:60:MET:H	1.69	0.57
8:Z:87:ILE:N	8:Z:87:ILE:HD12	2.20	0.57
2:B:123:PRO:HB3	2:B:515:LEU:HG	1.85	0.57
3:D:33:PRO:HD3	3:D:537:ASP:OD1	2.03	0.57
8:Z:229:TYR:HB3	8:Z:344:LEU:HB3	1.87	0.57
8:Z:354:THR:CG2	8:Z:359:LYS:HG3	2.35	0.57
2:B:297:TYR:HB3	2:B:300:PRO:HD2	1.87	0.57
7:Q:405:ASP:HB2	7:Q:502:LEU:HD22	1.87	0.57
3:D:371:ASN:HD22	3:D:394:ARG:HE	1.52	0.57
8:Z:378:GLY:HA3	8:Z:384:LEU:HD21	1.85	0.56
3:D:245:GLU:HG3	3:D:246:LYS:CD	2.31	0.56
5:G:91:VAL:HG11	5:G:501:VAL:HA	1.86	0.56
6:H:225:PHE:HB3	6:H:228:GLN:HG3	1.85	0.56
7:Q:377:LEU:O	7:Q:378:ARG:HD2	2.04	0.56
2:B:220:LEU:HD13	2:B:319:GLY:HA3	1.87	0.56
4:E:186:ALA:O	4:E:190:VAL:HG23	2.05	0.56
7:Q:20:LYS:HD3	7:Q:528:LYS:H	1.70	0.56
5:G:401:VAL:HG13	5:G:402:LEU:HD13	1.87	0.56
4:E:156:LEU:CB	4:E:161:ASN:HB3	2.34	0.56
7:Q:55:MET:CG	7:Q:63:LEU:HD11	2.35	0.56
2:B:100:THR:O	2:B:104:VAL:HG23	2.05	0.56
3:D:539:VAL:HG12	3:D:541:THR:H	1.70	0.56
8:Z:46:MET:HG3	8:Z:54:ILE:HG23	1.86	0.56
5:G:479:GLY:O	5:G:487:LEU:HD12	2.05	0.56
2:B:518:ASP:O	2:B:519:ASN:HB2	2.06	0.56
3:D:317:LEU:HG	3:D:321:ASN:HD21	1.71	0.56
7:Q:205:CYS:HG	7:Q:376:VAL:HA	1.70	0.56
6:H:239:LEU:O	6:H:240:LEU:HD23	2.05	0.56
6:H:521:LYS:HG2	7:Q:57:ILE:O	2.05	0.56
5:G:433:GLU:CD	5:G:433:GLU:H	2.08	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:LYS:HE2	1:A:317:LYS:CE	2.35	0.56
3:D:487:HIS:CE1	3:D:492:LYS:HA	2.40	0.56
5:G:165:ILE:HG21	5:G:390:ASN:CB	2.35	0.56
8:Z:139:VAL:HB	8:Z:407:VAL:O	2.04	0.56
4:E:250:ILE:HG21	4:E:341:ILE:HG12	1.87	0.56
2:B:111:ARG:NH1	2:B:111:ARG:HG2	2.19	0.56
5:G:491:LYS:HA	5:G:496:TRP:NE1	2.18	0.56
1:A:24:ALA:HA	5:G:9:VAL:HG22	1.88	0.56
4:E:208:LEU:O	4:E:383:VAL:HG22	2.04	0.56
4:E:472:GLN:O	4:E:475:THR:HB	2.06	0.56
2:B:411:GLY:HA3	2:B:447:PRO:HB3	1.87	0.56
3:D:29:ASP:HB2	3:D:540:ASN:CG	2.25	0.56
7:Q:523:GLN:HB3	8:Z:45:LYS:CE	2.36	0.56
2:B:11:ILE:O	4:E:84:ASP:N	2.33	0.56
5:G:74:HIS:HB2	8:Z:5:LYS:CB	2.31	0.56
7:Q:392:VAL:O	7:Q:396:VAL:HG23	2.05	0.56
4:E:156:LEU:HG	4:E:156:LEU:O	2.06	0.56
3:D:236:VAL:HG11	3:D:329:LYS:HD3	1.86	0.56
3:D:175:ASN:HA	3:D:180:SER:CB	2.36	0.56
3:D:292:GLN:HA	3:D:295:LYS:HE2	1.87	0.56
3:D:424:LEU:HD12	3:D:424:LEU:O	2.05	0.56
8:Z:31:GLN:HG2	8:Z:97:LEU:HA	1.87	0.56
2:B:53:LEU:HB3	3:D:542:ARG:NH1	2.21	0.56
4:E:117:LEU:CD2	4:E:524:VAL:HG13	2.36	0.56
4:E:117:LEU:HD21	4:E:524:VAL:HG13	1.88	0.56
1:A:410:PRO:O	1:A:414:ALA:HB3	2.05	0.56
4:E:156:LEU:HB3	4:E:161:ASN:CB	2.32	0.56
8:Z:407:VAL:CG2	8:Z:495:TRP:HB3	2.36	0.56
6:H:142:THR:HG22	6:H:404:SER:OG	2.05	0.56
3:D:24:LYS:CD	3:D:28:GLN:HE22	2.17	0.56
5:G:137:LEU:HD11	5:G:506:TYR:CD2	2.40	0.56
5:G:289:VAL:HG11	5:G:350:LEU:HD13	1.88	0.56
4:E:98:GLN:HE22	4:E:515:GLN:HG2	1.71	0.56
3:D:249:ILE:HG13	3:D:343:ILE:HD13	1.87	0.56
8:Z:127:LYS:NZ	8:Z:509:THR:HB	2.21	0.56
5:G:20:ARG:O	5:G:20:ARG:HG2	2.05	0.56
6:H:215:ALA:HB3	6:H:373:ILE:CD1	2.32	0.56
3:D:416:ARG:HH11	3:D:420:LYS:HZ1	1.53	0.56
4:E:247:LYS:HE3	4:E:298:ASN:ND2	2.20	0.56
1:A:107:LEU:O	1:A:112:ILE:HB	2.05	0.56
5:G:347:ALA:HB3	5:G:365:GLU:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:476:LEU:HD22	8:Z:490:ALA:CB	2.36	0.56
5:G:52:ASP:HB3	8:Z:525:GLY:O	2.06	0.56
3:D:151:LEU:HD21	3:D:435:LEU:HD11	1.87	0.56
2:B:52:LEU:HD11	2:B:70:ILE:HA	1.88	0.56
6:H:281:ILE:HG21	6:H:289:VAL:HG21	1.88	0.56
7:Q:410:PRO:HB2	7:Q:492:MET:HB2	1.87	0.56
2:B:29:PHE:HB3	2:B:110:LEU:HB3	1.88	0.56
1:A:456:ALA:HB3	1:A:490:LEU:HD22	1.88	0.56
4:E:34:LEU:H	4:E:34:LEU:HD22	1.71	0.56
8:Z:333:LEU:HB2	8:Z:339:LEU:HD23	1.88	0.56
8:Z:501:LYS:O	8:Z:504:LEU:HB3	2.06	0.56
4:E:18:ILE:HG22	4:E:19:ILE:H	1.70	0.56
8:Z:109:TYR:HB3	8:Z:114:LEU:HD13	1.86	0.55
5:G:72:VAL:HG12	5:G:73:GLN:N	2.21	0.55
2:B:221:ASP:CG	2:B:359:LEU:HG	2.26	0.55
5:G:358:GLU:HB3	5:G:360:PHE:CE1	2.41	0.55
4:E:204:VAL:CB	4:E:410:ARG:HG3	2.32	0.55
5:G:445:GLU:O	5:G:449:ARG:HG3	2.05	0.55
5:G:89:GLU:HA	5:G:389:ARG:HH22	1.69	0.55
6:H:150:GLU:OE2	6:H:400:ILE:HG23	2.06	0.55
3:D:37:ARG:HG3	3:D:536:ASP:OD1	2.06	0.55
5:G:49:MET:HB2	5:G:59:MET:CE	2.36	0.55
6:H:161:THR:HG21	6:H:491:PHE:CB	2.37	0.55
1:A:133:SER:HA	1:A:136:LEU:HD21	1.88	0.55
5:G:105:MET:CE	5:G:510:VAL:HA	2.36	0.55
2:B:116:LEU:HA	2:B:119:LYS:HD2	1.88	0.55
4:E:451:PHE:O	4:E:455:LEU:HG	2.07	0.55
7:Q:17:GLU:HG2	8:Z:70:GLN:NE2	2.20	0.55
5:G:37:ILE:HD11	5:G:99:ILE:HG21	1.87	0.55
2:B:229:PRO:CG	2:B:232:ILE:HD11	2.35	0.55
6:H:350:GLU:HA	6:H:358:TYR:O	2.06	0.55
6:H:198:LYS:HZ3	6:H:217:LYS:CE	2.19	0.55
7:Q:143:LEU:N	7:Q:144:PRO:HD2	2.22	0.55
8:Z:83:ALA:O	8:Z:87:ILE:HD13	2.05	0.55
1:A:352:VAL:HG22	1:A:353:GLN:N	2.20	0.55
7:Q:117:GLU:O	7:Q:121:LEU:HG	2.07	0.55
3:D:226:LEU:CD1	3:D:389:VAL:HB	2.36	0.55
6:H:448:GLN:HG3	6:H:452:ASN:ND2	2.21	0.55
8:Z:135:GLU:HG3	8:Z:138:LYS:NZ	2.21	0.55
8:Z:150:ASP:O	8:Z:154:THR:HG23	2.06	0.55
5:G:168:TRP:CD1	5:G:209:ILE:HB	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:139:VAL:HB	8:Z:407:VAL:HG13	1.87	0.55
8:Z:127:LYS:HD2	8:Z:509:THR:HG21	1.88	0.55
5:G:330:ARG:HD2	5:G:342:ASP:OD1	2.06	0.55
8:Z:376:ILE:HG22	8:Z:384:LEU:HD22	1.89	0.55
3:D:137:SER:OG	3:D:533:LEU:HB2	2.06	0.55
6:H:349:GLU:HG3	6:H:360:PHE:HD2	1.70	0.55
7:Q:206:LYS:HD3	7:Q:389:GLU:OE1	2.07	0.55
7:Q:69:ALA:HB3	7:Q:101:THR:HG22	1.89	0.55
1:A:74:VAL:O	1:A:78:LEU:HG	2.06	0.55
8:Z:98:ILE:HD11	8:Z:447:ILE:HD11	1.88	0.55
1:A:17:ILE:O	1:A:20:GLN:HG2	2.07	0.55
5:G:48:LYS:HA	8:Z:518:VAL:HG13	1.89	0.55
5:G:417:ALA:HB2	5:G:476:GLU:HG3	1.88	0.55
2:B:513:VAL:HG13	2:B:516:ARG:NH1	2.20	0.55
4:E:229:ILE:HB	4:E:384:THR:HG21	1.89	0.55
2:B:390:LEU:O	2:B:394:LEU:HG	2.06	0.55
7:Q:58:ASN:ND2	7:Q:62:LYS:HB2	2.19	0.55
8:Z:459:LEU:HD23	8:Z:460:GLN:N	2.22	0.55
6:H:79:LEU:HA	6:H:82:ILE:HD12	1.89	0.55
7:Q:188:VAL:HG13	7:Q:197:PHE:CE1	2.41	0.55
1:A:521:ALA:HA	1:A:524:ILE:HD12	1.89	0.55
7:Q:13:GLN:OE1	8:Z:72:PRO:HD2	2.06	0.55
1:A:17:ILE:HG13	1:A:21:ASN:HD21	1.71	0.55
4:E:83:VAL:HG13	4:E:88:ALA:HB3	1.88	0.55
6:H:341:VAL:O	6:H:341:VAL:HG12	2.07	0.55
8:Z:273:LYS:HD3	8:Z:337:ASP:OD1	2.07	0.55
4:E:145:ILE:CD1	4:E:514:LYS:HA	2.36	0.55
5:G:224:VAL:HG21	5:G:352:ILE:HG21	1.88	0.55
4:E:444:GLU:O	4:E:448:MET:HG3	2.07	0.55
2:B:292:ASN:HD22	2:B:293:ARG:N	2.05	0.55
1:A:226:PRO:CG	1:A:229:ILE:HD11	2.37	0.55
5:G:118:HIS:CD2	5:G:119:PRO:HD2	2.42	0.55
7:Q:312:LEU:HD23	7:Q:313:VAL:N	2.22	0.55
1:A:529:ASP:O	3:D:62:LYS:HD2	2.07	0.55
3:D:207:ASP:O	3:D:210:ASP:HB2	2.07	0.55
5:G:72:VAL:CG2	5:G:81:ILE:HD11	2.37	0.55
1:A:43:LYS:HE3	5:G:520:ASP:OD2	2.07	0.55
3:D:178:VAL:HG12	3:D:178:VAL:O	2.07	0.55
7:Q:475:ASN:O	7:Q:477:ASN:N	2.40	0.55
7:Q:242:TYR:OH	7:Q:283:ILE:HG12	2.07	0.55
2:B:322:ARG:O	2:B:326:VAL:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:355:LEU:HD22	8:Z:377:LYS:HE3	1.87	0.55
1:A:323:SER:HB2	1:A:347:GLN:N	2.22	0.55
3:D:294:LYS:HD3	3:D:325:ILE:HD11	1.87	0.55
5:G:200:ARG:NE	5:G:322:ARG:NH1	2.55	0.55
3:D:124:THR:HA	3:D:127:LEU:HD12	1.89	0.55
4:E:387:ILE:CG2	4:E:395:ILE:HG23	2.37	0.55
5:G:359:TYR:N	5:G:359:TYR:HD1	2.02	0.55
2:B:497:PHE:CZ	2:B:501:ARG:HD3	2.41	0.55
1:A:456:ALA:CB	1:A:490:LEU:HD22	2.38	0.55
1:A:96:ILE:O	1:A:100:LEU:HG	2.07	0.55
7:Q:15:LEU:HA	8:Z:71:HIS:ND1	2.22	0.54
3:D:197:VAL:HG12	3:D:387:LYS:CA	2.33	0.54
3:D:211:ILE:HG23	3:D:389:VAL:CG2	2.28	0.54
6:H:163:LEU:HD22	6:H:168:ILE:HG21	1.90	0.54
7:Q:164:LEU:O	7:Q:168:VAL:HG13	2.07	0.54
5:G:203:LYS:HB2	5:G:384:LEU:HD11	1.89	0.54
3:D:239:SER:HB2	3:D:321:ASN:CB	2.32	0.54
3:D:21:GLY:O	3:D:22:ARG:HG2	2.08	0.54
4:E:215:VAL:HB	4:E:392:LYS:NZ	2.22	0.54
7:Q:118:LEU:HD21	7:Q:440:LYS:HG3	1.89	0.54
1:A:80:ASP:O	1:A:84:LYS:HD3	2.06	0.54
7:Q:114:LEU:HD11	7:Q:443:GLU:OE2	2.07	0.54
4:E:130:PRO:HB3	4:E:528:LEU:HD22	1.88	0.54
6:H:190:LEU:HD11	6:H:195:ILE:CD1	2.31	0.54
5:G:136:THR:O	5:G:140:ILE:HG23	2.06	0.54
2:B:474:THR:O	2:B:474:THR:HG22	2.07	0.54
7:Q:390:ARG:HA	7:Q:390:ARG:CZ	2.37	0.54
4:E:170:LYS:HZ2	4:E:183:ARG:HA	1.70	0.54
3:D:251:LEU:HD23	3:D:345:THR:OG1	2.07	0.54
6:H:487:ASN:HA	6:H:490:ALA:HB3	1.89	0.54
4:E:290:ARG:O	4:E:294:GLU:HG3	2.07	0.54
1:A:201:HIS:HA	1:A:379:GLY:O	2.08	0.54
6:H:156:GLU:HA	6:H:180:VAL:HG21	1.89	0.54
8:Z:37:ASN:HA	8:Z:43:THR:H	1.73	0.54
7:Q:203:ARG:HH11	7:Q:221:MET:HG2	1.73	0.54
5:G:407:LEU:O	5:G:407:LEU:HD12	2.08	0.54
7:Q:160:VAL:O	7:Q:164:LEU:HG	2.07	0.54
3:D:170:ALA:HB2	3:D:415:ILE:HD11	1.89	0.54
8:Z:350:VAL:HA	8:Z:362:PHE:O	2.07	0.54
1:A:132:ILE:O	1:A:136:LEU:HG	2.07	0.54
2:B:172:LEU:O	2:B:176:LYS:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:338:PRO:N	7:Q:339:PRO:CD	2.70	0.54
3:D:230:LEU:HD13	3:D:338:PHE:HB3	1.89	0.54
7:Q:191:PHE:H	7:Q:192:PRO:CD	2.20	0.54
8:Z:422:LEU:HB3	8:Z:437:VAL:HG12	1.90	0.54
2:B:167:LEU:HD13	2:B:179:PHE:HB2	1.90	0.54
4:E:254:PRO:HB3	4:E:304:TRP:HB3	1.89	0.54
2:B:204:LYS:O	2:B:376:ARG:HA	2.07	0.54
1:A:105:ASP:HA	1:A:108:VAL:HB	1.90	0.54
2:B:236:LYS:HD2	2:B:286:GLY:O	2.07	0.54
6:H:226:GLU:O	6:H:227:MET:CB	2.55	0.54
3:D:443:SER:HB3	3:D:451:SER:HA	1.89	0.54
7:Q:378:ARG:HH11	7:Q:378:ARG:HG3	1.71	0.54
2:B:131:ARG:O	2:B:135:LYS:HG3	2.06	0.54
2:B:192:GLY:O	2:B:193:SER:HB2	2.07	0.54
2:B:420:ALA:O	2:B:424:LEU:HG	2.08	0.54
7:Q:129:ILE:HG22	7:Q:133:GLU:HG3	1.89	0.54
7:Q:477:ASN:HB3	7:Q:491:ASP:OD1	2.07	0.54
2:B:408:TYR:CE2	2:B:489:SER:HB3	2.43	0.54
6:H:488:PHE:HA	6:H:493:TRP:CZ2	2.43	0.54
2:B:203:LYS:O	2:B:203:LYS:HG3	2.07	0.54
1:A:105:ASP:O	1:A:109:LYS:HG3	2.08	0.54
2:B:9:VAL:HA	4:E:85:HIS:NE2	2.22	0.54
4:E:524:VAL:HA	4:E:527:ILE:CD1	2.38	0.54
6:H:521:LYS:HG2	7:Q:57:ILE:HB	1.89	0.54
5:G:209:ILE:HG22	5:G:209:ILE:O	2.07	0.54
8:Z:445:LEU:O	8:Z:449:LYS:HG3	2.08	0.54
7:Q:80:HIS:HB3	7:Q:83:ALA:CB	2.38	0.54
2:B:219:LEU:HD21	2:B:359:LEU:HD23	1.90	0.54
5:G:350:LEU:HG	5:G:363:ILE:HG12	1.90	0.54
6:H:227:MET:HA	6:H:230:LYS:HZ2	1.68	0.54
5:G:424:GLU:O	5:G:427:LYS:HG2	2.07	0.54
4:E:392:LYS:O	4:E:396:GLU:HG3	2.07	0.54
1:A:275:ILE:HD11	1:A:296:CYS:HB3	1.90	0.54
7:Q:225:LYS:HD2	7:Q:352:LEU:HD13	1.89	0.54
5:G:144:VAL:HG21	5:G:407:LEU:CD2	2.37	0.54
1:A:59:ALA:O	1:A:63:LYS:HG3	2.08	0.54
3:D:72:THR:HG21	3:D:83:GLN:NE2	2.23	0.54
4:E:236:HIS:CG	4:E:237:PRO:HD2	2.43	0.54
8:Z:414:VAL:O	8:Z:418:MET:HG3	2.08	0.54
7:Q:206:LYS:HB3	7:Q:385:MET:CG	2.36	0.54
7:Q:55:MET:HG2	7:Q:65:VAL:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:141:LEU:HD21	2:B:413:SER:OG	2.08	0.54
3:D:467:THR:O	3:D:470:GLU:HB3	2.07	0.54
5:G:18:SER:H	5:G:21:LYS:HB2	1.73	0.54
5:G:85:ARG:HA	5:G:85:ARG:NE	2.23	0.54
8:Z:109:TYR:HB3	8:Z:114:LEU:CD1	2.38	0.54
3:D:29:ASP:HB2	3:D:540:ASN:HB2	1.89	0.54
7:Q:523:GLN:HG2	8:Z:33:VAL:HG13	1.90	0.54
7:Q:104:VAL:HG13	7:Q:105:LEU:N	2.23	0.54
7:Q:327:THR:HG22	7:Q:366:GLU:CD	2.28	0.54
5:G:286:LYS:HD2	5:G:340:GLU:OE2	2.08	0.54
7:Q:146:LEU:HD12	7:Q:147:VAL:N	2.23	0.54
4:E:25:LYS:HE2	4:E:536:PRO:HB3	1.89	0.54
6:H:9:LEU:HD22	6:H:13:THR:HG21	1.90	0.54
6:H:406:VAL:HB	6:H:412:ILE:CD1	2.38	0.54
4:E:121:GLU:HA	4:E:124:LEU:HD12	1.90	0.54
5:G:52:ASP:HB3	8:Z:525:GLY:C	2.28	0.54
8:Z:133:PHE:HA	8:Z:136:GLN:OE1	2.07	0.54
2:B:52:LEU:C	2:B:53:LEU:HD12	2.28	0.53
5:G:70:ILE:HG21	8:Z:6:THR:HG22	1.90	0.53
2:B:202:ILE:HG12	2:B:372:THR:CG2	2.38	0.53
5:G:156:ILE:HG12	5:G:398:CYS:HB2	1.91	0.53
6:H:274:LEU:HD22	6:H:299:ALA:HB2	1.89	0.53
4:E:149:ASP:OD2	4:E:510:LEU:HD21	2.07	0.53
6:H:294:PRO:HG3	6:H:313:ARG:HD3	1.88	0.53
2:B:97:ASP:C	2:B:99:THR:H	2.10	0.53
2:B:43:LEU:HD23	2:B:449:ILE:HB	1.89	0.53
5:G:112:PHE:CE2	5:G:436:PRO:HA	2.42	0.53
4:E:44:VAL:HG11	4:E:91:MET:HG3	1.90	0.53
7:Q:191:PHE:HE2	7:Q:373:SER:HG	1.56	0.53
7:Q:436:TYR:O	7:Q:440:LYS:HG2	2.08	0.53
8:Z:222:LYS:HB2	8:Z:311:ILE:CD1	2.38	0.53
1:A:86:VAL:HG11	1:A:509:VAL:HA	1.91	0.53
3:D:312:LEU:HB3	3:D:329:LYS:HD2	1.90	0.53
1:A:150:ASN:O	1:A:154:THR:HG23	2.09	0.53
2:B:508:ALA:O	2:B:512:GLU:HG3	2.08	0.53
1:A:383:PHE:HA	1:A:386:ASP:OD2	2.07	0.53
3:D:36:ILE:CG2	3:D:536:ASP:HA	2.38	0.53
7:Q:238:LYS:HB3	7:Q:344:MET:HB3	1.90	0.53
4:E:318:ASP:C	4:E:319:LEU:HD12	2.29	0.53
4:E:119:GLU:HG3	4:E:454:ALA:HB2	1.89	0.53
5:G:83:ILE:HG23	5:G:508:THR:CG2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:294:GLN:HE22	8:Z:318:ARG:HD3	1.71	0.53
1:A:526:ARG:HG3	3:D:60:MET:HA	1.91	0.53
4:E:289:ILE:HD11	4:E:310:ALA:HB1	1.91	0.53
2:B:70:ILE:O	2:B:74:ILE:HG13	2.08	0.53
7:Q:222:VAL:CG1	7:Q:360:VAL:HB	2.39	0.53
5:G:50:LEU:HD23	8:Z:521:ILE:O	2.07	0.53
1:A:112:ILE:HA	1:A:433:ARG:NH2	2.23	0.53
5:G:225:THR:HB	5:G:311:ALA:O	2.07	0.53
1:A:60:THR:O	1:A:64:LEU:HG	2.08	0.53
5:G:164:VAL:HB	5:G:386:GLU:HG2	1.90	0.53
3:D:224:CYS:SG	3:D:393:VAL:HA	2.49	0.53
8:Z:450:VAL:HG12	8:Z:454:ASN:ND2	2.24	0.53
8:Z:179:ILE:HD13	8:Z:191:VAL:CG2	2.38	0.53
5:G:49:MET:HG2	5:G:49:MET:O	2.09	0.53
6:H:111:TYR:HB3	6:H:116:LEU:HD22	1.90	0.53
8:Z:350:VAL:HG13	8:Z:363:ILE:HG12	1.90	0.53
6:H:238:ALA:N	6:H:288:VAL:O	2.41	0.53
3:D:256:LEU:HD13	3:D:312:LEU:HD13	1.90	0.53
4:E:42:LYS:HG2	4:E:46:ASN:HD21	1.72	0.53
5:G:12:GLN:O	5:G:13:ASN:HB2	2.09	0.53
5:G:217:GLY:HA3	5:G:364:THR:HA	1.91	0.53
4:E:256:GLU:HB2	4:E:257:PRO:HD2	1.89	0.53
7:Q:225:LYS:HZ2	7:Q:352:LEU:HB2	1.70	0.53
3:D:515:LEU:O	3:D:519:VAL:HG23	2.09	0.53
6:H:153:LYS:O	6:H:157:LYS:HG3	2.08	0.53
6:H:9:LEU:HD13	6:H:13:THR:CG2	2.38	0.53
3:D:433:ILE:HG13	3:D:483:LEU:CD2	2.39	0.53
2:B:43:LEU:HD12	2:B:44:GLY:N	2.22	0.53
7:Q:204:VAL:HG13	7:Q:377:LEU:HG	1.89	0.53
2:B:399:GLN:O	2:B:403:ASP:HB3	2.08	0.53
1:A:45:LEU:HD13	1:A:64:LEU:HB2	1.90	0.53
2:B:432:GLU:O	2:B:436:MET:HG3	2.07	0.53
1:A:211:ILE:HG12	1:A:376:ILE:CG1	2.38	0.53
8:Z:44:MET:HB3	8:Z:58:LYS:HG2	1.91	0.53
7:Q:347:CYS:SG	7:Q:363:PHE:HB3	2.48	0.53
1:A:17:ILE:HG23	1:A:18:ARG:N	2.21	0.53
6:H:23:VAL:CG1	6:H:109:LYS:HZ1	2.18	0.53
1:A:137:ILE:CD1	1:A:410:PRO:HD3	2.35	0.53
6:H:394:MET:O	6:H:397:ARG:HB3	2.08	0.53
1:A:59:ALA:HB1	1:A:63:LYS:HE3	1.91	0.53
6:H:225:PHE:CB	6:H:228:GLN:HG3	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:PHE:HD2	1:A:330:THR:HA	1.74	0.53
5:G:396:GLN:NE2	5:G:399:ARG:HB3	2.24	0.53
2:B:72:LYS:HZ1	2:B:89:ARG:HG3	1.74	0.53
5:G:247:TYR:HB2	5:G:275:ILE:HD11	1.91	0.53
6:H:418:LYS:HZ2	6:H:469:ALA:HA	1.74	0.53
2:B:224:ILE:O	2:B:224:ILE:HG13	2.09	0.53
8:Z:175:SER:O	8:Z:179:ILE:HG12	2.09	0.53
1:A:351:VAL:CG2	1:A:364:ILE:HG23	2.37	0.53
5:G:282:ILE:HG22	5:G:287:PRO:HG3	1.90	0.53
6:H:48:LEU:CG	6:H:58:ILE:HG12	2.37	0.53
1:A:115:THR:HG23	3:D:58:LYS:CE	2.39	0.53
7:Q:226:GLU:HG3	7:Q:314:ARG:CG	2.39	0.53
3:D:420:LYS:HB2	3:D:516:LEU:HD12	1.90	0.53
3:D:82:LYS:CE	3:D:99:LYS:HZ3	2.22	0.53
3:D:24:LYS:HZ2	3:D:539:VAL:HG11	1.73	0.53
4:E:94:LEU:HD11	4:E:523:MET:CB	2.39	0.53
7:Q:15:LEU:HA	8:Z:71:HIS:CE1	2.44	0.53
7:Q:113:GLU:HA	7:Q:116:GLU:OE2	2.09	0.53
5:G:71:GLN:HB3	8:Z:8:ASN:HB2	1.91	0.53
5:G:107:SER:HA	5:G:110:GLU:OE2	2.08	0.53
4:E:405:ALA:O	4:E:409:ILE:HG13	2.08	0.53
5:G:442:GLN:HA	5:G:445:GLU:OE2	2.09	0.53
2:B:190:LEU:HD12	2:B:190:LEU:N	2.24	0.53
6:H:520:ILE:O	7:Q:56:VAL:HA	2.09	0.53
8:Z:161:HIS:CE1	8:Z:164:LEU:HB3	2.44	0.52
3:D:194:VAL:HA	3:D:197:VAL:CG2	2.38	0.52
5:G:184:GLN:OE1	5:G:402:LEU:HD23	2.10	0.52
5:G:285:LEU:HD22	5:G:339:ARG:HA	1.90	0.52
8:Z:218:HIS:HB2	8:Z:302:LEU:HB3	1.91	0.52
6:H:73:HIS:HB3	6:H:76:ALA:HB3	1.92	0.52
8:Z:180:LYS:HB3	8:Z:186:ILE:HG12	1.92	0.52
2:B:275:MET:HA	2:B:278:LYS:HD2	1.91	0.52
1:A:213:GLY:O	1:A:374:SER:N	2.42	0.52
8:Z:176:ILE:HA	8:Z:179:ILE:HG12	1.91	0.52
8:Z:290:VAL:HA	8:Z:311:ILE:O	2.10	0.52
5:G:355:ILE:HB	5:G:360:PHE:CD2	2.44	0.52
6:H:133:VAL:HG12	6:H:137:LYS:HZ2	1.74	0.52
4:E:437:ALA:CB	4:E:448:MET:HB2	2.38	0.52
2:B:455:GLY:HA3	3:D:135:ILE:CG1	2.39	0.52
6:H:191:GLN:HB3	6:H:194:MET:SD	2.48	0.52
1:A:528:ASP:OD2	3:D:53:THR:HG21	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:355:LEU:HD13	8:Z:375:LEU:HD21	1.90	0.52
6:H:278:LEU:CD2	6:H:302:TYR:HB2	2.40	0.52
6:H:27:SER:O	6:H:31:VAL:HG23	2.10	0.52
1:A:458:GLN:O	1:A:459:ASP:C	2.48	0.52
2:B:446:LEU:HB3	2:B:447:PRO:CD	2.40	0.52
4:E:18:ILE:HG13	6:H:73:HIS:CD2	2.44	0.52
1:A:532:LYS:HG2	3:D:65:GLN:HB3	1.91	0.52
5:G:72:VAL:HG22	8:Z:6:THR:O	2.09	0.52
8:Z:230:ILE:O	8:Z:344:LEU:HA	2.09	0.52
5:G:407:LEU:HA	5:G:499:LEU:N	2.25	0.52
2:B:520:ILE:HD12	4:E:60:MET:CB	2.37	0.52
1:A:133:SER:HA	1:A:136:LEU:HD11	1.91	0.52
5:G:80:MET:HA	5:G:83:ILE:HD12	1.92	0.52
2:B:19:GLU:HB3	2:B:24:ALA:HA	1.91	0.52
8:Z:48:VAL:HG13	8:Z:53:ASP:O	2.09	0.52
7:Q:221:MET:HA	7:Q:374:THR:HG1	1.72	0.52
5:G:71:GLN:H	8:Z:524:ALA:HB1	1.74	0.52
8:Z:14:ALA:HB1	8:Z:19:ALA:HB2	1.92	0.52
2:B:218:PHE:HA	2:B:372:THR:OG1	2.09	0.52
4:E:237:PRO:HG2	4:E:238:GLN:H	1.75	0.52
6:H:133:VAL:HG12	6:H:137:LYS:HZ1	1.72	0.52
1:A:214:TYR:HA	1:A:374:SER:OG	2.09	0.52
8:Z:333:LEU:HD23	8:Z:339:LEU:HD23	1.90	0.52
8:Z:514:ASN:O	8:Z:518:VAL:HG23	2.10	0.52
6:H:17:GLN:O	6:H:20:PRO:HD2	2.10	0.52
3:D:404:ALA:O	3:D:408:ILE:HG13	2.10	0.52
8:Z:103:LEU:CD2	8:Z:516:LEU:HD21	2.36	0.52
2:B:407:VAL:CG2	2:B:495:GLU:HB2	2.37	0.52
5:G:396:GLN:HE22	5:G:399:ARG:HD3	1.74	0.52
1:A:9:GLY:HA2	1:A:533:LEU:HD22	1.92	0.52
6:H:443:GLU:O	6:H:447:ARG:HB2	2.10	0.52
3:D:226:LEU:HD11	3:D:389:VAL:HB	1.91	0.52
2:B:11:ILE:HA	4:E:85:HIS:HB2	1.92	0.52
3:D:237:ALA:HA	3:D:317:LEU:HD11	1.91	0.52
4:E:299:LEU:HD12	4:E:320:PRO:O	2.09	0.52
3:D:247:ALA:HA	3:D:299:ASN:ND2	2.20	0.52
1:A:75:LEU:HB3	1:A:94:VAL:HG13	1.90	0.52
3:D:290:VAL:HG13	3:D:320:LEU:HD23	1.91	0.52
2:B:231:ARG:NH2	2:B:348:LEU:HD11	2.23	0.52
6:H:73:HIS:HB3	6:H:76:ALA:CB	2.39	0.52
8:Z:422:LEU:HA	8:Z:425:TYR:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:SER:HA	3:D:87:LEU:HD11	1.91	0.52
2:B:53:LEU:HD23	3:D:542:ARG:NH2	2.25	0.52
3:D:36:ILE:HG23	3:D:536:ASP:HA	1.92	0.52
5:G:46:MET:CA	8:Z:517:LEU:HB3	2.40	0.52
5:G:62:ASP:OD2	5:G:64:ASN:HB3	2.10	0.52
7:Q:292:VAL:HG21	7:Q:324:LEU:CD2	2.39	0.52
7:Q:138:LYS:O	7:Q:142:ILE:HG13	2.10	0.52
5:G:226:HIS:ND1	5:G:227:PRO:HD2	2.25	0.52
3:D:450:GLU:O	3:D:454:ILE:HG13	2.10	0.52
7:Q:93:GLN:HE22	7:Q:97:VAL:HG22	1.74	0.52
8:Z:426:LYS:N	8:Z:427:PRO:CD	2.73	0.52
4:E:45:ALA:CB	4:E:114:GLY:HA3	2.40	0.52
8:Z:118:ILE:H	8:Z:118:ILE:CD1	2.20	0.52
4:E:204:VAL:HB	4:E:410:ARG:CG	2.33	0.52
2:B:144:SER:CB	2:B:474:THR:HG21	2.33	0.52
2:B:90:VAL:O	2:B:94:GLU:HG2	2.10	0.52
2:B:79:PRO:CG	2:B:522:LYS:HG3	2.40	0.52
5:G:165:ILE:HG21	5:G:390:ASN:HB3	1.92	0.52
6:H:36:VAL:HG23	6:H:95:THR:HG23	1.92	0.52
8:Z:109:TYR:HA	8:Z:112:GLU:CD	2.30	0.52
1:A:356:ILE:HG23	1:A:378:ARG:CZ	2.40	0.52
6:H:78:THR:HA	6:H:81:ASP:OD2	2.09	0.52
7:Q:448:ILE:N	7:Q:448:ILE:HD12	2.25	0.52
6:H:133:VAL:HG13	6:H:500:ILE:HG23	1.92	0.52
6:H:118:PRO:O	6:H:121:ILE:HB	2.10	0.52
7:Q:188:VAL:HG13	7:Q:197:PHE:CZ	2.45	0.52
7:Q:33:ILE:HG13	7:Q:112:LEU:CB	2.28	0.51
4:E:161:ASN:HD22	4:E:164:PRO:CB	2.20	0.51
3:D:431:PRO:HG2	3:D:432:GLU:OE1	2.09	0.51
6:H:71:VAL:HB	6:H:77:LYS:HE3	1.90	0.51
8:Z:462:THR:HA	8:Z:465:LYS:HE2	1.90	0.51
5:G:51:LEU:HD13	8:Z:521:ILE:HG23	1.93	0.51
2:B:202:ILE:HG13	2:B:219:LEU:HD23	1.92	0.51
8:Z:222:LYS:HB2	8:Z:311:ILE:CG1	2.41	0.51
8:Z:225:VAL:HG21	8:Z:290:VAL:HG22	1.92	0.51
5:G:404:ASP:OD2	5:G:406:GLN:HG2	2.09	0.51
5:G:286:LYS:N	5:G:287:PRO:CD	2.73	0.51
6:H:230:LYS:O	6:H:349:GLU:HA	2.09	0.51
2:B:194:GLY:CA	2:B:401:VAL:HG21	2.38	0.51
3:D:230:LEU:CD1	3:D:338:PHE:HB3	2.40	0.51
1:A:438:ILE:O	1:A:441:PHE:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LYS:HA	1:A:277:LYS:NZ	2.24	0.51
1:A:427:ALA:O	1:A:435:GLN:HG3	2.11	0.51
6:H:216:PHE:CE2	6:H:318:ASP:HB3	2.45	0.51
7:Q:523:GLN:HB3	8:Z:45:LYS:HE3	1.92	0.51
3:D:197:VAL:CG1	3:D:387:LYS:HA	2.35	0.51
2:B:513:VAL:HG13	2:B:516:ARG:HH12	1.74	0.51
6:H:238:ALA:CB	6:H:289:VAL:HG22	2.38	0.51
8:Z:138:LYS:HD2	8:Z:406:CYS:SG	2.50	0.51
2:B:196:LEU:HD11	2:B:395:CYS:HA	1.93	0.51
8:Z:164:LEU:HD13	8:Z:202:THR:HG22	1.91	0.51
5:G:380:SER:O	5:G:384:LEU:HB2	2.11	0.51
3:D:178:VAL:HB	3:D:403:GLU:CG	2.36	0.51
3:D:206:VAL:HG21	3:D:419:VAL:HG21	1.92	0.51
4:E:248:ILE:HG12	4:E:299:LEU:HD23	1.92	0.51
3:D:300:VAL:HG13	3:D:326:MET:HE1	1.91	0.51
8:Z:144:ASP:O	8:Z:148:LEU:HG	2.11	0.51
4:E:463:ALA:HB2	4:E:473:THR:HG21	1.92	0.51
2:B:135:LYS:O	2:B:139:GLN:HG3	2.11	0.51
2:B:509:GLU:HA	2:B:512:GLU:OE1	2.11	0.51
8:Z:160:VAL:CG2	8:Z:386:GLN:HG2	2.40	0.51
4:E:93:GLU:HB2	4:E:523:MET:HE1	1.93	0.51
5:G:51:LEU:HD13	8:Z:521:ILE:CG2	2.40	0.51
1:A:222:SER:OG	1:A:225:MET:HG2	2.11	0.51
3:D:119:LEU:HB3	3:D:140:PHE:HE2	1.75	0.51
2:B:239:ILE:HB	2:B:331:ILE:HA	1.93	0.51
2:B:351:GLU:HG3	2:B:360:ILE:HD13	1.92	0.51
6:H:150:GLU:O	6:H:151:GLN:HB3	2.11	0.51
6:H:152:ARG:O	6:H:156:GLU:HG3	2.10	0.51
7:Q:296:ARG:HH12	7:Q:315:LEU:HD11	1.75	0.51
7:Q:225:LYS:HD2	7:Q:352:LEU:HD22	1.92	0.51
5:G:49:MET:HB2	5:G:59:MET:HE2	1.92	0.51
7:Q:327:THR:OG1	7:Q:372:ILE:HB	2.10	0.51
5:G:476:GLU:O	5:G:476:GLU:HG2	2.10	0.51
7:Q:230:ASP:CB	7:Q:311:MET:HA	2.38	0.51
2:B:279:VAL:HG11	2:B:303:LEU:CB	2.41	0.51
3:D:144:LEU:HG	3:D:526:THR:HB	1.92	0.51
4:E:445:GLN:O	4:E:449:ARG:HG3	2.10	0.51
1:A:487:GLY:CA	1:A:498:ASN:HD21	2.23	0.51
3:D:463:VAL:HG23	3:D:464:ILE:N	2.26	0.51
1:A:32:VAL:HB	1:A:91:THR:HG23	1.93	0.51
7:Q:337:ASN:H	7:Q:338:PRO:CD	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:391:LEU:O	5:G:395:MET:HG3	2.11	0.51
8:Z:292:ILE:HD13	8:Z:313:LEU:HD13	1.93	0.51
7:Q:425:SER:O	7:Q:429:THR:HG23	2.11	0.51
8:Z:311:ILE:N	8:Z:311:ILE:HD12	2.26	0.51
5:G:406:GLN:O	5:G:499:LEU:N	2.35	0.51
3:D:179:VAL:HG11	3:D:407:SER:HB2	1.93	0.51
4:E:248:ILE:HD12	4:E:337:THR:HG21	1.92	0.51
6:H:316:GLU:HG2	6:H:320:LYS:HE3	1.93	0.51
2:B:479:ASP:OD1	2:B:482:GLU:HG2	2.10	0.51
2:B:446:LEU:HB3	2:B:447:PRO:HD3	1.93	0.51
6:H:411:ALA:HB2	6:H:487:ASN:ND2	2.25	0.51
3:D:82:LYS:NZ	3:D:99:LYS:NZ	2.58	0.51
4:E:133:ILE:HB	4:E:528:LEU:HD11	1.93	0.51
7:Q:520:ARG:O	7:Q:522:ASP:N	2.44	0.51
2:B:52:LEU:O	2:B:53:LEU:HD12	2.11	0.51
1:A:137:ILE:HG21	1:A:499:LYS:HG3	1.92	0.51
2:B:516:ARG:HG2	4:E:57:LEU:HA	1.92	0.51
5:G:512:THR:O	5:G:516:LEU:HG	2.11	0.51
7:Q:171:LYS:HB2	7:Q:173:TYR:CD1	2.45	0.51
6:H:294:PRO:HG3	6:H:313:ARG:CG	2.41	0.51
6:H:9:LEU:HB3	6:H:13:THR:HB	1.92	0.51
7:Q:337:ASN:N	7:Q:338:PRO:CD	2.74	0.51
4:E:123:LEU:HB3	4:E:128:ILE:HD12	1.91	0.51
3:D:333:ARG:O	3:D:337:GLU:HG3	2.11	0.51
6:H:378:ALA:HB3	6:H:381:PHE:HD1	1.76	0.51
3:D:525:ALA:O	3:D:529:VAL:HG23	2.11	0.51
3:D:417:CYS:HA	3:D:516:LEU:CD1	2.41	0.51
3:D:196:LYS:HB3	3:D:386:GLY:N	2.25	0.51
4:E:443:LEU:CD2	4:E:443:LEU:N	2.74	0.51
7:Q:155:ARG:HH22	7:Q:192:PRO:CG	2.24	0.51
1:A:164:ASN:HB3	1:A:206:MET:HE1	1.91	0.51
8:Z:209:GLY:HA3	8:Z:364:GLU:HA	1.92	0.51
7:Q:24:GLY:O	7:Q:27:GLU:HB3	2.11	0.50
1:A:105:ASP:O	1:A:108:VAL:HB	2.11	0.50
4:E:87:ILE:HG23	4:E:88:ALA:N	2.26	0.50
1:A:408:VAL:HG22	1:A:409:VAL:N	2.26	0.50
5:G:407:LEU:CB	5:G:498:PRO:HA	2.40	0.50
7:Q:156:ASP:O	7:Q:160:VAL:HG23	2.11	0.50
1:A:401:ARG:NH2	1:A:506:PRO:HG2	2.27	0.50
2:B:186:ALA:HB2	2:B:214:LEU:HD11	1.92	0.50
7:Q:68:ASP:O	7:Q:72:ILE:HG13	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:GLU:HB2	2:B:342:LYS:HD3	1.91	0.50
1:A:167:PHE:HB2	1:A:206:MET:HE1	1.93	0.50
2:B:35:ILE:HB	2:B:84:LEU:CD1	2.41	0.50
6:H:92:ASP:CG	6:H:93:GLY:N	2.64	0.50
7:Q:140:HIS:HE2	7:Q:508:ILE:HB	1.76	0.50
4:E:231:ASP:OD1	4:E:371:MET:HE3	2.11	0.50
8:Z:412:GLY:HA2	8:Z:415:GLU:CD	2.32	0.50
2:B:124:GLN:HG2	4:E:55:ASN:HD21	1.73	0.50
3:D:194:VAL:O	3:D:198:ILE:HG23	2.10	0.50
6:H:215:ALA:CB	6:H:373:ILE:HD11	2.33	0.50
3:D:86:VAL:CG1	3:D:91:ALA:HB3	2.42	0.50
6:H:26:ILE:HG23	6:H:105:LEU:CB	2.36	0.50
2:B:461:LEU:CD2	2:B:478:LEU:HD13	2.42	0.50
2:B:89:ARG:HH11	2:B:89:ARG:HG2	1.76	0.50
2:B:29:PHE:CZ	2:B:515:LEU:HA	2.46	0.50
7:Q:20:LYS:HB3	7:Q:525:ILE:HG13	1.93	0.50
8:Z:13:VAL:HG13	8:Z:522:MET:HG2	1.94	0.50
5:G:137:LEU:HA	5:G:140:ILE:CD1	2.41	0.50
8:Z:99:ILE:HG13	8:Z:512:ALA:HB2	1.92	0.50
7:Q:155:ARG:HH22	7:Q:192:PRO:HG2	1.75	0.50
4:E:416:ASN:O	4:E:417:ARG:HG2	2.12	0.50
8:Z:422:LEU:HB2	8:Z:441:ALA:HB2	1.93	0.50
8:Z:164:LEU:HG	8:Z:167:VAL:HB	1.93	0.50
8:Z:168:LEU:O	8:Z:172:VAL:HG23	2.12	0.50
5:G:462:LEU:O	5:G:466:LEU:HB2	2.12	0.50
8:Z:293:ASN:HD22	8:Z:297:ILE:CD1	2.23	0.50
8:Z:198:HIS:O	8:Z:199:LYS:HB2	2.11	0.50
3:D:98:SER:O	3:D:109:THR:HG23	2.11	0.50
4:E:344:ARG:NH2	4:E:345:PHE:CD2	2.80	0.50
4:E:426:GLU:HB3	4:E:455:LEU:O	2.11	0.50
7:Q:408:LEU:O	7:Q:408:LEU:HD12	2.10	0.50
4:E:134:ALA:HB1	4:E:525:ARG:HG3	1.93	0.50
1:A:349:GLU:HB3	1:A:366:ASN:CB	2.35	0.50
3:D:187:SER:O	3:D:191:VAL:HG23	2.11	0.50
7:Q:138:LYS:HD2	7:Q:141:GLU:OE1	2.11	0.50
4:E:115:ALA:HB1	4:E:457:VAL:HG11	1.94	0.50
6:H:213:GLY:O	6:H:370:CYS:HA	2.12	0.50
3:D:252:ILE:HD11	3:D:354:PHE:CG	2.45	0.50
1:A:498:ASN:HB3	1:A:503:VAL:HB	1.92	0.50
1:A:322:ALA:O	1:A:369:ALA:HB3	2.12	0.50
8:Z:328:CYS:SG	8:Z:366:CYS:SG	3.06	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:333:LEU:HB2	8:Z:339:LEU:CD2	2.42	0.50
6:H:331:GLN:CG	6:H:341:VAL:HG11	2.41	0.50
6:H:331:GLN:HG2	6:H:341:VAL:HG11	1.94	0.50
1:A:24:ALA:HB1	1:A:72:ALA:HB2	1.93	0.50
1:A:398:VAL:O	1:A:402:VAL:HG23	2.12	0.50
3:D:483:LEU:HD22	3:D:496:ILE:HD11	1.92	0.50
8:Z:409:PRO:O	8:Z:414:VAL:HG23	2.11	0.50
3:D:486:ARG:HG3	3:D:503:ILE:HG12	1.93	0.50
2:B:487:ASP:O	2:B:491:LEU:HG	2.11	0.50
5:G:283:ILE:HG12	5:G:309:ILE:CD1	2.42	0.50
4:E:300:ALA:HB3	4:E:321:ALA:HB2	1.94	0.50
4:E:318:ASP:O	4:E:319:LEU:HD12	2.12	0.50
7:Q:215:SER:HA	7:Q:378:ARG:HG2	1.93	0.50
1:A:447:VAL:HG13	1:A:448:ILE:N	2.27	0.50
2:B:408:TYR:CZ	2:B:489:SER:HB3	2.46	0.50
4:E:215:VAL:HB	4:E:392:LYS:HZ2	1.77	0.50
8:Z:142:GLU:HG3	8:Z:144:ASP:H	1.77	0.50
1:A:277:LYS:NZ	1:A:280:ALA:HB3	2.26	0.50
4:E:73:ASP:O	4:E:77:ILE:HG13	2.10	0.50
1:A:5:LEU:CD1	1:A:11:ARG:HB2	2.40	0.50
2:B:11:ILE:HD11	4:E:40:ALA:HB1	1.93	0.50
5:G:95:THR:O	5:G:99:ILE:HG12	2.12	0.50
1:A:409:VAL:HB	1:A:410:PRO:HD2	1.94	0.50
5:G:203:LYS:HB2	5:G:384:LEU:HD21	1.93	0.50
6:H:238:ALA:O	6:H:289:VAL:HA	2.12	0.50
6:H:50:VAL:HG13	6:H:54:GLY:O	2.12	0.50
2:B:51:ILE:N	3:D:538:VAL:HG13	2.26	0.50
1:A:474:ALA:O	1:A:483:LEU:HB2	2.11	0.50
3:D:249:ILE:O	3:D:359:LEU:HA	2.12	0.50
3:D:487:HIS:HE1	3:D:492:LYS:HA	1.77	0.50
2:B:408:TYR:OH	2:B:489:SER:HB3	2.12	0.50
5:G:230:ARG:NE	5:G:308:ASN:HB3	2.27	0.50
6:H:63:ALA:H	6:H:94:THR:HG21	1.76	0.50
1:A:114:PRO:HB3	1:A:525:LEU:HD22	1.93	0.50
8:Z:232:THR:O	8:Z:339:LEU:HD21	2.11	0.50
7:Q:171:LYS:HB2	7:Q:173:TYR:HE1	1.77	0.50
3:D:421:LYS:CG	3:D:515:LEU:HB3	2.39	0.50
4:E:27:ARG:NH2	4:E:534:ARG:NH2	2.59	0.50
3:D:82:LYS:HZ3	3:D:99:LYS:HZ3	1.60	0.50
8:Z:139:VAL:O	8:Z:407:VAL:HG12	2.11	0.50
8:Z:415:GLU:OE2	8:Z:447:ILE:HG21	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:35:ARG:HD2	8:Z:450:VAL:HG22	1.94	0.49
8:Z:55:LYS:HE2	8:Z:62:VAL:HG11	1.94	0.49
8:Z:62:VAL:O	8:Z:66:GLU:HG2	2.12	0.49
7:Q:353:SER:O	7:Q:360:VAL:HG22	2.11	0.49
5:G:46:MET:HG2	8:Z:517:LEU:CD2	2.42	0.49
5:G:110:GLU:HA	5:G:113:LEU:HD12	1.94	0.49
3:D:179:VAL:HG12	3:D:404:ALA:HA	1.93	0.49
3:D:515:LEU:HG	3:D:519:VAL:HG23	1.91	0.49
4:E:385:ILE:O	4:E:387:ILE:HD12	2.12	0.49
2:B:465:LEU:HD12	2:B:485:ILE:HD12	1.93	0.49
4:E:251:LEU:O	4:E:302:CYS:HA	2.12	0.49
2:B:51:ILE:H	3:D:538:VAL:HG13	1.76	0.49
5:G:171:LEU:O	5:G:175:ILE:HG13	2.12	0.49
8:Z:23:ASN:O	8:Z:73:THR:HG21	2.12	0.49
3:D:169:SER:HB2	3:D:418:LEU:HD22	1.94	0.49
2:B:477:GLY:HA3	2:B:488:MET:HG2	1.93	0.49
7:Q:44:ARG:HE	7:Q:451:ALA:HB2	1.77	0.49
1:A:532:LYS:HZ2	3:D:65:GLN:HB2	1.77	0.49
5:G:23:GLN:NE2	5:G:113:LEU:HD22	2.27	0.49
3:D:105:ALA:N	3:D:416:ARG:HH22	2.10	0.49
4:E:306:PHE:HB3	4:E:323:ARG:HD3	1.94	0.49
2:B:505:LEU:O	2:B:509:GLU:HG2	2.12	0.49
4:E:340:ARG:HD2	4:E:352:LYS:HD3	1.94	0.49
4:E:178:VAL:HG21	4:E:185:MET:HG3	1.93	0.49
7:Q:246:PHE:CB	7:Q:297:VAL:HG13	2.42	0.49
1:A:31:ILE:CG1	5:G:16:ARG:HH12	2.24	0.49
8:Z:224:ARG:NH1	8:Z:349:LEU:HD11	2.28	0.49
1:A:125:CYS:O	1:A:129:VAL:HG23	2.12	0.49
4:E:145:ILE:HG23	4:E:149:ASP:OD1	2.12	0.49
2:B:522:LYS:HE2	2:B:523:ALA:H	1.77	0.49
3:D:122:SER:HB2	3:D:456:ALA:HB1	1.93	0.49
4:E:363:SER:HA	4:E:370:LYS:HA	1.94	0.49
7:Q:474:GLY:HA3	7:Q:478:VAL:CG2	2.42	0.49
8:Z:15:ARG:O	8:Z:18:ALA:HB3	2.12	0.49
7:Q:218:LEU:HD13	7:Q:362:VAL:CG1	2.42	0.49
4:E:400:ARG:O	4:E:403:HIS:HB3	2.12	0.49
7:Q:92:MET:O	7:Q:96:GLU:HG2	2.12	0.49
1:A:119:SER:O	1:A:123:LEU:HG	2.12	0.49
3:D:61:ASP:O	3:D:62:LYS:HD3	2.12	0.49
2:B:218:PHE:CB	2:B:326:VAL:HG11	2.31	0.49
6:H:390:HIS:O	6:H:394:MET:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:401:VAL:HG13	5:G:402:LEU:CD1	2.42	0.49
1:A:82:GLN:NE2	1:A:86:VAL:HG21	2.27	0.49
6:H:289:VAL:HB	6:H:310:CYS:SG	2.52	0.49
7:Q:49:PRO:CA	7:Q:170:SER:HA	2.42	0.49
1:A:474:ALA:HB3	1:A:486:ILE:HG13	1.94	0.49
3:D:469:ALA:HB1	3:D:474:LEU:HB2	1.93	0.49
3:D:466:SER:OG	3:D:480:VAL:HG21	2.13	0.49
6:H:378:ALA:HB3	6:H:381:PHE:CD1	2.48	0.49
5:G:65:ALA:O	5:G:69:GLU:HG2	2.13	0.49
5:G:325:ARG:HG2	5:G:325:ARG:HH11	1.78	0.49
8:Z:35:ARG:HG2	8:Z:453:GLN:HE22	1.77	0.49
3:D:24:LYS:HG3	3:D:30:ARG:HH11	1.77	0.49
4:E:94:LEU:HG	4:E:523:MET:HG2	1.95	0.49
3:D:317:LEU:HG	3:D:321:ASN:ND2	2.27	0.49
1:A:86:VAL:HG13	1:A:512:LYS:HZ1	1.74	0.49
4:E:511:ILE:H	4:E:511:ILE:CD1	2.23	0.49
2:B:215:ASP:O	2:B:371:CYS:HB3	2.12	0.49
8:Z:473:SER:HB2	8:Z:477:VAL:CG2	2.43	0.49
7:Q:417:ILE:HG13	7:Q:467:LEU:HD21	1.95	0.49
7:Q:410:PRO:HG3	7:Q:476:LYS:HG2	1.95	0.49
3:D:132:HIS:HB3	3:D:135:ILE:CD1	2.42	0.49
5:G:477:THR:O	5:G:489:ASP:HA	2.13	0.49
7:Q:17:GLU:CB	8:Z:68:GLN:HG2	2.43	0.49
3:D:36:ILE:HG21	3:D:536:ASP:C	2.33	0.49
4:E:193:VAL:HG11	4:E:409:ILE:HG22	1.95	0.49
3:D:89:PRO:HA	3:D:92:ARG:HD2	1.94	0.49
2:B:158:ASP:O	2:B:162:ILE:HG12	2.13	0.49
6:H:443:GLU:OE1	6:H:461:LEU:HD11	2.13	0.49
5:G:38:ARG:HG3	5:G:100:ILE:CD1	2.42	0.49
7:Q:218:LEU:HD13	7:Q:362:VAL:HG13	1.94	0.49
7:Q:14:MET:HG3	8:Z:70:GLN:OE1	2.12	0.49
7:Q:112:LEU:HD22	7:Q:519:LEU:CD2	2.36	0.49
4:E:87:ILE:CD1	4:E:527:ILE:HD13	2.43	0.49
7:Q:292:VAL:HG21	7:Q:324:LEU:HD21	1.95	0.49
1:A:224:GLY:HA3	1:A:301:VAL:HG13	1.94	0.49
5:G:285:LEU:HD11	5:G:338:LEU:HB3	1.94	0.49
5:G:203:LYS:CD	5:G:384:LEU:HG	2.34	0.49
1:A:2:GLU:CB	3:D:90:ALA:HB3	2.43	0.49
2:B:239:ILE:HD12	2:B:329:GLY:O	2.13	0.49
8:Z:131:LEU:CD2	8:Z:505:LEU:HD12	2.41	0.49
5:G:424:GLU:HA	5:G:427:LYS:HZ3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:132:GLN:O	8:Z:136:GLN:HG3	2.11	0.49
7:Q:524:ILE:CG2	8:Z:46:MET:N	2.73	0.49
1:A:59:ALA:HB2	1:A:90:THR:HG21	1.93	0.49
5:G:352:ILE:HD11	5:G:359:TYR:HB3	1.95	0.49
5:G:523:VAL:HG12	5:G:524:SER:N	2.28	0.49
1:A:445:LEU:N	1:A:446:PRO:CD	2.76	0.49
3:D:431:PRO:HG2	3:D:432:GLU:CD	2.33	0.49
3:D:470:GLU:C	3:D:472:ALA:H	2.16	0.49
4:E:75:ALA:HB2	4:E:106:THR:HG21	1.95	0.49
2:B:163:ALA:HB3	2:B:180:THR:HG23	1.95	0.49
8:Z:97:LEU:HB3	8:Z:446:ILE:HD13	1.94	0.49
4:E:90:LEU:HA	4:E:93:GLU:CD	2.33	0.49
2:B:187:VAL:CG2	2:B:397:LEU:HD13	2.41	0.49
3:D:251:LEU:CB	3:D:347:PRO:HA	2.43	0.49
4:E:173:LEU:HD13	4:E:185:MET:HB2	1.94	0.49
4:E:95:SER:HB2	4:E:106:THR:HG22	1.95	0.49
2:B:353:MET:HA	2:B:357:ASP:O	2.13	0.49
7:Q:44:ARG:HE	7:Q:451:ALA:CB	2.25	0.49
7:Q:239:ILE:O	7:Q:344:MET:HA	2.12	0.49
7:Q:407:ARG:HB2	7:Q:501:TYR:HB3	1.94	0.49
6:H:154:LEU:HA	6:H:157:LYS:HZ3	1.78	0.49
6:H:226:GLU:HB3	6:H:227:MET:HE2	1.94	0.49
4:E:20:LYS:HZ3	6:H:32:ILE:CG1	2.26	0.49
2:B:522:LYS:NZ	3:D:22:ARG:O	2.46	0.49
1:A:483:LEU:O	1:A:486:ILE:HG12	2.13	0.49
7:Q:448:ILE:HD12	7:Q:448:ILE:H	1.78	0.49
2:B:487:ASP:HB3	2:B:490:VAL:HB	1.94	0.49
2:B:74:ILE:HA	3:D:541:THR:OG1	2.13	0.48
7:Q:316:ASN:OD1	7:Q:320:ASP:HB2	2.13	0.48
7:Q:222:VAL:HG23	7:Q:374:THR:HG21	1.94	0.48
5:G:72:VAL:HA	8:Z:6:THR:O	2.12	0.48
8:Z:13:VAL:HG13	8:Z:522:MET:CG	2.43	0.48
5:G:23:GLN:NE2	5:G:113:LEU:HD13	2.16	0.48
1:A:506:PRO:HB2	1:A:509:VAL:CG2	2.37	0.48
5:G:183:VAL:HG23	5:G:194:ASP:OD2	2.13	0.48
6:H:450:CYS:HA	6:H:479:ILE:CD1	2.43	0.48
2:B:287:ILE:CG2	2:B:343:LEU:HD21	2.43	0.48
1:A:57:ASP:O	1:A:61:ILE:HG13	2.12	0.48
8:Z:410:GLY:HA3	8:Z:496:ASP:OD1	2.13	0.48
7:Q:246:PHE:HB2	7:Q:297:VAL:HG13	1.94	0.48
4:E:34:LEU:O	4:E:38:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:226:LEU:HD21	3:D:389:VAL:HG11	1.95	0.48
3:D:174:LEU:HB2	3:D:183:SER:OG	2.13	0.48
7:Q:138:LYS:HG2	7:Q:426:TYR:CD2	2.48	0.48
5:G:101:LEU:HG	5:G:447:ILE:HD11	1.95	0.48
3:D:395:GLY:O	3:D:401:ILE:HD11	2.12	0.48
2:B:79:PRO:HD3	2:B:522:LYS:CD	2.40	0.48
7:Q:174:GLY:HA2	7:Q:177:VAL:CG1	2.41	0.48
5:G:209:ILE:HD13	5:G:387:VAL:HG21	1.94	0.48
2:B:198:ALA:HB1	2:B:369:GLU:O	2.13	0.48
8:Z:161:HIS:C	8:Z:163:GLU:H	2.15	0.48
2:B:11:ILE:HA	4:E:85:HIS:N	2.24	0.48
1:A:350:GLU:HB3	1:A:366:ASN:HD22	1.77	0.48
5:G:79:SER:O	5:G:83:ILE:HG13	2.13	0.48
3:D:483:LEU:HD22	3:D:496:ILE:CD1	2.42	0.48
4:E:315:LEU:C	4:E:315:LEU:HD23	2.34	0.48
1:A:483:LEU:HD12	1:A:485:TRP:CH2	2.48	0.48
7:Q:351:TYR:CE2	7:Q:364:LYS:HE2	2.49	0.48
7:Q:227:THR:HG23	7:Q:302:LEU:HD22	1.94	0.48
7:Q:103:PHE:CE1	7:Q:448:ILE:HG12	2.42	0.48
4:E:18:ILE:HG22	4:E:19:ILE:HG13	1.95	0.48
6:H:418:LYS:NZ	6:H:469:ALA:HA	2.27	0.48
1:A:271:THR:HA	1:A:274:ARG:NH2	2.28	0.48
6:H:199:LYS:O	6:H:199:LYS:HG3	2.13	0.48
7:Q:486:VAL:O	7:Q:486:VAL:HG13	2.14	0.48
7:Q:428:GLU:HA	7:Q:435:GLN:NE2	2.12	0.48
7:Q:199:VAL:CG1	7:Q:396:VAL:HG12	2.35	0.48
4:E:459:PRO:HA	4:E:462:LEU:HG	1.95	0.48
6:H:214:VAL:HG23	6:H:361:PHE:HB2	1.95	0.48
2:B:46:LYS:O	2:B:453:ASN:HB3	2.14	0.48
6:H:366:LYS:O	6:H:368:LYS:N	2.46	0.48
6:H:129:THR:O	6:H:133:VAL:HG23	2.14	0.48
6:H:496:ALA:O	6:H:500:ILE:HG13	2.13	0.48
6:H:516:VAL:HG22	7:Q:53:ASN:O	2.13	0.48
7:Q:55:MET:SD	7:Q:63:LEU:HD21	2.53	0.48
1:A:35:SER:HA	1:A:41:LEU:H	1.78	0.48
6:H:86:GLN:HE21	6:H:90:VAL:CG2	2.26	0.48
1:A:384:MET:N	1:A:384:MET:SD	2.87	0.48
3:D:31:ASP:HB3	3:D:36:ILE:CB	2.27	0.48
1:A:4:PRO:O	1:A:5:LEU:HD23	2.13	0.48
7:Q:239:ILE:CD1	7:Q:328:VAL:HG11	2.42	0.48
6:H:169:SER:HA	6:H:172:LYS:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:420:LYS:HD2	3:D:516:LEU:HD11	1.95	0.48
4:E:456:GLU:C	4:E:459:PRO:HD2	2.34	0.48
5:G:105:MET:HE1	5:G:510:VAL:HA	1.95	0.48
5:G:445:GLU:O	5:G:448:PRO:HG2	2.14	0.48
2:B:196:LEU:HD11	2:B:398:ALA:HB2	1.94	0.48
3:D:79:THR:O	3:D:83:GLN:HG3	2.13	0.48
1:A:9:GLY:HA2	1:A:533:LEU:CD2	2.44	0.48
7:Q:417:ILE:HG13	7:Q:467:LEU:CD2	2.44	0.48
5:G:352:ILE:HG23	5:G:352:ILE:O	2.14	0.48
4:E:375:GLU:HG3	4:E:376:GLN:HG2	1.95	0.48
5:G:468:ALA:O	5:G:472:GLN:HG3	2.14	0.48
3:D:464:ILE:O	3:D:468:LEU:HG	2.13	0.48
2:B:238:LEU:HD22	2:B:287:ILE:HG21	1.95	0.48
2:B:287:ILE:HD11	2:B:290:PHE:HB2	1.95	0.48
7:Q:188:VAL:O	7:Q:188:VAL:HG12	2.12	0.48
3:D:364:LEU:HD11	3:D:366:GLU:HB3	1.95	0.48
3:D:486:ARG:C	3:D:494:THR:HG21	2.34	0.48
3:D:26:ALA:O	3:D:27:TYR:HB2	2.14	0.48
2:B:202:ILE:HB	2:B:374:VAL:HA	1.96	0.48
1:A:205:GLN:HA	1:A:378:ARG:O	2.14	0.48
7:Q:71:THR:O	7:Q:75:GLU:HG2	2.14	0.48
8:Z:459:LEU:C	8:Z:459:LEU:HD23	2.34	0.48
3:D:476:PRO:O	3:D:480:VAL:HG23	2.14	0.48
2:B:290:PHE:CE2	2:B:292:ASN:HB2	2.48	0.48
7:Q:391:ALA:HA	7:Q:394:ASP:OD2	2.13	0.48
2:B:316:ASP:OD2	2:B:318:VAL:HG12	2.14	0.48
1:A:286:ILE:N	1:A:286:ILE:HD12	2.29	0.48
2:B:37:ASP:O	2:B:40:LYS:HB3	2.13	0.48
8:Z:161:HIS:NE2	8:Z:168:LEU:HB2	2.28	0.48
5:G:74:HIS:CB	8:Z:5:LYS:HB2	2.33	0.48
2:B:519:ASN:C	2:B:520:ILE:HD13	2.34	0.48
4:E:297:ALA:HB2	4:E:353:LEU:HD21	1.96	0.48
5:G:350:LEU:HA	5:G:362:PHE:O	2.14	0.48
6:H:288:VAL:HA	6:H:309:PHE:O	2.13	0.48
3:D:430:ALA:N	3:D:431:PRO:HD2	2.29	0.48
7:Q:453:ALA:HB1	7:Q:458:VAL:HB	1.96	0.48
6:H:191:GLN:HB3	6:H:194:MET:HG3	1.96	0.48
1:A:286:ILE:HB	1:A:307:ALA:HB2	1.95	0.48
8:Z:40:PRO:HA	8:Z:158:THR:HA	1.95	0.48
5:G:473:GLU:HB3	5:G:478:TRP:HE1	1.79	0.48
1:A:13:THR:O	1:A:16:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:204:ILE:HD12	5:G:375:LEU:HD13	1.96	0.48
2:B:232:ILE:HG22	2:B:235:ALA:HB2	1.95	0.48
4:E:163:GLU:O	4:E:167:GLN:HG3	2.14	0.48
3:D:454:ILE:O	3:D:457:PHE:HB3	2.13	0.48
1:A:450:ASN:OD1	1:A:464:VAL:HG21	2.14	0.48
7:Q:191:PHE:H	7:Q:192:PRO:HD3	1.79	0.48
1:A:41:LEU:HA	5:G:518:ARG:HD2	1.96	0.48
3:D:535:ILE:HG22	3:D:535:ILE:O	2.13	0.48
3:D:190:SER:O	3:D:194:VAL:HG23	2.14	0.48
2:B:219:LEU:HB3	2:B:372:THR:CG2	2.43	0.48
1:A:93:VAL:HG13	1:A:94:VAL:N	2.28	0.48
1:A:112:ILE:HG23	1:A:433:ARG:CD	2.36	0.48
8:Z:181:LYS:HE2	8:Z:370:ARG:NH1	2.28	0.48
7:Q:45:THR:HA	7:Q:455:ASN:OD1	2.13	0.48
6:H:155:LEU:HD22	6:H:396:VAL:HG13	1.96	0.48
3:D:370:LEU:HD13	3:D:392:VAL:HG21	1.94	0.48
8:Z:160:VAL:HG21	8:Z:386:GLN:HG2	1.95	0.48
6:H:134:ASN:HD22	6:H:134:ASN:N	2.12	0.48
8:Z:38:LEU:HD23	8:Z:450:VAL:HG11	1.95	0.48
8:Z:14:ALA:O	8:Z:520:GLU:HB3	2.14	0.48
1:A:137:ILE:HD13	1:A:499:LYS:CG	2.43	0.48
7:Q:241:VAL:HG22	7:Q:324:LEU:HD23	1.96	0.48
6:H:240:LEU:HD13	6:H:334:VAL:HG22	1.95	0.48
8:Z:133:PHE:HD1	8:Z:136:GLN:OE1	1.96	0.48
8:Z:50:GLY:C	8:Z:52:GLY:H	2.17	0.48
3:D:29:ASP:HB2	3:D:540:ASN:CB	2.44	0.47
7:Q:113:GLU:O	7:Q:117:GLU:HG3	2.14	0.47
4:E:410:ARG:O	4:E:413:ILE:HG22	2.14	0.47
1:A:137:ILE:HG23	1:A:499:LYS:HZ1	1.79	0.47
5:G:515:LEU:O	5:G:519:ILE:HG13	2.14	0.47
3:D:174:LEU:HD13	3:D:183:SER:HA	1.96	0.47
3:D:186:LEU:HD23	3:D:189:MET:HE1	1.95	0.47
1:A:398:VAL:HG23	1:A:399:VAL:N	2.29	0.47
7:Q:205:CYS:SG	7:Q:207:ILE:HD11	2.53	0.47
1:A:330:THR:HG22	1:A:332:ALA:H	1.79	0.47
3:D:46:ALA:HA	3:D:49:ASP:OD2	2.14	0.47
8:Z:181:LYS:CD	8:Z:370:ARG:HH12	2.27	0.47
2:B:238:LEU:HB2	2:B:343:LEU:HD23	1.96	0.47
2:B:399:GLN:O	2:B:403:ASP:N	2.47	0.47
2:B:223:LYS:HZ1	2:B:351:GLU:HB2	1.77	0.47
7:Q:525:ILE:CG2	7:Q:526:MET:H	2.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:397:VAL:HA	5:G:400:ASN:ND2	2.26	0.47
6:H:214:VAL:HA	6:H:371:THR:HB	1.95	0.47
4:E:312:HIS:O	4:E:315:LEU:HB3	2.14	0.47
2:B:281:ARG:HA	2:B:284:LYS:HD2	1.95	0.47
3:D:249:ILE:CG2	3:D:345:THR:HG21	2.42	0.47
5:G:211:ASP:C	5:G:377:ARG:HG3	2.35	0.47
2:B:156:ARG:HA	2:B:159:LEU:HD12	1.96	0.47
7:Q:22:PHE:CD1	7:Q:22:PHE:N	2.83	0.47
3:D:421:LYS:HE2	3:D:515:LEU:CD2	2.37	0.47
3:D:88:HIS:CE1	3:D:90:ALA:H	2.31	0.47
4:E:454:ALA:O	4:E:457:VAL:HG22	2.14	0.47
6:H:224:GLY:HA3	6:H:228:GLN:OE1	2.14	0.47
5:G:82:GLU:O	5:G:86:THR:HG23	2.15	0.47
3:D:433:ILE:CD1	3:D:465:PRO:HG3	2.42	0.47
8:Z:221:MET:HG2	8:Z:306:ALA:HB2	1.97	0.47
7:Q:212:VAL:HA	7:Q:378:ARG:O	2.14	0.47
6:H:117:HIS:O	6:H:121:ILE:HG13	2.14	0.47
1:A:413:GLY:HA3	1:A:449:PRO:HB3	1.95	0.47
2:B:123:PRO:O	2:B:126:ILE:HB	2.13	0.47
4:E:426:GLU:N	4:E:426:GLU:OE1	2.48	0.47
7:Q:446:GLU:O	7:Q:450:ARG:HB2	2.14	0.47
2:B:228:GLN:NE2	2:B:301:GLU:HG2	2.29	0.47
7:Q:222:VAL:HA	7:Q:361:VAL:O	2.14	0.47
2:B:33:ILE:CG2	2:B:111:ARG:HD3	2.43	0.47
5:G:200:ARG:O	5:G:373:THR:HA	2.14	0.47
5:G:137:LEU:HD11	5:G:506:TYR:HE2	1.78	0.47
2:B:346:CYS:SG	2:B:349:ILE:HG13	2.54	0.47
6:H:224:GLY:O	6:H:300:THR:HG23	2.14	0.47
1:A:385:CYS:HA	1:A:388:MET:HE3	1.95	0.47
1:A:121:TYR:HB3	1:A:518:THR:CG2	2.43	0.47
3:D:78:ALA:HB2	3:D:109:THR:CG2	2.42	0.47
2:B:340:LEU:HD12	2:B:343:LEU:HD12	1.97	0.47
1:A:115:THR:HA	1:A:118:ILE:HD12	1.96	0.47
3:D:24:LYS:HG3	3:D:30:ARG:NH1	2.30	0.47
7:Q:13:GLN:CG	8:Z:71:HIS:HA	2.45	0.47
2:B:9:VAL:HG13	4:E:36:SER:HB2	1.97	0.47
5:G:416:MET:HE3	5:G:466:LEU:HD22	1.97	0.47
5:G:286:LYS:N	5:G:287:PRO:HD3	2.30	0.47
7:Q:21:HIS:CD2	7:Q:21:HIS:H	2.31	0.47
2:B:39:VAL:HA	2:B:50:LYS:HZ1	1.79	0.47
6:H:516:VAL:HA	7:Q:53:ASN:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:251:LEU:HD12	3:D:336:ILE:HD12	1.95	0.47
1:A:369:ALA:C	1:A:371:THR:H	2.18	0.47
1:A:289:THR:OG1	1:A:316:LEU:HD22	2.14	0.47
5:G:44:LYS:HD3	5:G:455:CYS:HA	1.96	0.47
8:Z:104:LYS:O	8:Z:108:LEU:HG	2.14	0.47
3:D:226:LEU:HG	3:D:389:VAL:HB	1.96	0.47
6:H:110:PRO:HG2	6:H:111:TYR:CD1	2.49	0.47
5:G:470:HIS:HE1	5:G:476:GLU:HG3	1.80	0.47
4:E:207:GLU:C	4:E:209:ILE:H	2.16	0.47
6:H:224:GLY:O	6:H:225:PHE:HB2	2.14	0.47
3:D:256:LEU:CD1	3:D:256:LEU:N	2.76	0.47
1:A:210:LEU:HD12	1:A:375:VAL:HG22	1.96	0.47
6:H:100:LEU:HD21	6:H:445:ILE:CD1	2.45	0.47
5:G:245:LEU:HD12	5:G:296:ILE:HG12	1.95	0.47
2:B:203:LYS:HB2	2:B:383:LEU:HG	1.95	0.47
2:B:35:ILE:HB	2:B:84:LEU:HD12	1.97	0.47
4:E:85:HIS:CE1	4:E:87:ILE:HG22	2.49	0.47
5:G:416:MET:HG2	5:G:466:LEU:CD2	2.40	0.47
4:E:410:ARG:HA	4:E:413:ILE:CG2	2.44	0.47
6:H:175:PHE:O	6:H:179:VAL:HG23	2.14	0.47
5:G:152:MET:HG3	5:G:401:VAL:HG11	1.95	0.47
8:Z:351:TYR:HB2	8:Z:353:TYR:CE1	2.50	0.47
3:D:43:ALA:O	3:D:47:VAL:HG23	2.15	0.47
3:D:239:SER:CB	3:D:321:ASN:HB3	2.37	0.47
7:Q:187:CYS:SG	7:Q:217:VAL:HG13	2.54	0.47
1:A:82:GLN:HG2	1:A:90:THR:HA	1.96	0.47
7:Q:390:ARG:HA	7:Q:390:ARG:NE	2.30	0.47
6:H:239:LEU:HD22	6:H:319:LEU:CD1	2.41	0.47
2:B:51:ILE:H	3:D:538:VAL:CG1	2.28	0.47
3:D:431:PRO:HG2	3:D:432:GLU:OE2	2.15	0.47
4:E:165:LEU:HD13	4:E:190:VAL:HG13	1.97	0.47
6:H:36:VAL:O	6:H:95:THR:HG21	2.14	0.47
4:E:109:VAL:HG13	4:E:110:VAL:N	2.29	0.47
1:A:292:ILE:HG13	1:A:309:ARG:HB3	1.97	0.47
2:B:232:ILE:HD12	2:B:288:ASN:O	2.15	0.47
1:A:132:ILE:HD12	1:A:511:VAL:HG22	1.97	0.47
1:A:85:GLU:HB3	1:A:512:LYS:NZ	2.30	0.47
5:G:319:ASP:O	5:G:323:ILE:HG13	2.14	0.47
7:Q:204:VAL:HG11	7:Q:389:GLU:HG3	1.97	0.47
7:Q:188:VAL:HG11	7:Q:399:PHE:CG	2.50	0.47
2:B:367:LEU:C	2:B:369:GLU:H	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:244:GLU:HB3	4:E:245:ASP:H	1.54	0.47
4:E:298:ASN:O	4:E:320:PRO:HD2	2.15	0.47
6:H:144:LYS:HD3	6:H:154:LEU:HD11	1.97	0.47
1:A:75:LEU:HD13	1:A:94:VAL:HG13	1.96	0.47
2:B:276:LYS:HB2	2:B:299:TYR:HE2	1.80	0.47
7:Q:409:VAL:N	7:Q:499:ASP:O	2.43	0.47
3:D:49:ASP:O	3:D:52:ARG:HB3	2.15	0.47
4:E:428:SER:HB2	4:E:487:PRO:HB3	1.97	0.47
6:H:186:LEU:HD12	6:H:186:LEU:H	1.80	0.47
3:D:156:ARG:HB3	3:D:424:LEU:CD1	2.44	0.47
4:E:522:GLN:CD	4:E:522:GLN:N	2.69	0.47
8:Z:382:HIS:O	8:Z:385:THR:HB	2.15	0.47
5:G:471:THR:O	5:G:471:THR:HG22	2.14	0.47
2:B:111:ARG:HA	2:B:114:GLU:OE2	2.15	0.47
4:E:61:MET:CE	4:E:81:MET:HB2	2.45	0.47
2:B:288:ASN:N	2:B:288:ASN:ND2	2.62	0.47
3:D:174:LEU:HD13	3:D:186:LEU:HB2	1.97	0.47
2:B:209:LEU:HD21	2:B:382:ILE:CG2	2.38	0.47
2:B:281:ARG:NH1	2:B:281:ARG:HG2	2.29	0.47
5:G:177:LEU:C	5:G:177:LEU:HD23	2.35	0.47
7:Q:188:VAL:HB	7:Q:399:PHE:CE2	2.49	0.47
4:E:417:ARG:HG3	4:E:417:ARG:HH11	1.79	0.47
7:Q:525:ILE:CG2	8:Z:67:MET:HG2	2.46	0.46
1:A:12:SER:HB2	1:A:17:ILE:CB	2.32	0.46
3:D:173:SER:CB	3:D:414:VAL:HG21	2.45	0.46
4:E:456:GLU:O	4:E:459:PRO:HD2	2.14	0.46
2:B:454:ALA:CB	2:B:480:MET:SD	2.98	0.46
3:D:348:VAL:HG21	3:D:354:PHE:HA	1.97	0.46
2:B:83:VAL:HA	2:B:86:ASP:OD2	2.14	0.46
6:H:522:ASN:CG	7:Q:77:GLU:HB2	2.35	0.46
6:H:233:HIS:CG	6:H:234:ASN:N	2.83	0.46
7:Q:364:LYS:O	7:Q:365:HIS:HB2	2.15	0.46
1:A:423:LEU:HD13	1:A:441:PHE:CD2	2.50	0.46
3:D:154:MET:HB3	3:D:492:LYS:CD	2.44	0.46
1:A:526:ARG:HD2	3:D:59:GLY:O	2.14	0.46
3:D:185:LEU:HD22	3:D:222:ASP:OD1	2.15	0.46
6:H:66:LEU:HB3	6:H:80:VAL:HG22	1.97	0.46
1:A:355:ARG:HA	1:A:359:ASP:O	2.15	0.46
4:E:90:LEU:HD23	4:E:93:GLU:OE1	2.15	0.46
7:Q:33:ILE:HG21	7:Q:116:GLU:OE2	2.14	0.46
5:G:46:MET:HB3	8:Z:517:LEU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:286:ILE:HG21	3:D:315:LEU:HB2	1.98	0.46
5:G:499:LEU:O	5:G:503:LEU:N	2.45	0.46
2:B:516:ARG:HG2	4:E:58:ASP:N	2.29	0.46
3:D:148:ILE:O	3:D:152:THR:HG23	2.15	0.46
1:A:395:ALA:HA	1:A:398:VAL:HG22	1.97	0.46
6:H:228:GLN:OE1	6:H:309:PHE:HA	2.15	0.46
2:B:95:VAL:HG23	2:B:96:GLY:N	2.21	0.46
6:H:213:GLY:O	6:H:371:THR:N	2.49	0.46
2:B:61:LEU:HD21	2:B:63:VAL:HG23	1.97	0.46
1:A:474:ALA:O	1:A:485:TRP:NE1	2.48	0.46
6:H:198:LYS:HZ3	6:H:217:LYS:CG	2.25	0.46
4:E:18:ILE:HG22	4:E:19:ILE:N	2.30	0.46
4:E:521:THR:HB	4:E:522:GLN:NE2	2.30	0.46
5:G:157:ASN:O	5:G:161:THR:HG23	2.14	0.46
5:G:163:LYS:H	5:G:166:SER:HB3	1.79	0.46
6:H:241:ASN:HD22	6:H:241:ASN:HA	1.52	0.46
7:Q:520:ARG:O	8:Z:43:THR:HB	2.16	0.46
7:Q:20:LYS:HD2	7:Q:525:ILE:HG13	1.97	0.46
5:G:200:ARG:NH1	5:G:202:GLU:HB2	2.31	0.46
4:E:62:VAL:HA	4:E:67:ASP:O	2.16	0.46
5:G:203:LYS:HB2	5:G:384:LEU:CG	2.45	0.46
8:Z:349:LEU:HG	8:Z:351:TYR:HD2	1.80	0.46
6:H:286:ALA:HB2	6:H:342:LEU:HD21	1.98	0.46
6:H:349:GLU:HG3	6:H:360:PHE:CD2	2.49	0.46
1:A:241:LEU:HG	1:A:331:LEU:CD2	2.44	0.46
4:E:20:LYS:HZ3	6:H:32:ILE:HG12	1.80	0.46
4:E:236:HIS:CD2	4:E:237:PRO:HD2	2.50	0.46
5:G:433:GLU:O	5:G:436:PRO:HD2	2.15	0.46
2:B:455:GLY:HA3	3:D:135:ILE:HG12	1.97	0.46
8:Z:188:LEU:HD11	8:Z:396:ARG:HD3	1.98	0.46
7:Q:16:LYS:HD2	7:Q:525:ILE:HB	1.96	0.46
8:Z:48:VAL:CG2	8:Z:54:ILE:HG12	2.39	0.46
7:Q:393:ASP:O	7:Q:396:VAL:HB	2.15	0.46
1:A:2:GLU:CD	3:D:44:ALA:H	2.16	0.46
1:A:90:THR:O	1:A:93:VAL:HG12	2.15	0.46
3:D:236:VAL:HG21	3:D:329:LYS:H	1.80	0.46
4:E:227:GLY:HA2	4:E:380:SER:OG	2.16	0.46
4:E:192:ALA:O	4:E:196:VAL:HG22	2.15	0.46
1:A:496:ARG:HG2	1:A:497:ASP:N	2.31	0.46
8:Z:34:LEU:HD11	8:Z:60:GLY:HA2	1.98	0.46
8:Z:179:ILE:HD13	8:Z:191:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:49:MET:HB3	8:Z:518:VAL:HG11	1.97	0.46
4:E:193:VAL:O	4:E:197:ALA:HB2	2.15	0.46
6:H:163:LEU:O	6:H:166:LYS:HB2	2.15	0.46
4:E:167:GLN:O	4:E:171:THR:HG23	2.15	0.46
6:H:226:GLU:HB3	6:H:227:MET:HE3	1.97	0.46
3:D:252:ILE:HD12	3:D:351:VAL:HA	1.98	0.46
2:B:187:VAL:HG21	2:B:397:LEU:CD1	2.43	0.46
3:D:335:ASP:O	3:D:339:ILE:HG13	2.15	0.46
5:G:129:ALA:O	5:G:132:ASP:HB2	2.16	0.46
7:Q:296:ARG:NH1	7:Q:315:LEU:HD11	2.31	0.46
2:B:320:VAL:HA	2:B:323:LEU:HD12	1.97	0.46
3:D:258:ALA:HB2	3:D:286:ILE:HG13	1.98	0.46
2:B:516:ARG:CG	4:E:57:LEU:HA	2.45	0.46
6:H:238:ALA:O	6:H:289:VAL:HG13	2.14	0.46
4:E:145:ILE:HD12	4:E:514:LYS:HG3	1.96	0.46
6:H:350:GLU:OE2	6:H:357:ARG:HD2	2.16	0.46
1:A:533:LEU:HD12	3:D:66:ASP:HA	1.96	0.46
6:H:197:ILE:CG2	6:H:386:GLU:HG3	2.44	0.46
7:Q:466:LYS:O	7:Q:470:VAL:HG23	2.16	0.46
1:A:370:ARG:C	1:A:372:SER:H	2.18	0.46
8:Z:123:PHE:CE1	8:Z:439:ALA:HB3	2.51	0.46
8:Z:34:LEU:HG	8:Z:93:THR:HG23	1.97	0.46
5:G:448:PRO:O	5:G:451:LEU:HB3	2.16	0.46
4:E:489:LEU:HD23	4:E:490:GLY:N	2.30	0.46
1:A:467:LEU:HB2	1:A:488:LEU:HD21	1.97	0.46
3:D:217:LEU:HG	3:D:401:ILE:HD12	1.98	0.46
8:Z:475:GLN:HG3	8:Z:475:GLN:O	2.15	0.46
3:D:251:LEU:HB3	3:D:347:PRO:HA	1.97	0.46
2:B:413:SER:O	2:B:417:MET:HG2	2.16	0.46
1:A:423:LEU:HD13	1:A:441:PHE:HD2	1.79	0.46
4:E:42:LYS:NZ	4:E:46:ASN:HD21	2.13	0.46
7:Q:197:PHE:CB	7:Q:403:THR:HG21	2.46	0.46
4:E:131:ILE:HD12	4:E:131:ILE:H	1.81	0.46
3:D:100:ALA:O	3:D:104:GLU:HG3	2.15	0.46
1:A:220:VAL:O	1:A:225:MET:SD	2.74	0.46
2:B:520:ILE:HD12	4:E:60:MET:N	2.30	0.46
1:A:176:VAL:O	1:A:180:LYS:HB2	2.16	0.46
4:E:317:ASN:O	4:E:318:ASP:HB2	2.15	0.46
4:E:315:LEU:O	4:E:315:LEU:HD23	2.16	0.46
2:B:231:ARG:HH21	2:B:348:LEU:CD1	2.27	0.46
3:D:195:MET:SD	3:D:196:LYS:HG3	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:36:GLY:O	2:B:104:VAL:HG22	2.15	0.46
1:A:520:ALA:O	1:A:524:ILE:HG13	2.16	0.46
6:H:315:PRO:HB2	6:H:318:ASP:OD2	2.15	0.46
6:H:122:ILE:HG23	6:H:511:CYS:SG	2.56	0.46
6:H:223:ALA:O	6:H:311:ALA:HA	2.16	0.46
3:D:24:LYS:CE	3:D:28:GLN:HE22	2.29	0.46
7:Q:13:GLN:N	7:Q:13:GLN:NE2	2.63	0.46
7:Q:16:LYS:HD2	7:Q:525:ILE:CB	2.45	0.46
8:Z:46:MET:CG	8:Z:54:ILE:HG23	2.45	0.46
8:Z:175:SER:O	8:Z:179:ILE:HG23	2.16	0.46
7:Q:168:VAL:O	7:Q:173:TYR:CE1	2.69	0.46
3:D:174:LEU:HD12	3:D:187:SER:OG	2.16	0.46
1:A:2:GLU:OE2	3:D:39:SER:O	2.34	0.46
1:A:190:TYR:HB3	1:A:400:LYS:HG3	1.97	0.46
7:Q:148:CYS:HB2	7:Q:476:LYS:NZ	2.31	0.46
6:H:411:ALA:HB2	6:H:487:ASN:HD21	1.81	0.46
8:Z:141:LYS:O	8:Z:142:GLU:HB3	2.16	0.46
1:A:275:ILE:HG23	1:A:300:PHE:CE1	2.50	0.46
6:H:36:VAL:CG2	6:H:95:THR:HG23	2.46	0.46
4:E:22:GLN:HG3	4:E:23:ASP:O	2.16	0.46
4:E:325:VAL:HB	4:E:330:ILE:HD11	1.98	0.46
8:Z:123:PHE:HD1	8:Z:440:PHE:HB2	1.81	0.46
3:D:36:ILE:HD11	3:D:40:ASN:HD21	1.81	0.46
3:D:61:ASP:C	3:D:62:LYS:HD3	2.36	0.46
5:G:84:SER:HB2	5:G:95:THR:CG2	2.45	0.46
3:D:416:ARG:HH11	3:D:420:LYS:HZ2	1.63	0.46
1:A:132:ILE:C	1:A:134:GLU:H	2.19	0.46
6:H:290:LEU:HD11	6:H:361:PHE:CE2	2.51	0.46
3:D:64:ILE:HG21	3:D:83:GLN:HB3	1.97	0.46
8:Z:217:ARG:HG2	8:Z:302:LEU:HD22	1.98	0.46
8:Z:218:HIS:HB3	8:Z:221:MET:CG	2.43	0.46
6:H:43:ARG:HH21	6:H:480:ASN:HA	1.77	0.46
7:Q:453:ALA:CB	7:Q:463:VAL:HG11	2.46	0.46
3:D:472:ALA:HB2	3:D:498:VAL:HB	1.98	0.46
4:E:518:SER:HA	4:E:522:GLN:HE21	1.81	0.46
3:D:475:ASN:HB3	3:D:478:SER:HB3	1.97	0.46
8:Z:24:ILE:HD13	8:Z:107:ASP:HB2	1.97	0.46
8:Z:161:HIS:C	8:Z:163:GLU:N	2.67	0.45
5:G:26:ASN:OD1	5:G:516:LEU:HB3	2.16	0.45
2:B:239:ILE:HG22	2:B:331:ILE:HG23	1.98	0.45
6:H:521:LYS:O	6:H:522:ASN:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:290:VAL:HG11	3:D:319:PHE:C	2.36	0.45
7:Q:227:THR:HB	7:Q:230:ASP:CG	2.36	0.45
8:Z:126:ALA:HB2	8:Z:437:VAL:HA	1.97	0.45
8:Z:123:PHE:HE1	8:Z:439:ALA:HB3	1.80	0.45
7:Q:73:LEU:HD12	7:Q:90:SER:OG	2.15	0.45
5:G:136:THR:O	5:G:140:ILE:HD12	2.16	0.45
6:H:300:THR:O	6:H:303:PHE:HB2	2.16	0.45
8:Z:135:GLU:HG3	8:Z:138:LYS:HZ2	1.80	0.45
4:E:236:HIS:HB3	4:E:239:MET:CG	2.42	0.45
7:Q:85:MET:O	7:Q:88:MET:HE2	2.16	0.45
4:E:443:LEU:HD23	4:E:444:GLU:H	1.80	0.45
5:G:296:ILE:HG13	5:G:313:ARG:HB3	1.98	0.45
7:Q:99:ASP:OD2	7:Q:398:THR:HG22	2.16	0.45
3:D:364:LEU:O	3:D:364:LEU:HG	2.17	0.45
2:B:396:VAL:O	2:B:400:THR:HG23	2.16	0.45
8:Z:447:ILE:N	8:Z:448:PRO:HD2	2.31	0.45
7:Q:13:GLN:HG3	8:Z:71:HIS:HA	1.98	0.45
6:H:190:LEU:CD2	6:H:397:ARG:HB2	2.40	0.45
3:D:170:ALA:O	3:D:174:LEU:HG	2.16	0.45
3:D:157:PRO:HA	3:D:423:ALA:HA	1.98	0.45
8:Z:99:ILE:O	8:Z:103:LEU:HG	2.17	0.45
3:D:462:GLU:O	3:D:465:PRO:HG2	2.15	0.45
3:D:302:LEU:HD13	3:D:339:ILE:HD13	1.98	0.45
5:G:165:ILE:CD1	5:G:387:VAL:HG13	2.45	0.45
1:A:118:ILE:CG2	1:A:522:ILE:HG23	2.45	0.45
6:H:445:ILE:N	6:H:446:PRO:HD2	2.30	0.45
1:A:286:ILE:HB	1:A:307:ALA:CB	2.46	0.45
2:B:415:MET:HE1	2:B:466:ARG:HB2	1.97	0.45
6:H:64:THR:O	6:H:68:LEU:HD12	2.15	0.45
7:Q:223:PHE:CZ	7:Q:316:ASN:HA	2.51	0.45
8:Z:333:LEU:HG	8:Z:338:ASP:O	2.16	0.45
2:B:219:LEU:HD22	2:B:374:VAL:CG2	2.47	0.45
5:G:347:ALA:O	5:G:349:LEU:HB2	2.16	0.45
7:Q:206:LYS:HD3	7:Q:389:GLU:CD	2.37	0.45
6:H:366:LYS:HB3	6:H:368:LYS:HE3	1.98	0.45
5:G:160:ILE:HG23	5:G:165:ILE:CG2	2.45	0.45
3:D:216:LYS:CE	3:D:376:LEU:HD11	2.47	0.45
5:G:85:ARG:HG3	5:G:85:ARG:HH11	1.82	0.45
6:H:92:ASP:CG	6:H:93:GLY:H	2.20	0.45
8:Z:82:THR:HG22	8:Z:86:ASP:OD2	2.16	0.45
2:B:368:GLY:C	2:B:370:ALA:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:529:LYS:HA	6:H:45:MET:SD	2.56	0.45
3:D:32:LYS:HZ1	3:D:33:PRO:HD2	1.80	0.45
8:Z:172:VAL:HG13	8:Z:395:LEU:HD23	1.99	0.45
5:G:27:ILE:HG13	5:G:106:LEU:HB3	1.98	0.45
6:H:163:LEU:HB2	6:H:172:LYS:HB2	1.98	0.45
4:E:188:ILE:HG21	4:E:385:ILE:HG23	1.98	0.45
4:E:511:ILE:HA	4:E:514:LYS:NZ	2.32	0.45
6:H:239:LEU:HD21	6:H:290:LEU:HD12	1.99	0.45
3:D:446:LEU:HD23	3:D:454:ILE:CD1	2.45	0.45
2:B:452:ASP:C	2:B:454:ALA:H	2.19	0.45
2:B:61:LEU:HD23	2:B:61:LEU:O	2.17	0.45
1:A:329:SER:OG	1:A:330:THR:N	2.50	0.45
7:Q:16:LYS:HG3	7:Q:525:ILE:HD13	1.99	0.45
5:G:107:SER:O	5:G:110:GLU:HG2	2.17	0.45
6:H:37:ARG:HG3	6:H:99:LEU:CD2	2.47	0.45
1:A:75:LEU:HD13	1:A:94:VAL:CG1	2.47	0.45
4:E:236:HIS:HD2	4:E:315:LEU:HD12	1.76	0.45
4:E:306:PHE:HB2	4:E:323:ARG:CB	2.42	0.45
4:E:443:LEU:H	4:E:443:LEU:HD22	1.82	0.45
8:Z:127:LYS:HZ2	8:Z:509:THR:HB	1.81	0.45
7:Q:110:ALA:O	7:Q:114:LEU:HD23	2.17	0.45
2:B:139:GLN:HA	2:B:142:LEU:CD1	2.47	0.45
1:A:470:PHE:HD2	1:A:495:PRO:HB2	1.81	0.45
3:D:26:ALA:C	3:D:28:GLN:H	2.20	0.45
8:Z:44:MET:HG3	8:Z:56:LEU:HD11	1.99	0.45
3:D:32:LYS:HZ3	3:D:33:PRO:HD2	1.77	0.45
2:B:11:ILE:HG12	4:E:85:HIS:CB	2.47	0.45
1:A:297:LEU:O	1:A:301:VAL:HG23	2.16	0.45
1:A:129:VAL:O	1:A:132:ILE:HB	2.17	0.45
6:H:289:VAL:O	6:H:310:CYS:HA	2.17	0.45
1:A:449:PRO:HA	1:A:452:LEU:HD12	1.99	0.45
1:A:487:GLY:HA3	1:A:498:ASN:ND2	2.31	0.45
4:E:153:ASP:O	4:E:154:SER:C	2.55	0.45
8:Z:148:LEU:HD22	8:Z:398:VAL:HG13	1.99	0.45
3:D:224:CYS:HA	3:D:392:VAL:O	2.16	0.45
7:Q:134:ILE:HD12	7:Q:434:GLU:CD	2.37	0.45
2:B:9:VAL:HG13	4:E:36:SER:CB	2.47	0.45
5:G:50:LEU:C	5:G:51:LEU:HD12	2.38	0.45
8:Z:277:LEU:HD22	8:Z:341:PRO:HD3	1.98	0.45
6:H:228:GLN:O	6:H:230:LYS:N	2.50	0.45
6:H:497:MET:CE	6:H:501:ASN:HB2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:119:GLN:HG2	7:Q:50:ASN:HD22	1.81	0.45
4:E:254:PRO:HB3	4:E:304:TRP:CB	2.46	0.45
5:G:453:GLN:C	5:G:455:CYS:H	2.20	0.45
3:D:108:GLY:O	3:D:110:THR:N	2.50	0.45
6:H:276:ASP:O	6:H:280:LYS:HG3	2.17	0.45
8:Z:114:LEU:CD2	8:Z:432:ARG:HD3	2.44	0.45
3:D:31:ASP:CB	3:D:36:ILE:HB	2.29	0.45
5:G:48:LYS:O	5:G:59:MET:HA	2.17	0.45
8:Z:230:ILE:HG13	8:Z:324:LEU:HD11	1.99	0.45
7:Q:126:SER:HB3	8:Z:41:LYS:HD3	1.99	0.45
3:D:119:LEU:HD12	3:D:529:VAL:CG2	2.39	0.45
4:E:224:LEU:HD12	4:E:384:THR:O	2.16	0.45
8:Z:352:GLU:HA	8:Z:360:PHE:O	2.17	0.45
2:B:172:LEU:CD1	2:B:209:LEU:HD13	2.47	0.45
2:B:94:GLU:O	2:B:395:CYS:HB3	2.16	0.45
5:G:242:ASP:O	5:G:293:GLU:HB3	2.17	0.45
7:Q:445:PHE:HA	7:Q:448:ILE:HD13	1.99	0.45
6:H:136:ILE:O	6:H:140:ALA:HB2	2.17	0.45
4:E:42:LYS:HG2	4:E:46:ASN:ND2	2.32	0.45
3:D:81:LEU:HD13	3:D:95:VAL:HA	1.99	0.45
4:E:446:TYR:CD1	4:E:446:TYR:N	2.85	0.45
7:Q:504:LYS:O	7:Q:508:ILE:HD12	2.17	0.45
3:D:161:SER:N	3:D:422:ARG:NH1	2.65	0.45
7:Q:514:ALA:O	7:Q:518:VAL:HG23	2.16	0.45
5:G:467:ARG:HG3	5:G:467:ARG:HH11	1.81	0.45
1:A:211:ILE:N	1:A:374:SER:O	2.50	0.45
1:A:213:GLY:HA3	1:A:365:LYS:CB	2.46	0.45
7:Q:521:VAL:CG1	7:Q:524:ILE:HD13	2.46	0.45
7:Q:223:PHE:C	7:Q:224:LYS:HD2	2.36	0.45
6:H:179:VAL:O	6:H:183:VAL:HG23	2.17	0.45
7:Q:407:ARG:HD2	7:Q:501:TYR:CD2	2.53	0.45
4:E:219:LEU:O	4:E:222:THR:HG23	2.16	0.45
3:D:300:VAL:HG12	3:D:300:VAL:O	2.16	0.45
6:H:214:VAL:HA	6:H:371:THR:CB	2.47	0.45
5:G:183:VAL:HG12	5:G:370:LYS:O	2.17	0.45
1:A:232:ALA:O	1:A:347:GLN:HA	2.17	0.45
2:B:280:GLU:O	2:B:284:LYS:HG3	2.17	0.45
6:H:407:ALA:HB1	6:H:487:ASN:HB2	1.99	0.45
3:D:484:ARG:HH11	3:D:484:ARG:HG3	1.82	0.45
8:Z:186:ILE:HB	8:Z:399:LYS:HG3	1.99	0.45
8:Z:304:ALA:O	8:Z:308:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:48:MET:HG2	4:E:110:VAL:HG11	1.97	0.45
1:A:390:ARG:HD2	1:A:390:ARG:HA	1.81	0.45
5:G:151:THR:HA	5:G:154:ASN:HD22	1.82	0.45
5:G:72:VAL:HG13	8:Z:5:LYS:O	2.17	0.44
5:G:70:ILE:CG2	8:Z:6:THR:HG22	2.46	0.44
5:G:27:ILE:HG22	5:G:28:ASN:N	2.32	0.44
3:D:136:ILE:HG22	3:D:533:LEU:HD13	1.99	0.44
3:D:420:LYS:CD	3:D:516:LEU:HD11	2.46	0.44
1:A:168:PHE:HZ	1:A:205:GLN:HB2	1.81	0.44
1:A:180:LYS:CD	1:A:190:TYR:HB2	2.47	0.44
3:D:77:GLY:HA2	3:D:80:ILE:HD12	1.99	0.44
3:D:483:LEU:HD22	3:D:496:ILE:HG13	1.99	0.44
6:H:417:SER:CA	6:H:439:ALA:HB1	2.45	0.44
4:E:357:GLY:HA3	4:E:376:GLN:HB2	1.98	0.44
1:A:206:MET:HE2	1:A:206:MET:HA	1.99	0.44
8:Z:127:LYS:HD2	8:Z:509:THR:CB	2.47	0.44
2:B:472:GLY:C	2:B:473:LYS:HD2	2.38	0.44
5:G:204:ILE:HD13	5:G:355:ILE:CG2	2.35	0.44
1:A:502:GLY:O	1:A:504:PHE:HD1	2.00	0.44
5:G:137:LEU:HB3	5:G:499:LEU:CD1	2.47	0.44
1:A:27:SER:CB	5:G:9:VAL:HG11	2.41	0.44
3:D:123:CYS:SG	3:D:533:LEU:HD22	2.57	0.44
3:D:88:HIS:HA	3:D:89:PRO:HD3	1.90	0.44
1:A:190:TYR:HD2	1:A:400:LYS:CB	2.23	0.44
1:A:395:ALA:O	1:A:398:VAL:HG22	2.17	0.44
4:E:297:ALA:HB2	4:E:353:LEU:CD2	2.46	0.44
4:E:510:LEU:HG	4:E:514:LYS:HZ1	1.78	0.44
5:G:101:LEU:HD23	5:G:446:VAL:CG2	2.47	0.44
6:H:135:LYS:HA	6:H:135:LYS:HD2	1.88	0.44
2:B:44:GLY:C	2:B:46:LYS:H	2.20	0.44
7:Q:204:VAL:HG22	7:Q:375:ILE:HD12	2.00	0.44
2:B:72:LYS:HZ3	2:B:89:ARG:HG3	1.77	0.44
3:D:444:ARG:O	3:D:444:ARG:HG2	2.18	0.44
1:A:233:LYS:HB3	1:A:345:LEU:HD13	1.98	0.44
4:E:86:GLN:H	4:E:86:GLN:CD	2.20	0.44
2:B:102:VAL:HG13	2:B:103:THR:N	2.32	0.44
6:H:455:PHE:HB2	6:H:482:GLU:CD	2.37	0.44
2:B:385:GLU:OE1	2:B:385:GLU:HA	2.17	0.44
5:G:145:ASP:OD2	5:G:148:ASN:HB2	2.17	0.44
5:G:366:CYS:O	5:G:369:PRO:HD3	2.17	0.44
5:G:458:SER:HB3	5:G:461:ARG:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:155:SER:OG	3:D:425:ILE:HG23	2.17	0.44
8:Z:59:ASP:OD2	8:Z:62:VAL:HG23	2.18	0.44
3:D:33:PRO:HA	3:D:536:ASP:OD2	2.17	0.44
1:A:5:LEU:HD21	1:A:531:ILE:HD13	1.99	0.44
4:E:40:ALA:CB	4:E:87:ILE:HG21	2.47	0.44
5:G:466:LEU:HG	5:G:487:LEU:CD1	2.44	0.44
1:A:137:ILE:HB	1:A:408:VAL:O	2.17	0.44
4:E:61:MET:HE2	4:E:81:MET:HB2	1.99	0.44
1:A:82:GLN:NE2	1:A:86:VAL:CG2	2.81	0.44
5:G:130:LEU:HA	5:G:133:MET:CE	2.46	0.44
4:E:20:LYS:HZ2	6:H:31:VAL:CG1	2.31	0.44
3:D:436:ALA:O	3:D:458:ALA:HB1	2.18	0.44
4:E:312:HIS:CE1	4:E:316:GLN:HE22	2.35	0.44
1:A:30:ASN:O	1:A:33:LYS:HB3	2.16	0.44
1:A:453:ALA:HB1	1:A:458:GLN:O	2.17	0.44
5:G:172:ALA:HA	5:G:175:ILE:HD12	2.00	0.44
5:G:424:GLU:HA	5:G:427:LYS:HZ1	1.81	0.44
6:H:46:ASP:O	6:H:47:LYS:HD3	2.17	0.44
2:B:455:GLY:CA	3:D:135:ILE:HD11	2.47	0.44
4:E:139:GLN:O	4:E:143:ILE:HG13	2.18	0.44
7:Q:32:ASN:OD1	7:Q:82:ALA:HB2	2.17	0.44
2:B:326:VAL:CG1	2:B:365:VAL:HG11	2.35	0.44
4:E:405:ALA:O	4:E:408:VAL:HG22	2.18	0.44
5:G:407:LEU:HA	5:G:499:LEU:H	1.81	0.44
8:Z:196:MET:HG2	8:Z:360:PHE:CZ	2.52	0.44
4:E:511:ILE:O	4:E:515:GLN:HB3	2.17	0.44
3:D:439:LEU:HD13	3:D:457:PHE:HD2	1.82	0.44
2:B:183:ALA:O	2:B:187:VAL:HG23	2.18	0.44
8:Z:186:ILE:HD12	8:Z:399:LYS:O	2.17	0.44
3:D:532:ILE:O	3:D:535:ILE:HB	2.18	0.44
7:Q:434:GLU:O	7:Q:438:ILE:HG13	2.17	0.44
7:Q:22:PHE:HB3	7:Q:525:ILE:HD12	2.00	0.44
7:Q:80:HIS:CE1	7:Q:82:ALA:HB3	2.52	0.44
7:Q:34:GLN:HA	7:Q:37:LYS:HE2	1.99	0.44
5:G:50:LEU:HD11	5:G:66:ILE:HG23	2.00	0.44
4:E:410:ARG:CA	4:E:413:ILE:HG22	2.47	0.44
1:A:222:SER:C	1:A:224:GLY:H	2.21	0.44
2:B:518:ASP:C	4:E:59:LYS:HZ2	2.21	0.44
3:D:414:VAL:HG23	3:D:415:ILE:N	2.33	0.44
6:H:9:LEU:HD13	6:H:13:THR:HG22	2.00	0.44
3:D:217:LEU:HA	3:D:401:ILE:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:235:LYS:HG2	3:D:367:GLU:CD	2.38	0.44
1:A:230:VAL:HB	1:A:231:ASN:H	1.60	0.44
2:B:337:HIS:N	2:B:338:PRO:CD	2.81	0.44
2:B:141:LEU:O	2:B:145:ALA:HB2	2.18	0.44
5:G:292:THR:HB	5:G:313:ARG:HA	2.00	0.44
8:Z:87:ILE:N	8:Z:87:ILE:CD1	2.81	0.44
5:G:430:THR:HA	5:G:434:GLN:NE2	2.31	0.44
7:Q:59:HIS:C	7:Q:61:GLU:H	2.21	0.44
7:Q:119:LEU:HD21	7:Q:125:VAL:HA	1.99	0.44
3:D:229:GLY:HA3	3:D:380:THR:HA	1.99	0.44
3:D:315:LEU:H	3:D:315:LEU:CD2	2.10	0.44
6:H:391:ASP:HA	6:H:394:MET:CG	2.48	0.44
3:D:137:SER:HG	3:D:533:LEU:HB2	1.83	0.44
4:E:511:ILE:HA	4:E:514:LYS:HZ3	1.82	0.44
5:G:130:LEU:HD21	5:G:507:LYS:HA	2.00	0.44
6:H:214:VAL:HG12	6:H:371:THR:OG1	2.18	0.44
3:D:429:GLY:O	3:D:433:ILE:HG12	2.18	0.44
6:H:366:LYS:HD3	6:H:368:LYS:HZ2	1.77	0.44
6:H:497:MET:HE3	6:H:500:ILE:HB	1.99	0.44
4:E:132:ARG:HG2	4:E:443:LEU:HG	1.99	0.44
2:B:458:SER:O	2:B:462:VAL:HG23	2.17	0.44
4:E:155:VAL:HG21	4:E:412:LEU:HD11	1.98	0.44
7:Q:27:GLU:O	7:Q:31:ARG:HG3	2.17	0.44
7:Q:297:VAL:HG23	7:Q:314:ARG:HB3	2.00	0.44
7:Q:225:LYS:CD	7:Q:352:LEU:HD13	2.48	0.44
1:A:18:ARG:HH12	1:A:108:VAL:HG13	1.83	0.44
1:A:530:LEU:HD11	3:D:63:MET:O	2.17	0.44
4:E:83:VAL:HG13	4:E:88:ALA:CB	2.47	0.44
5:G:64:ASN:HD21	5:G:68:ARG:HD2	1.83	0.44
5:G:462:LEU:O	5:G:462:LEU:HD13	2.18	0.44
2:B:520:ILE:CD1	4:E:60:MET:HB3	2.38	0.44
2:B:521:ILE:O	4:E:62:VAL:HB	2.18	0.44
6:H:37:ARG:NH2	6:H:444:ILE:HG13	2.33	0.44
4:E:164:PRO:O	4:E:167:GLN:HB2	2.18	0.44
8:Z:204:THR:HG22	8:Z:377:LYS:N	2.32	0.44
5:G:133:MET:SD	5:G:444:LEU:HD11	2.58	0.44
2:B:189:ARG:NH1	2:B:189:ARG:HB3	2.33	0.44
2:B:196:LEU:HD21	2:B:394:LEU:O	2.18	0.44
2:B:397:LEU:O	2:B:401:VAL:HG13	2.17	0.44
1:A:533:LEU:CD1	3:D:66:ASP:HA	2.47	0.44
8:Z:470:HIS:HA	8:Z:477:VAL:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:374:ILE:HD13	5:G:391:LEU:HD21	1.99	0.44
2:B:408:TYR:CD1	2:B:494:THR:HG22	2.52	0.44
5:G:41:LEU:HD22	5:G:100:ILE:HD12	2.00	0.44
2:B:29:PHE:CE1	2:B:515:LEU:HA	2.52	0.44
8:Z:356:GLY:O	8:Z:357:GLU:HB2	2.18	0.44
5:G:415:GLU:H	5:G:415:GLU:CD	2.21	0.44
1:A:16:ALA:O	1:A:20:GLN:HG2	2.18	0.44
1:A:408:VAL:HG23	1:A:505:GLU:C	2.37	0.44
7:Q:160:VAL:HG11	7:Q:185:GLN:HG2	1.99	0.44
8:Z:274:ILE:HD11	8:Z:336:LEU:CD2	2.48	0.44
3:D:179:VAL:HB	3:D:186:LEU:CD1	2.47	0.44
3:D:78:ALA:CB	3:D:109:THR:HG21	2.45	0.44
3:D:144:LEU:HD23	3:D:526:THR:OG1	2.17	0.44
3:D:339:ILE:HG23	3:D:343:ILE:HD12	2.00	0.44
6:H:117:HIS:NE2	7:Q:454:GLU:O	2.51	0.44
1:A:448:ILE:N	1:A:449:PRO:HD2	2.33	0.44
3:D:430:ALA:HB1	3:D:492:LYS:O	2.17	0.44
2:B:155:PHE:CD2	2:B:157:GLN:HB3	2.53	0.44
5:G:325:ARG:HG2	5:G:325:ARG:NH1	2.32	0.44
5:G:44:LYS:CD	5:G:455:CYS:HA	2.48	0.44
2:B:439:TYR:OH	2:B:504:LEU:HD22	2.17	0.44
3:D:226:LEU:HA	3:D:390:THR:O	2.17	0.44
1:A:392:LEU:O	1:A:396:LEU:HG	2.18	0.44
4:E:208:LEU:HD22	4:E:381:ARG:O	2.17	0.44
4:E:102:ILE:HG12	4:E:515:GLN:OE1	2.18	0.44
4:E:25:LYS:CE	4:E:536:PRO:HB3	2.48	0.44
4:E:20:LYS:HZ1	6:H:31:VAL:HB	1.76	0.44
3:D:289:LEU:O	3:D:293:ILE:HG13	2.17	0.44
2:B:398:ALA:O	2:B:401:VAL:HG22	2.18	0.44
7:Q:234:VAL:HG11	7:Q:289:ASN:CG	2.38	0.44
3:D:76:ASP:OD2	3:D:78:ALA:HB3	2.18	0.44
8:Z:30:LEU:HD21	8:Z:64:LEU:HD22	2.00	0.44
1:A:513:SER:OG	1:A:514:LEU:N	2.51	0.44
4:E:478:ARG:O	4:E:482:VAL:HG23	2.18	0.44
2:B:375:LEU:CD1	2:B:387:GLU:HA	2.48	0.44
3:D:28:GLN:HG3	3:D:541:THR:CA	2.47	0.43
3:D:193:ALA:HB2	3:D:226:LEU:HD11	2.00	0.43
8:Z:341:PRO:HA	8:Z:344:LEU:CD1	2.47	0.43
5:G:143:PRO:HA	5:G:406:GLN:OE1	2.17	0.43
2:B:229:PRO:O	2:B:310:MET:HG3	2.17	0.43
6:H:521:LYS:O	6:H:522:ASN:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:470:HIS:ND1	8:Z:477:VAL:HB	2.32	0.43
4:E:225:ILE:HG22	4:E:227:GLY:H	1.83	0.43
4:E:325:VAL:HG12	4:E:330:ILE:HG12	1.98	0.43
6:H:208:SER:HA	6:H:375:ARG:HH11	1.82	0.43
8:Z:75:SER:O	8:Z:78:ALA:HB3	2.18	0.43
2:B:48:MET:HB3	3:D:534:LYS:O	2.18	0.43
8:Z:118:ILE:HG21	8:Z:432:ARG:CB	2.42	0.43
7:Q:527:ALA:HB2	8:Z:66:GLU:O	2.17	0.43
8:Z:168:LEU:HD23	8:Z:172:VAL:HG23	1.99	0.43
8:Z:331:ILE:HD12	8:Z:343:CYS:SG	2.57	0.43
2:B:11:ILE:HD11	4:E:40:ALA:CA	2.48	0.43
5:G:282:ILE:HG12	5:G:338:LEU:HD13	1.98	0.43
2:B:68:ALA:HB2	2:B:99:THR:HG21	2.01	0.43
6:H:9:LEU:HD23	7:Q:77:GLU:O	2.18	0.43
2:B:61:LEU:HD23	2:B:61:LEU:C	2.39	0.43
5:G:79:SER:HA	5:G:82:GLU:OE1	2.17	0.43
8:Z:368:ASN:OD1	8:Z:370:ARG:HB2	2.18	0.43
7:Q:454:GLU:C	7:Q:456:SER:H	2.21	0.43
6:H:431:GLN:O	6:H:435:ILE:HG13	2.17	0.43
8:Z:142:GLU:HG3	8:Z:144:ASP:HB2	2.01	0.43
7:Q:460:ALA:HA	7:Q:463:VAL:CG1	2.48	0.43
7:Q:460:ALA:O	7:Q:464:ILE:HG13	2.18	0.43
7:Q:125:VAL:O	7:Q:128:VAL:HB	2.17	0.43
5:G:409:PRO:HA	5:G:495:ILE:O	2.17	0.43
7:Q:459:LYS:HE2	7:Q:461:ASN:HB2	2.00	0.43
8:Z:321:MET:O	8:Z:325:THR:HG23	2.17	0.43
6:H:72:VAL:HG12	6:H:72:VAL:O	2.18	0.43
2:B:52:LEU:HB2	2:B:62:MET:HB3	2.00	0.43
2:B:66:ASP:O	2:B:70:ILE:HG13	2.18	0.43
8:Z:225:VAL:HG21	8:Z:290:VAL:CG2	2.48	0.43
1:A:285:VAL:HA	1:A:306:MET:O	2.18	0.43
4:E:61:MET:O	4:E:69:THR:HB	2.19	0.43
7:Q:231:VAL:HG23	7:Q:311:MET:HB2	2.00	0.43
3:D:426:ALA:O	3:D:431:PRO:HD3	2.18	0.43
7:Q:140:HIS:CE1	7:Q:509:LYS:HB2	2.53	0.43
7:Q:140:HIS:HB3	7:Q:505:TYR:HE1	1.83	0.43
6:H:242:VAL:HG22	6:H:243:GLU:N	2.32	0.43
5:G:233:ILE:N	5:G:233:ILE:HD12	2.33	0.43
3:D:32:LYS:C	3:D:36:ILE:HG22	2.38	0.43
7:Q:221:MET:O	7:Q:363:PHE:HD1	2.01	0.43
1:A:137:ILE:N	1:A:408:VAL:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:232:ILE:HG21	2:B:235:ALA:HB2	1.98	0.43
2:B:288:ASN:HD22	2:B:288:ASN:N	2.16	0.43
3:D:241:ILE:HD11	3:D:324:LYS:HB3	2.01	0.43
2:B:83:VAL:O	2:B:87:MET:HG3	2.19	0.43
5:G:33:ILE:HD13	5:G:80:MET:HB2	2.00	0.43
1:A:446:PRO:O	1:A:450:ASN:HB2	2.19	0.43
7:Q:191:PHE:N	7:Q:192:PRO:HD2	2.33	0.43
6:H:176:ALA:O	6:H:180:VAL:HG23	2.18	0.43
4:E:369:ASP:O	4:E:370:LYS:C	2.56	0.43
4:E:329:GLU:O	4:E:333:ILE:HG13	2.19	0.43
8:Z:156:LEU:HD11	8:Z:168:LEU:HD22	2.01	0.43
5:G:49:MET:HG3	5:G:59:MET:CG	2.46	0.43
5:G:72:VAL:CG1	5:G:73:GLN:N	2.82	0.43
2:B:517:VAL:CG2	2:B:520:ILE:HD11	2.48	0.43
6:H:13:THR:HG22	6:H:13:THR:O	2.17	0.43
2:B:51:ILE:CG2	2:B:61:LEU:HG	2.48	0.43
3:D:217:LEU:CD1	3:D:401:ILE:HD12	2.49	0.43
5:G:396:GLN:HE22	5:G:399:ARG:HH11	1.66	0.43
3:D:192:ASP:HA	3:D:195:MET:CG	2.48	0.43
7:Q:414:ALA:HB1	7:Q:476:LYS:O	2.19	0.43
1:A:145:ARG:O	1:A:146:ASP:C	2.56	0.43
1:A:317:LYS:O	1:A:321:LYS:HG3	2.18	0.43
1:A:447:VAL:O	1:A:451:THR:HG23	2.18	0.43
8:Z:154:THR:HA	8:Z:157:ARG:CD	2.48	0.43
6:H:415:GLU:HG2	6:H:473:MET:HG3	2.00	0.43
1:A:278:ILE:HG21	1:A:286:ILE:HG12	2.00	0.43
7:Q:336:LEU:N	7:Q:336:LEU:HD12	2.34	0.43
1:A:39:VAL:HG21	1:A:455:ASN:O	2.19	0.43
8:Z:445:LEU:O	8:Z:448:PRO:HG2	2.18	0.43
3:D:540:ASN:HB3	3:D:542:ARG:CD	2.27	0.43
7:Q:246:PHE:HB2	7:Q:297:VAL:HA	2.01	0.43
5:G:49:MET:CE	5:G:57:ILE:HD13	2.49	0.43
5:G:316:ARG:HB2	5:G:319:ASP:OD2	2.18	0.43
6:H:51:ASP:C	6:H:53:ARG:H	2.22	0.43
6:H:352:GLN:HG2	6:H:357:ARG:CG	2.48	0.43
5:G:89:GLU:CD	5:G:389:ARG:HH22	2.21	0.43
8:Z:417:ALA:CA	8:Z:470:HIS:HE2	2.31	0.43
7:Q:204:VAL:CG1	7:Q:377:LEU:HG	2.49	0.43
8:Z:69:ILE:CG2	8:Z:74:ALA:HB3	2.49	0.43
6:H:127:THR:O	6:H:131:LEU:HG	2.19	0.43
1:A:357:CYS:O	1:A:358:ASP:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:497:ASN:HB3	8:Z:499:CYS:SG	2.59	0.43
3:D:162:ASP:HB3	3:D:165:THR:OG1	2.18	0.43
8:Z:378:GLY:CA	8:Z:384:LEU:HD21	2.47	0.43
2:B:10:ASN:O	4:E:85:HIS:N	2.51	0.43
6:H:189:LEU:O	6:H:190:LEU:O	2.37	0.43
3:D:170:ALA:HB3	3:D:187:SER:HB3	2.01	0.43
2:B:61:LEU:CD2	2:B:63:VAL:HG23	2.49	0.43
2:B:461:LEU:HD13	2:B:461:LEU:C	2.39	0.43
3:D:294:LYS:CD	3:D:325:ILE:HD11	2.48	0.43
2:B:131:ARG:HG3	2:B:131:ARG:HH11	1.83	0.43
2:B:127:ILE:HG23	2:B:512:GLU:HB3	2.01	0.43
6:H:194:MET:O	6:H:369:THR:HA	2.18	0.43
1:A:240:SER:HB3	1:A:290:GLY:HA3	2.01	0.43
1:A:104:ALA:O	1:A:108:VAL:HG23	2.19	0.43
1:A:17:ILE:HG21	1:A:528:ASP:O	2.18	0.43
5:G:71:GLN:CG	8:Z:8:ASN:HB2	2.49	0.43
2:B:352:VAL:HG23	2:B:354:ILE:HG13	2.00	0.43
1:A:220:VAL:CG1	1:A:225:MET:HG3	2.48	0.43
8:Z:233:CYS:SG	8:Z:336:LEU:HG	2.59	0.43
4:E:211:VAL:HG13	4:E:387:ILE:HD13	2.00	0.43
8:Z:355:LEU:HD22	8:Z:377:LYS:CE	2.49	0.43
4:E:249:ALA:HB2	4:E:297:ALA:CB	2.49	0.43
4:E:205:ASP:OD2	4:E:207:GLU:HB2	2.19	0.43
4:E:20:LYS:NZ	6:H:32:ILE:N	2.67	0.43
1:A:69:HIS:CE1	1:A:71:ALA:HB3	2.54	0.43
5:G:93:ASP:CG	5:G:94:GLY:N	2.72	0.43
4:E:112:LEU:HD21	4:E:517:ILE:HA	2.01	0.43
2:B:45:PRO:HA	2:B:169:SER:HA	2.01	0.43
5:G:49:MET:HE3	5:G:57:ILE:HD13	2.01	0.43
5:G:66:ILE:O	5:G:70:ILE:HG13	2.19	0.43
6:H:23:VAL:CA	6:H:109:LYS:HZ1	2.30	0.43
2:B:326:VAL:O	2:B:365:VAL:HB	2.18	0.43
1:A:43:LYS:HG2	5:G:520:ASP:CG	2.39	0.43
7:Q:146:LEU:HD22	7:Q:418:GLU:OE1	2.19	0.43
6:H:37:ARG:CG	6:H:448:GLN:HG2	2.49	0.43
6:H:101:ALA:O	6:H:105:LEU:HG	2.18	0.43
7:Q:165:HIS:HB2	7:Q:181:LYS:HD3	2.00	0.43
7:Q:85:MET:HA	7:Q:88:MET:CE	2.48	0.43
4:E:225:ILE:HG22	4:E:227:GLY:N	2.33	0.43
8:Z:235:VAL:HG22	8:Z:236:SER:N	2.34	0.43
3:D:28:GLN:HG2	3:D:29:ASP:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:33:PRO:O	3:D:536:ASP:OD1	2.36	0.43
2:B:11:ILE:CA	4:E:85:HIS:HB2	2.48	0.43
5:G:49:MET:CG	5:G:59:MET:HG2	2.46	0.43
2:B:218:PHE:CD1	2:B:326:VAL:HG21	2.54	0.43
5:G:462:LEU:HD11	5:G:480:VAL:HG22	2.00	0.43
6:H:54:GLY:O	6:H:55:LYS:C	2.56	0.43
6:H:520:ILE:HG21	7:Q:76:LEU:HD22	2.00	0.43
5:G:80:MET:HA	5:G:83:ILE:CD1	2.49	0.43
6:H:497:MET:HE2	6:H:501:ASN:HB2	2.00	0.43
3:D:212:LYS:HD2	3:D:230:LEU:HD11	2.01	0.43
5:G:245:LEU:HD12	5:G:296:ILE:CG1	2.49	0.43
8:Z:407:VAL:HG22	8:Z:495:TRP:CG	2.53	0.43
4:E:305:GLY:HA2	4:E:324:TRP:CE2	2.54	0.43
4:E:446:TYR:HD1	4:E:446:TYR:N	2.16	0.43
1:A:236:CYS:HB3	1:A:316:LEU:HD11	2.00	0.43
8:Z:380:ASN:HA	8:Z:380:ASN:HD22	1.66	0.43
6:H:471:GLY:HA3	6:H:475:TYR:CE1	2.53	0.43
8:Z:91:GLY:O	8:Z:92:THR:C	2.57	0.42
7:Q:41:GLN:HA	7:Q:44:ARG:HB2	2.00	0.42
1:A:20:GLN:HE21	5:G:7:VAL:N	2.17	0.42
3:D:131:ILE:HG12	3:D:449:MET:HE2	2.01	0.42
7:Q:89:ALA:HB1	7:Q:104:VAL:HG21	2.00	0.42
4:E:189:ALA:HA	4:E:406:LEU:HD21	1.99	0.42
1:A:2:GLU:O	1:A:3:GLY:O	2.36	0.42
6:H:228:GLN:CB	6:H:229:PRO:HD2	2.49	0.42
5:G:421:ALA:O	5:G:424:GLU:HB3	2.19	0.42
8:Z:76:LEU:O	8:Z:80:VAL:HG23	2.19	0.42
7:Q:225:LYS:CA	7:Q:313:VAL:HG22	2.44	0.42
1:A:12:SER:OG	1:A:17:ILE:HD13	2.19	0.42
3:D:226:LEU:CG	3:D:389:VAL:HB	2.49	0.42
5:G:40:CYS:HA	5:G:45:SER:HB2	2.00	0.42
8:Z:511:ILE:HA	8:Z:514:ASN:HD22	1.83	0.42
8:Z:8:ASN:CG	8:Z:9:PRO:HD2	2.40	0.42
6:H:16:SER:O	6:H:21:GLN:HB2	2.19	0.42
3:D:115:ILE:O	3:D:119:LEU:HG	2.20	0.42
3:D:170:ALA:HB1	3:D:187:SER:HA	2.00	0.42
3:D:416:ARG:O	3:D:420:LYS:HG3	2.19	0.42
3:D:515:LEU:HG	3:D:519:VAL:HG21	2.02	0.42
6:H:448:GLN:HG3	6:H:452:ASN:HD21	1.81	0.42
1:A:138:ILE:HG21	1:A:406:LYS:NZ	2.34	0.42
7:Q:351:TYR:HE2	7:Q:364:LYS:HE2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:194:ASP:HB3	5:G:399:ARG:HG3	2.01	0.42
7:Q:212:VAL:C	7:Q:214:SER:H	2.22	0.42
1:A:328:LEU:HD22	1:A:328:LEU:N	2.34	0.42
2:B:131:ARG:HG2	2:B:135:LYS:HE2	2.01	0.42
3:D:132:HIS:CD2	3:D:133:PRO:HD2	2.54	0.42
7:Q:408:LEU:CD1	7:Q:498:LEU:HD13	2.49	0.42
7:Q:201:ASN:HB3	7:Q:371:ALA:O	2.19	0.42
7:Q:358:THR:O	7:Q:358:THR:HG23	2.19	0.42
8:Z:101:GLU:O	8:Z:104:LYS:HB3	2.20	0.42
1:A:5:LEU:HD13	1:A:531:ILE:HG21	2.02	0.42
3:D:378:LYS:HE2	3:D:380:THR:CG2	2.49	0.42
6:H:110:PRO:HG2	6:H:111:TYR:HD1	1.84	0.42
1:A:137:ILE:HG22	1:A:137:ILE:O	2.19	0.42
6:H:168:ILE:HD11	6:H:175:PHE:CE1	2.55	0.42
4:E:62:VAL:HG22	4:E:68:VAL:HA	2.01	0.42
6:H:448:GLN:HE21	6:H:452:ASN:CG	2.21	0.42
6:H:348:PHE:HE2	6:H:361:PHE:CE2	2.38	0.42
2:B:187:VAL:HG11	2:B:397:LEU:HB3	2.00	0.42
8:Z:217:ARG:HG2	8:Z:302:LEU:CD2	2.49	0.42
7:Q:93:GLN:NE2	7:Q:97:VAL:HG22	2.34	0.42
7:Q:148:CYS:HB2	7:Q:476:LYS:HZ2	1.83	0.42
2:B:414:GLU:HB3	2:B:443:LEU:O	2.19	0.42
2:B:243:GLY:HA2	2:B:292:ASN:OD1	2.20	0.42
3:D:99:LYS:O	3:D:103:ILE:HG13	2.19	0.42
1:A:242:GLN:HG3	1:A:291:GLY:O	2.19	0.42
8:Z:415:GLU:N	8:Z:415:GLU:OE1	2.44	0.42
8:Z:35:ARG:HG3	8:Z:450:VAL:CG1	2.49	0.42
7:Q:524:ILE:HG21	8:Z:46:MET:N	2.24	0.42
4:E:520:ALA:O	4:E:524:VAL:HG23	2.19	0.42
5:G:37:ILE:O	5:G:40:CYS:HB2	2.20	0.42
5:G:72:VAL:HG22	8:Z:6:THR:CG2	2.47	0.42
7:Q:168:VAL:HA	7:Q:173:TYR:OH	2.19	0.42
3:D:477:ILE:H	3:D:477:ILE:CD1	2.28	0.42
1:A:176:VAL:HG22	1:A:190:TYR:CZ	2.55	0.42
8:Z:196:MET:SD	8:Z:197:LYS:N	2.92	0.42
4:E:115:ALA:CB	4:E:457:VAL:HG11	2.50	0.42
1:A:136:LEU:O	1:A:138:ILE:N	2.52	0.42
6:H:294:PRO:HG3	6:H:313:ARG:CD	2.49	0.42
6:H:348:PHE:HE2	6:H:361:PHE:CZ	2.37	0.42
2:B:465:LEU:O	2:B:469:HIS:HB2	2.19	0.42
6:H:414:MET:HE3	6:H:464:LEU:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:185:PHE:CZ	5:G:370:LYS:HB3	2.54	0.42
3:D:340:CYS:HB2	3:D:347:PRO:HD3	2.00	0.42
1:A:233:LYS:HB3	1:A:345:LEU:HB3	2.00	0.42
4:E:532:ASP:O	6:H:47:LYS:HD2	2.19	0.42
4:E:52:LEU:HD12	4:E:53:GLY:H	1.84	0.42
3:D:36:ILE:CD1	3:D:40:ASN:HD21	2.32	0.42
2:B:10:ASN:H	4:E:85:HIS:CD2	2.37	0.42
8:Z:9:PRO:O	8:Z:10:LYS:HB2	2.20	0.42
5:G:27:ILE:HG23	5:G:106:LEU:CB	2.45	0.42
2:B:520:ILE:HG22	2:B:521:ILE:N	2.35	0.42
3:D:186:LEU:HA	3:D:189:MET:HE3	2.02	0.42
7:Q:187:CYS:C	7:Q:189:SER:H	2.22	0.42
4:E:535:LYS:HA	4:E:536:PRO:HD2	1.93	0.42
5:G:101:LEU:O	5:G:105:MET:HG3	2.19	0.42
2:B:96:GLY:O	2:B:97:ASP:O	2.37	0.42
2:B:203:LYS:HA	2:B:383:LEU:HD11	2.00	0.42
5:G:49:MET:N	8:Z:518:VAL:HG13	2.34	0.42
6:H:237:ILE:HG21	6:H:328:GLY:HA3	2.01	0.42
6:H:51:ASP:O	6:H:53:ARG:N	2.47	0.42
2:B:95:VAL:O	2:B:392:ASP:HB3	2.19	0.42
3:D:217:LEU:CD1	3:D:398:LYS:HG3	2.45	0.42
5:G:368:ASP:C	5:G:370:LYS:H	2.23	0.42
2:B:231:ARG:HE	2:B:348:LEU:HD11	1.84	0.42
2:B:478:LEU:HD12	2:B:479:ASP:H	1.84	0.42
2:B:418:ALA:O	2:B:440:ALA:HB1	2.20	0.42
5:G:356:GLY:O	5:G:357:ASP:HB2	2.19	0.42
2:B:181:LYS:O	2:B:185:GLU:HB2	2.20	0.42
6:H:374:LEU:HB3	6:H:382:MET:CE	2.50	0.42
8:Z:91:GLY:O	8:Z:93:THR:N	2.52	0.42
8:Z:97:LEU:N	8:Z:97:LEU:HD12	2.35	0.42
8:Z:55:LYS:CE	8:Z:62:VAL:HG11	2.50	0.42
3:D:378:LYS:HE2	3:D:380:THR:HG21	2.02	0.42
2:B:219:LEU:HD22	2:B:374:VAL:HG21	2.02	0.42
1:A:222:SER:HG	1:A:301:VAL:HG22	1.85	0.42
4:E:248:ILE:CD1	4:E:337:THR:HG21	2.50	0.42
2:B:186:ALA:O	2:B:190:LEU:HD13	2.18	0.42
2:B:244:MET:O	2:B:300:PRO:HG2	2.20	0.42
6:H:165:SER:HB3	6:H:480:ASN:CB	2.48	0.42
7:Q:379:GLY:N	7:Q:385:MET:SD	2.93	0.42
1:A:326:THR:HB	1:A:344:MET:HB3	2.02	0.42
5:G:354:LYS:HA	5:G:359:TYR:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:132:ARG:CG	4:E:443:LEU:HG	2.50	0.42
1:A:450:ASN:O	1:A:454:VAL:HG23	2.19	0.42
4:E:304:TRP:HB3	4:E:305:GLY:H	1.74	0.42
1:A:311:VAL:HG12	1:A:315:ASP:HB2	2.01	0.42
1:A:169:ALA:O	1:A:173:VAL:HG23	2.20	0.42
8:Z:450:VAL:O	8:Z:453:GLN:HB3	2.18	0.42
1:A:376:ILE:N	1:A:376:ILE:HD13	2.35	0.42
2:B:75:GLY:N	3:D:541:THR:OG1	2.51	0.42
5:G:144:VAL:HG11	5:G:407:LEU:HD21	2.01	0.42
7:Q:156:ASP:OD2	7:Q:158:ASP:HB2	2.20	0.42
8:Z:297:ILE:HG13	8:Z:314:ARG:HB3	2.02	0.42
4:E:234:PHE:HE2	4:E:240:PRO:O	2.03	0.42
7:Q:179:LEU:HG	7:Q:183:ILE:HD11	2.01	0.42
6:H:313:ARG:CG	6:H:313:ARG:HH11	2.18	0.42
4:E:362:ILE:HB	4:E:364:PHE:HE1	1.77	0.42
6:H:136:ILE:HG21	6:H:500:ILE:HG13	2.01	0.42
1:A:97:ALA:HA	1:A:100:LEU:HD12	2.01	0.42
2:B:31:GLY:O	2:B:35:ILE:HG12	2.20	0.42
7:Q:59:HIS:CD2	7:Q:59:HIS:H	2.38	0.42
6:H:103:GLU:OE2	6:H:106:LYS:HD3	2.20	0.42
7:Q:25:LEU:HD22	7:Q:26:GLU:OE1	2.20	0.42
1:A:159:LYS:HB2	1:A:161:ILE:HG22	2.01	0.42
7:Q:13:GLN:CD	8:Z:72:PRO:HD2	2.40	0.42
5:G:23:GLN:HG3	5:G:24:SER:H	1.84	0.42
4:E:189:ALA:O	4:E:193:VAL:HG23	2.20	0.42
5:G:285:LEU:HD22	5:G:339:ARG:C	2.39	0.42
3:D:41:ILE:HG21	3:D:124:THR:CG2	2.49	0.42
7:Q:142:ILE:HD13	7:Q:422:GLN:CB	2.50	0.42
5:G:105:MET:HE2	5:G:105:MET:HB3	1.71	0.42
2:B:171:LEU:HD21	2:B:382:ILE:HG12	2.02	0.42
2:B:373:ILE:HG21	2:B:390:LEU:HD21	2.02	0.42
5:G:77:ALA:O	5:G:80:MET:HB2	2.20	0.42
5:G:83:ILE:HG23	5:G:508:THR:HG22	2.02	0.42
1:A:483:LEU:HD12	1:A:485:TRP:CZ2	2.55	0.42
1:A:115:THR:HG21	3:D:471:ASN:O	2.19	0.42
5:G:296:ILE:CG1	5:G:313:ARG:HB3	2.49	0.42
2:B:139:GLN:HA	2:B:142:LEU:HD12	2.01	0.42
3:D:182:TYR:CD2	3:D:221:ILE:HB	2.54	0.42
8:Z:446:ILE:HG23	8:Z:447:ILE:N	2.34	0.42
3:D:37:ARG:NE	3:D:536:ASP:OD2	2.53	0.42
8:Z:195:GLU:HB2	8:Z:384:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:LEU:HD21	3:D:63:MET:HB3	2.02	0.42
1:A:2:GLU:OE2	3:D:44:ALA:N	2.39	0.42
4:E:156:LEU:CD2	4:E:161:ASN:HB3	2.47	0.42
1:A:136:LEU:HB3	1:A:407:SER:HB3	2.01	0.42
1:A:507:THR:O	1:A:511:VAL:HG23	2.20	0.42
6:H:238:ALA:HB2	6:H:286:ALA:CB	2.44	0.42
7:Q:333:LEU:HD21	7:Q:343:GLU:CG	2.49	0.42
7:Q:401:VAL:O	7:Q:405:ASP:N	2.53	0.42
8:Z:131:LEU:HD21	8:Z:505:LEU:HB2	2.02	0.42
8:Z:413:ALA:HA	8:Z:477:VAL:O	2.18	0.42
6:H:460:ILE:CG2	6:H:461:LEU:N	2.82	0.42
1:A:445:LEU:C	1:A:447:VAL:H	2.23	0.42
5:G:153:LEU:HD13	5:G:177:LEU:HD12	2.02	0.42
7:Q:124:SER:O	7:Q:128:VAL:HG23	2.19	0.42
8:Z:176:ILE:HD11	8:Z:395:LEU:CB	2.49	0.41
8:Z:228:ALA:HB1	8:Z:290:VAL:HG23	1.99	0.41
5:G:202:GLU:O	5:G:375:LEU:HA	2.20	0.41
5:G:285:LEU:HD22	5:G:339:ARG:CA	2.50	0.41
3:D:137:SER:HA	3:D:533:LEU:HD12	2.02	0.41
3:D:213:ILE:HD11	3:D:412:LEU:CD1	2.46	0.41
8:Z:352:GLU:CG	8:Z:359:LYS:HB3	2.50	0.41
3:D:439:LEU:HB2	3:D:458:ALA:HB2	2.01	0.41
6:H:522:ASN:ND2	7:Q:75:GLU:O	2.52	0.41
7:Q:502:LEU:HD12	7:Q:502:LEU:HA	1.87	0.41
8:Z:134:LEU:CD2	8:Z:414:VAL:HG11	2.50	0.41
8:Z:476:LEU:HD22	8:Z:490:ALA:HB2	2.01	0.41
7:Q:356:GLY:O	7:Q:357:ASP:CB	2.67	0.41
3:D:132:HIS:HB3	3:D:135:ILE:HD12	2.02	0.41
1:A:381:ASN:HB2	1:A:384:MET:SD	2.60	0.41
3:D:104:GLU:OE1	3:D:524:LEU:HD11	2.19	0.41
1:A:73:LYS:O	1:A:76:CYS:HB2	2.19	0.41
4:E:147:HIS:O	4:E:150:LYS:HB3	2.20	0.41
8:Z:177:LEU:O	8:Z:177:LEU:HD23	2.20	0.41
8:Z:412:GLY:HA2	8:Z:415:GLU:OE1	2.20	0.41
8:Z:331:ILE:HB	8:Z:343:CYS:SG	2.60	0.41
3:D:197:VAL:HG21	3:D:211:ILE:HD11	2.02	0.41
3:D:123:CYS:SG	3:D:136:ILE:HG21	2.60	0.41
1:A:176:VAL:HG21	1:A:399:VAL:HG11	2.02	0.41
8:Z:352:GLU:HG2	8:Z:359:LYS:HB3	2.02	0.41
8:Z:350:VAL:HG22	8:Z:363:ILE:HG23	2.01	0.41
3:D:256:LEU:HD13	3:D:312:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:432:GLU:N	3:D:432:GLU:CD	2.73	0.41
3:D:371:ASN:ND2	3:D:394:ARG:HD3	2.36	0.41
5:G:245:LEU:HD12	5:G:296:ILE:HD13	2.02	0.41
3:D:346:LYS:HD2	3:D:358:MET:SD	2.60	0.41
7:Q:281:LYS:HA	7:Q:308:TYR:HE2	1.84	0.41
4:E:343:PRO:HG2	4:E:347:GLU:HG3	2.02	0.41
8:Z:70:GLN:O	8:Z:72:PRO:HD3	2.20	0.41
1:A:220:VAL:HG12	1:A:225:MET:HG3	2.02	0.41
5:G:394:ALA:O	5:G:397:VAL:HG22	2.20	0.41
1:A:2:GLU:N	3:D:88:HIS:HB3	2.35	0.41
7:Q:423:ILE:O	7:Q:426:TYR:HB3	2.20	0.41
1:A:507:THR:HG23	1:A:508:ILE:N	2.36	0.41
5:G:289:VAL:HG12	5:G:310:THR:HB	2.02	0.41
1:A:484:LYS:O	1:A:486:ILE:N	2.46	0.41
1:A:328:LEU:HD21	1:A:344:MET:CB	2.48	0.41
6:H:198:LYS:HZ3	6:H:217:LYS:HE3	1.85	0.41
3:D:232:LEU:HD21	3:D:339:ILE:CD1	2.47	0.41
3:D:343:ILE:HG12	3:D:382:CYS:SG	2.60	0.41
4:E:344:ARG:HG3	4:E:345:PHE:N	2.35	0.41
4:E:417:ARG:NH1	4:E:417:ARG:HG3	2.35	0.41
7:Q:415:THR:O	7:Q:419:LEU:HG	2.19	0.41
4:E:129:HIS:HA	4:E:130:PRO:HD3	1.95	0.41
2:B:367:LEU:O	2:B:369:GLU:N	2.54	0.41
7:Q:130:GLU:O	7:Q:134:ILE:HG13	2.18	0.41
5:G:243:SER:OG	5:G:335:PRO:HD3	2.21	0.41
8:Z:374:LEU:CD2	8:Z:391:ILE:HD13	2.47	0.41
7:Q:353:SER:OG	7:Q:360:VAL:HG23	2.20	0.41
4:E:466:SER:HB3	4:E:493:CYS:HG	1.84	0.41
5:G:71:GLN:H	8:Z:524:ALA:CB	2.32	0.41
8:Z:7:LEU:HD21	8:Z:522:MET:HB3	2.02	0.41
2:B:365:VAL:O	2:B:366:ALA:C	2.59	0.41
5:G:416:MET:HE2	5:G:466:LEU:HD13	2.02	0.41
6:H:391:ASP:HA	6:H:394:MET:HG3	2.02	0.41
3:D:411:ALA:O	3:D:415:ILE:HG13	2.19	0.41
3:D:421:LYS:CE	3:D:515:LEU:HD23	2.42	0.41
3:D:237:ALA:CA	3:D:317:LEU:HD11	2.49	0.41
6:H:37:ARG:HD2	6:H:99:LEU:HD11	2.02	0.41
1:A:138:ILE:HG21	1:A:406:LYS:HZ1	1.85	0.41
5:G:238:ILE:HD13	5:G:323:ILE:CG2	2.40	0.41
5:G:130:LEU:HD11	5:G:507:LYS:CD	2.43	0.41
2:B:97:ASP:C	2:B:99:THR:N	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:142:LYS:HZ2	3:D:446:LEU:HD21	1.85	0.41
6:H:415:GLU:O	6:H:418:LYS:HB3	2.20	0.41
1:A:420:SER:HA	1:A:442:ALA:HB1	2.01	0.41
8:Z:13:VAL:HG22	8:Z:522:MET:CG	2.45	0.41
8:Z:225:VAL:HG22	8:Z:311:ILE:HG12	2.03	0.41
7:Q:147:VAL:HG21	7:Q:501:TYR:HB2	2.02	0.41
4:E:145:ILE:HA	4:E:145:ILE:HD13	1.94	0.41
4:E:25:LYS:HB3	4:E:26:SER:H	1.68	0.41
5:G:149:ARG:CG	5:G:177:LEU:HD11	2.50	0.41
4:E:41:ALA:O	4:E:42:LYS:C	2.58	0.41
7:Q:191:PHE:CE1	7:Q:197:PHE:HE1	2.38	0.41
3:D:151:LEU:HD21	3:D:435:LEU:CD1	2.49	0.41
8:Z:73:THR:O	8:Z:76:LEU:HB2	2.19	0.41
1:A:77:GLU:O	1:A:81:LEU:HG	2.21	0.41
1:A:234:ILE:HD11	1:A:364:ILE:HG21	2.03	0.41
1:A:137:ILE:HG23	1:A:499:LYS:CE	2.49	0.41
3:D:173:SER:HB2	3:D:414:VAL:HG11	2.02	0.41
1:A:356:ILE:HD12	1:A:361:LEU:HB2	2.02	0.41
1:A:107:LEU:O	1:A:110:GLN:HB2	2.21	0.41
3:D:98:SER:HB2	3:D:109:THR:HG22	2.02	0.41
3:D:345:THR:HB	3:D:360:GLY:HA3	2.02	0.41
8:Z:426:LYS:HB2	8:Z:434:GLN:HG2	2.02	0.41
4:E:416:ASN:C	4:E:417:ARG:HG2	2.40	0.41
5:G:119:PRO:O	5:G:122:VAL:HB	2.20	0.41
2:B:477:GLY:HA3	2:B:488:MET:CG	2.51	0.41
3:D:118:SER:OG	3:D:460:ALA:HB1	2.20	0.41
2:B:26:LEU:O	2:B:30:ILE:HG13	2.20	0.41
2:B:521:ILE:HG13	4:E:61:MET:CE	2.51	0.41
1:A:356:ILE:CD1	1:A:361:LEU:HB2	2.50	0.41
4:E:459:PRO:HA	4:E:462:LEU:CD1	2.51	0.41
6:H:231:LYS:HE3	6:H:347:VAL:HG13	2.03	0.41
3:D:252:ILE:HB	3:D:303:ILE:CD1	2.46	0.41
2:B:297:TYR:HB3	2:B:300:PRO:CD	2.50	0.41
5:G:383:ILE:HG22	5:G:383:ILE:O	2.21	0.41
5:G:523:VAL:HG12	5:G:524:SER:H	1.85	0.41
5:G:467:ARG:HG3	5:G:467:ARG:NH1	2.36	0.41
1:A:62:LEU:HD12	1:A:79:ALA:CB	2.51	0.41
5:G:440:VAL:O	5:G:443:ALA:HB3	2.20	0.41
4:E:35:LYS:CA	4:E:38:ILE:HD12	2.46	0.41
7:Q:327:THR:HG22	7:Q:366:GLU:OE2	2.20	0.41
3:D:186:LEU:HD23	3:D:189:MET:CE	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:PHE:O	1:A:172:VAL:HG23	2.21	0.41
1:A:508:ILE:HG23	1:A:509:VAL:N	2.36	0.41
6:H:346:GLN:HG3	6:H:347:VAL:HG23	2.03	0.41
2:B:189:ARG:HH11	2:B:189:ARG:HB3	1.86	0.41
2:B:94:GLU:HA	2:B:94:GLU:OE1	2.20	0.41
6:H:464:LEU:HD13	6:H:476:GLY:O	2.21	0.41
6:H:464:LEU:HA	6:H:484:ILE:HG21	2.02	0.41
1:A:484:LYS:C	1:A:486:ILE:H	2.24	0.41
5:G:399:ARG:NH1	5:G:399:ARG:HG2	2.36	0.41
1:A:448:ILE:HB	1:A:449:PRO:HD3	2.03	0.41
5:G:168:TRP:CZ3	5:G:210:GLU:HB2	2.56	0.41
5:G:236:PRO:HA	5:G:288:ASP:OD2	2.21	0.41
4:E:378:LYS:HB2	4:E:378:LYS:HE3	1.90	0.41
8:Z:109:TYR:HA	8:Z:112:GLU:OE1	2.20	0.41
7:Q:525:ILE:HG13	7:Q:526:MET:N	2.35	0.41
7:Q:526:MET:O	7:Q:527:ALA:HB2	2.21	0.41
8:Z:374:LEU:HD22	8:Z:391:ILE:HG21	2.02	0.41
5:G:46:MET:O	5:G:48:LYS:NZ	2.53	0.41
8:Z:520:GLU:C	8:Z:521:ILE:HD12	2.41	0.41
4:E:104:ASP:OD2	4:E:408:VAL:HG12	2.21	0.41
3:D:41:ILE:HG23	3:D:120:LEU:CB	2.47	0.41
3:D:179:VAL:HG11	3:D:404:ALA:HA	2.00	0.41
3:D:206:VAL:HG23	3:D:419:VAL:HG21	2.00	0.41
1:A:172:VAL:HG12	1:A:399:VAL:HG21	2.01	0.41
1:A:403:LEU:HD12	1:A:403:LEU:HA	1.80	0.41
4:E:247:LYS:HD2	4:E:296:GLY:O	2.21	0.41
4:E:457:VAL:HG23	4:E:458:ILE:H	1.84	0.41
5:G:447:ILE:N	5:G:448:PRO:HD2	2.35	0.41
2:B:209:LEU:HD11	2:B:382:ILE:HG23	2.02	0.41
6:H:65:ILE:O	6:H:69:LEU:HG	2.21	0.41
3:D:111:SER:O	3:D:112:VAL:C	2.59	0.41
7:Q:97:VAL:HG12	7:Q:401:VAL:HG22	2.03	0.41
1:A:230:VAL:O	1:A:232:ALA:N	2.54	0.41
6:H:416:LEU:O	6:H:420:LEU:HG	2.21	0.41
3:D:249:ILE:HG13	3:D:343:ILE:HG21	2.03	0.41
2:B:238:LEU:CD2	2:B:287:ILE:HG21	2.51	0.41
6:H:435:ILE:O	6:H:438:TYR:HB3	2.20	0.41
4:E:481:GLN:NE2	4:E:487:PRO:HB3	2.36	0.41
3:D:371:ASN:HD22	3:D:394:ARG:NE	2.16	0.41
7:Q:155:ARG:HA	7:Q:155:ARG:HD3	1.82	0.41
5:G:117:MET:O	5:G:118:HIS:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:486:ASP:OD1	6:H:488:PHE:HB3	2.21	0.41
7:Q:504:LYS:O	7:Q:507:ALA:HB3	2.21	0.41
1:A:369:ALA:C	1:A:371:THR:N	2.74	0.41
4:E:95:SER:HB2	4:E:106:THR:CG2	2.50	0.41
4:E:518:SER:CA	4:E:522:GLN:HE21	2.34	0.41
8:Z:325:THR:HB	8:Z:330:GLY:O	2.21	0.41
5:G:504:GLN:HA	5:G:504:GLN:HE21	1.86	0.41
4:E:252:THR:HG23	4:E:303:GLN:OE1	2.21	0.41
7:Q:126:SER:CB	8:Z:41:LYS:HD3	2.51	0.41
2:B:521:ILE:HG12	4:E:61:MET:SD	2.60	0.41
6:H:214:VAL:HA	6:H:371:THR:OG1	2.21	0.41
5:G:208:ILE:HG13	5:G:210:GLU:H	1.86	0.41
8:Z:422:LEU:HB3	8:Z:437:VAL:CG1	2.51	0.41
2:B:437:GLU:HG3	2:B:441:LYS:HE3	2.03	0.41
1:A:105:ASP:O	1:A:109:LYS:N	2.50	0.40
4:E:441:PRO:O	4:E:442:THR:O	2.39	0.40
4:E:527:ILE:H	4:E:527:ILE:HG13	1.53	0.40
6:H:168:ILE:HG13	6:H:168:ILE:O	2.21	0.40
3:D:237:ALA:CB	3:D:327:VAL:HG12	2.49	0.40
8:Z:194:MET:HE1	8:Z:360:PHE:HE2	1.85	0.40
2:B:133:ALA:HB1	2:B:421:VAL:HG11	2.02	0.40
4:E:237:PRO:O	4:E:239:MET:N	2.54	0.40
7:Q:475:ASN:O	7:Q:476:LYS:C	2.59	0.40
3:D:332:GLU:HB3	3:D:335:ASP:OD2	2.21	0.40
3:D:345:THR:O	3:D:345:THR:HG23	2.21	0.40
6:H:117:HIS:HA	6:H:118:PRO:HD3	1.93	0.40
2:B:414:GLU:OE1	2:B:414:GLU:HA	2.21	0.40
7:Q:197:PHE:HB3	7:Q:403:THR:HG21	2.04	0.40
8:Z:407:VAL:HG23	8:Z:495:TRP:HB3	2.03	0.40
2:B:441:LYS:HA	2:B:444:ARG:HE	1.87	0.40
1:A:354:GLU:HG3	1:A:363:LEU:HD12	2.02	0.40
3:D:507:LEU:HD12	3:D:512:VAL:HG12	2.03	0.40
3:D:540:ASN:C	3:D:542:ARG:H	2.24	0.40
4:E:524:VAL:HA	4:E:527:ILE:HD12	2.04	0.40
5:G:46:MET:CE	8:Z:517:LEU:HA	2.52	0.40
1:A:137:ILE:O	1:A:408:VAL:HG12	2.21	0.40
5:G:470:HIS:CE1	5:G:476:GLU:HG3	2.56	0.40
2:B:517:VAL:HA	4:E:58:ASP:O	2.21	0.40
2:B:161:ASN:O	2:B:165:THR:HG23	2.21	0.40
4:E:248:ILE:CG1	4:E:299:LEU:HD23	2.50	0.40
1:A:136:LEU:HB3	1:A:407:SER:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:LEU:HD23	1:A:533:LEU:H	1.86	0.40
4:E:142:ARG:NH2	6:H:167:LEU:HD13	2.36	0.40
6:H:420:LEU:HB2	6:H:439:ALA:HB2	2.03	0.40
7:Q:174:GLY:CA	7:Q:177:VAL:HG13	2.48	0.40
2:B:414:GLU:HG3	2:B:446:LEU:HD22	2.03	0.40
1:A:460:SER:O	1:A:464:VAL:HG23	2.22	0.40
1:A:44:MET:SD	1:A:52:VAL:HG13	2.62	0.40
6:H:71:VAL:HG12	6:H:77:LYS:HG2	2.03	0.40
7:Q:508:ILE:H	7:Q:508:ILE:HD12	1.86	0.40
3:D:169:SER:CB	3:D:418:LEU:HD22	2.51	0.40
4:E:363:SER:HB3	4:E:370:LYS:HG3	2.03	0.40
6:H:241:ASN:HB2	6:H:332:THR:HA	2.02	0.40
4:E:430:ALA:O	4:E:452:ALA:HB1	2.21	0.40
8:Z:91:GLY:O	8:Z:94:SER:N	2.54	0.40
1:A:11:ARG:CB	1:A:531:ILE:HG12	2.51	0.40
6:H:19:ILE:O	6:H:23:VAL:HG23	2.20	0.40
2:B:111:ARG:HG3	2:B:114:GLU:OE2	2.21	0.40
3:D:416:ARG:NH1	3:D:420:LYS:HZ2	2.18	0.40
3:D:300:VAL:HG13	3:D:326:MET:SD	2.61	0.40
6:H:323:MET:HA	6:H:328:GLY:O	2.20	0.40
4:E:25:LYS:NZ	4:E:536:PRO:HB3	2.33	0.40
5:G:104:GLU:HG2	5:G:446:VAL:CG1	2.48	0.40
3:D:142:LYS:NZ	3:D:446:LEU:HD21	2.37	0.40
8:Z:404:ASP:C	8:Z:406:CYS:H	2.24	0.40
2:B:191:LYS:HZ3	2:B:401:VAL:HG12	1.86	0.40
7:Q:448:ILE:N	7:Q:449:PRO:HD2	2.36	0.40
7:Q:491:ASP:OD1	7:Q:493:LEU:HB3	2.22	0.40
1:A:441:PHE:O	1:A:445:LEU:HG	2.21	0.40
5:G:275:ILE:HD13	5:G:299:LEU:HD12	2.04	0.40
4:E:215:VAL:HB	4:E:392:LYS:HE3	2.04	0.40
2:B:223:LYS:CE	2:B:360:ILE:HD12	2.51	0.40
3:D:151:LEU:HD21	3:D:435:LEU:CG	2.51	0.40
3:D:506:ILE:HG23	3:D:511:VAL:HB	2.04	0.40
3:D:254:PHE:HB2	3:D:350:HIS:HA	2.04	0.40
7:Q:521:VAL:HG12	7:Q:524:ILE:HD13	2.02	0.40
3:D:32:LYS:HZ3	3:D:32:LYS:HB3	1.86	0.40
1:A:2:GLU:HB3	3:D:91:ALA:N	2.36	0.40
4:E:240:PRO:HD2	4:E:320:PRO:HD3	2.04	0.40
6:H:238:ALA:CB	6:H:286:ALA:HB1	2.42	0.40
5:G:447:ILE:HB	5:G:448:PRO:HD3	2.04	0.40
2:B:172:LEU:HD13	2:B:209:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:465:LEU:HD12	2:B:485:ILE:CD1	2.51	0.40
5:G:347:ALA:HB3	5:G:365:GLU:CB	2.44	0.40
7:Q:231:VAL:HG22	7:Q:309:ASN:O	2.21	0.40
4:E:225:ILE:CG2	4:E:375:GLU:HB3	2.52	0.40
6:H:398:ARG:HB3	6:H:495:PRO:HG3	2.03	0.40
8:Z:142:GLU:C	8:Z:144:ASP:N	2.73	0.40
8:Z:23:ASN:HD22	8:Z:23:ASN:N	2.19	0.40
8:Z:520:GLU:OE1	8:Z:522:MET:HG3	2.22	0.40
8:Z:324:LEU:HD12	8:Z:324:LEU:O	2.22	0.40
7:Q:160:VAL:CG1	7:Q:185:GLN:HG2	2.50	0.40
5:G:203:LYS:HB2	5:G:384:LEU:CD1	2.52	0.40
3:D:421:LYS:C	3:D:423:ALA:H	2.25	0.40
8:Z:355:LEU:HD11	8:Z:362:PHE:HZ	1.87	0.40
6:H:351:THR:OG1	6:H:360:PHE:HE2	2.05	0.40
1:A:385:CYS:O	1:A:389:GLU:HB2	2.22	0.40
6:H:361:PHE:CD1	6:H:361:PHE:N	2.89	0.40
6:H:6:VAL:O	6:H:7:ILE:HB	2.22	0.40
7:Q:66:THR:HG21	7:Q:71:THR:CG2	2.51	0.40
5:G:165:ILE:HD11	5:G:172:ALA:CB	2.51	0.40
7:Q:188:VAL:HG11	7:Q:399:PHE:CD1	2.55	0.40
6:H:126:ARG:HH11	6:H:126:ARG:HG3	1.87	0.40
2:B:102:VAL:HA	2:B:503:VAL:HG13	2.03	0.40
8:Z:407:VAL:HG22	8:Z:495:TRP:HB3	2.03	0.40
2:B:242:THR:HA	2:B:294:GLN:NE2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	471/556 (85%)	390 (83%)	63 (13%)	18 (4%)	4 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	351/556 (63%)	283 (81%)	50 (14%)	18 (5%)	2	29
2	B	473/535 (88%)	398 (84%)	62 (13%)	13 (3%)	6	44
2	b	353/535 (66%)	301 (85%)	42 (12%)	10 (3%)	6	44
3	D	469/542 (86%)	385 (82%)	70 (15%)	14 (3%)	5	42
3	d	351/542 (65%)	300 (86%)	42 (12%)	9 (3%)	7	45
4	E	471/541 (87%)	392 (83%)	60 (13%)	19 (4%)	4	35
4	e	351/541 (65%)	295 (84%)	39 (11%)	17 (5%)	3	31
5	G	471/545 (86%)	396 (84%)	62 (13%)	13 (3%)	6	44
5	g	351/545 (64%)	291 (83%)	51 (14%)	9 (3%)	7	45
6	H	473/543 (87%)	384 (81%)	73 (15%)	16 (3%)	5	40
6	h	353/543 (65%)	289 (82%)	54 (15%)	10 (3%)	6	44
7	Q	473/548 (86%)	406 (86%)	45 (10%)	22 (5%)	3	32
7	q	351/548 (64%)	292 (83%)	48 (14%)	11 (3%)	5	42
8	Z	473/531 (89%)	400 (85%)	57 (12%)	16 (3%)	5	40
8	z	473/531 (89%)	403 (85%)	57 (12%)	13 (3%)	6	44
All	All	6708/8682 (77%)	5605 (84%)	875 (13%)	228 (3%)	5	40

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	GLY
1	A	145	ARG
1	A	146	ASP
1	A	230	VAL
2	B	54	SER
2	B	97	ASP
2	B	193	SER
2	B	519	ASN
3	D	33	PRO
4	E	63	ASP
4	E	244	GLU
4	E	441	PRO
5	G	148	ASN
5	G	333	SER
5	G	519	ILE
6	H	190	LEU
6	H	233	HIS

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Mol	Chain	Res	Type
6	H	237	ILE
7	Q	235	LYS
7	Q	476	LYS
7	Q	497	VAL
7	Q	526	MET
7	Q	527	ALA
8	Z	226	GLU
8	Z	379	PRO
1	a	1004	PRO
1	a	1011	ARG
1	a	1047	ASP
1	a	1533	LEU
2	b	1018	GLU
2	b	1054	SER
2	b	1148	HIS
4	e	1063	ASP
6	h	1018	GLY
6	h	1189	LEU
6	h	1190	LEU
7	q	1015	LEU
7	q	1016	LYS
8	z	1016	ALA
8	z	1050	GLY
8	z	1051	ALA
8	z	1157	ARG
8	z	1522	MET
1	A	48	ASP
1	A	459	ASP
1	A	485	TRP
2	B	429	PRO
2	B	506	SER
4	E	237	PRO
4	E	242	GLN
4	E	248	ILE
4	E	343	PRO
4	E	370	LYS
4	E	390	GLY
4	E	415	ASP
4	E	442	THR
5	G	11	SER
5	G	45	SER
5	G	93	ASP

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Mol	Chain	Res	Type
5	G	349	LEU
5	G	359	TYR
5	G	468	ALA
5	G	523	VAL
5	G	524	SER
6	H	227	MET
6	H	367	ALA
6	H	498	VAL
7	Q	17	GLU
7	Q	334	PRO
7	Q	475	ASN
7	Q	487	PRO
7	Q	521	VAL
8	Z	407	VAL
8	Z	522	MET
1	a	1006	SER
1	a	1158	SER
1	a	1485	TRP
2	b	1046	LYS
2	b	1168	SER
2	b	1508	ALA
2	b	1523	ALA
3	d	1498	VAL
4	e	1104	ASP
4	e	1177	VAL
4	e	1390	GLY
4	e	1442	THR
4	e	1533	ILE
5	g	1008	LEU
5	g	1011	SER
5	g	1162	THR
5	g	1371	ALA
6	h	1372	ILE
6	h	1507	SER
7	q	1188	VAL
7	q	1487	PRO
8	z	1017	GLN
1	A	461	THR
2	B	233	GLU
2	B	333	SER
2	B	508	ALA
3	D	42	SER

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Mol	Chain	Res	Type
3	D	66	ASP
3	D	109	THR
3	D	249	ILE
3	D	541	THR
4	E	154	SER
4	E	238	GLN
4	E	518	SER
6	H	55	LYS
7	Q	60	LEU
7	Q	169	MET
7	Q	405	ASP
7	Q	525	ILE
8	Z	51	ALA
8	Z	510	VAL
1	a	1088	ASP
1	a	1146	ASP
3	d	1541	THR
4	e	1023	ASP
4	e	1441	PRO
4	e	1518	SER
5	g	1148	ASN
6	h	1051	ASP
7	q	1019	ALA
8	z	1335	SER
1	A	88	ASP
1	A	380	ALA
1	A	460	SER
2	B	10	ASN
3	D	162	ASP
3	D	241	ILE
3	D	245	GLU
3	D	424	LEU
4	E	26	SER
6	H	19	ILE
6	H	189	LEU
6	H	432	GLN
7	Q	105	LEU
7	Q	156	ASP
7	Q	191	PHE
8	Z	92	THR
8	Z	430	LYS
1	a	1111	LYS

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Mol	Chain	Res	Type
1	a	1411	GLY
1	a	1531	ILE
2	b	1014	ALA
2	b	1429	PRO
3	d	1066	ASP
3	d	1428	GLY
4	e	1135	ASP
4	e	1161	ASN
4	e	1381	ARG
4	e	1416	ASN
4	e	1536	PRO
5	g	1521	ASP
6	h	1504	THR
6	h	1518	GLU
7	q	1526	MET
8	z	1189	PHE
8	z	1333	LEU
1	A	133	SER
1	A	231	ASN
1	A	322	ALA
1	A	376	ILE
1	A	432	SER
2	B	499	VAL
3	D	112	VAL
3	D	510	LEU
4	E	22	GLN
6	H	7	ILE
6	H	225	PHE
7	Q	147	VAL
7	Q	332	ALA
8	Z	68	GLN
8	Z	142	GLU
8	Z	143	MET
8	Z	157	ARG
8	Z	504	LEU
1	a	1031	ILE
1	a	1203	ARG
1	a	1432	SER
3	d	1206	VAL
3	d	1224	CYS
5	g	1040	CYS
7	q	1191	PHE

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Mol	Chain	Res	Type
7	q	1505	TYR
8	z	1430	LYS
8	z	1471	SER
1	A	137	ILE
3	D	422	ARG
4	E	240	PRO
4	E	477	VAL
5	G	9	VAL
6	H	23	VAL
7	Q	81	PRO
7	Q	188	VAL
7	Q	505	TYR
3	d	1535	ILE
7	q	1025	LEU
7	q	1173	TYR
1	A	9	GLY
4	E	486	ASN
5	G	410	GLY
6	H	516	VAL
1	a	1211	ILE
2	b	1407	VAL
3	d	1130	GLY
7	q	1516	VAL
2	B	368	GLY
6	H	229	PRO
8	Z	500	VAL
4	e	1178	VAL
4	e	1422	GLY
5	g	1514	VAL
6	h	1139	ILE
8	z	1510	VAL
2	B	194	GLY
6	H	522	ASN
8	Z	518	VAL
8	z	1089	GLY
3	D	300	VAL
8	Z	494	ILE
1	a	1086	VAL
1	a	1415	VAL
3	d	1476	PRO
4	e	1486	ASN
5	g	1122	VAL

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Mol	Chain	Res	Type
6	h	1516	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	395/461 (86%)	368 (93%)	27 (7%)	20	57
1	a	297/461 (64%)	269 (91%)	28 (9%)	11	42
2	B	382/429 (89%)	372 (97%)	10 (3%)	54	80
2	b	281/429 (66%)	263 (94%)	18 (6%)	22	59
3	D	407/454 (90%)	388 (95%)	19 (5%)	32	68
3	d	303/454 (67%)	285 (94%)	18 (6%)	24	61
4	E	400/455 (88%)	371 (93%)	29 (7%)	17	55
4	e	298/455 (66%)	283 (95%)	15 (5%)	30	66
5	G	416/470 (88%)	402 (97%)	14 (3%)	44	76
5	g	307/470 (65%)	288 (94%)	19 (6%)	23	60
6	H	394/445 (88%)	381 (97%)	13 (3%)	45	76
6	h	292/445 (66%)	274 (94%)	18 (6%)	23	60
7	Q	398/452 (88%)	380 (96%)	18 (4%)	34	69
7	q	296/452 (66%)	279 (94%)	17 (6%)	25	62
8	Z	398/440 (90%)	386 (97%)	12 (3%)	48	77
8	z	398/440 (90%)	374 (94%)	24 (6%)	24	61
All	All	5662/7212 (78%)	5363 (95%)	299 (5%)	28	65

All (299) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	12	SER
1	A	39	VAL

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Mol	Chain	Res	Type
1	A	84	LYS
1	A	105	ASP
1	A	116	SER
1	A	147	CYS
1	A	222	SER
1	A	225	MET
1	A	231	ASN
1	A	240	SER
1	A	243	LYS
1	A	277	LYS
1	A	358	ASP
1	A	372	SER
1	A	381	ASN
1	A	382	ASP
1	A	384	MET
1	A	387	GLU
1	A	403	LEU
1	A	430	MET
1	A	523	THR
1	A	529	ASP
1	A	530	LEU
1	A	532	LYS
1	A	533	LEU
1	A	534	HIS
2	B	19	GLU
2	B	99	THR
2	B	221	ASP
2	B	287	ILE
2	B	288	ASN
2	B	292	ASN
2	B	334	THR
2	B	381	GLN
2	B	406	THR
2	B	480	MET
3	D	32	LYS
3	D	33	PRO
3	D	63	MET
3	D	110	THR
3	D	123	CYS
3	D	195	MET
3	D	210	ASP
3	D	217	LEU

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Mol	Chain	Res	Type
3	D	224	CYS
3	D	256	LEU
3	D	315	LEU
3	D	340	CYS
3	D	364	LEU
3	D	371	ASN
3	D	444	ARG
3	D	452	TYR
3	D	516	LEU
3	D	537	ASP
3	D	542	ARG
4	E	28	LEU
4	E	29	MET
4	E	48	MET
4	E	63	ASP
4	E	84	ASP
4	E	86	GLN
4	E	102	ILE
4	E	107	THR
4	E	148	LEU
4	E	160	LYS
4	E	203	ASP
4	E	219	LEU
4	E	244	GLU
4	E	306	PHE
4	E	345	PHE
4	E	351	GLU
4	E	369	ASP
4	E	381	ARG
4	E	384	THR
4	E	388	ARG
4	E	397	GLU
4	E	426	GLU
4	E	443	LEU
4	E	446	TYR
4	E	509	THR
4	E	515	GLN
4	E	527	ILE
4	E	528	LEU
4	E	535	LYS
5	G	10	LEU
5	G	97	SER

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Mol	Chain	Res	Type
5	G	140	ILE
5	G	225	THR
5	G	234	LYS
5	G	235	ASN
5	G	284	GLN
5	G	336	GLU
5	G	341	GLU
5	G	359	TYR
5	G	382	GLU
5	G	427	LYS
5	G	503	LEU
5	G	504	GLN
6	H	8	LEU
6	H	10	LYS
6	H	11	GLU
6	H	16	SER
6	H	21	GLN
6	H	134	ASN
6	H	138	GLU
6	H	198	LYS
6	H	227	MET
6	H	241	ASN
6	H	345	CYS
6	H	403	ASP
6	H	521	LYS
7	Q	13	GLN
7	Q	14	MET
7	Q	15	LEU
7	Q	17	GLU
7	Q	141	GLU
7	Q	173	TYR
7	Q	175	ASN
7	Q	227	THR
7	Q	383	ASN
7	Q	399	PHE
7	Q	406	LYS
7	Q	428	GLU
7	Q	473	GLU
7	Q	509	LYS
7	Q	518	VAL
7	Q	524	ILE
7	Q	526	MET

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Mol	Chain	Res	Type
7	Q	528	LYS
8	Z	196	MET
8	Z	197	LYS
8	Z	217	ARG
8	Z	225	VAL
8	Z	227	ASP
8	Z	370	ARG
8	Z	374	LEU
8	Z	380	ASN
8	Z	507	SER
8	Z	508	CYS
8	Z	519	ASP
8	Z	523	ARG
1	a	1006	SER
1	a	1010	ASP
1	a	1018	ARG
1	a	1035	SER
1	a	1047	ASP
1	a	1049	ILE
1	a	1068	GLU
1	a	1088	ASP
1	a	1110	GLN
1	a	1125	CYS
1	a	1137	ILE
1	a	1138	ILE
1	a	1143	LEU
1	a	1146	ASP
1	a	1158	SER
1	a	1168	PHE
1	a	1172	VAL
1	a	1177	LEU
1	a	1180	LYS
1	a	1181	TYR
1	a	1212	ASN
1	a	1372	SER
1	a	1382	ASP
1	a	1400	LYS
1	a	1403	LEU
1	a	1523	THR
1	a	1526	ARG
1	a	1534	HIS
2	b	1017	ASP

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Mol	Chain	Res	Type
2	b	1049	ASP
2	b	1062	MET
2	b	1172	LEU
2	b	1195	ASN
2	b	1209	LEU
2	b	1376	ARG
2	b	1388	ARG
2	b	1390	LEU
2	b	1396	VAL
2	b	1427	ARG
2	b	1431	LYS
2	b	1470	SER
2	b	1495	GLU
2	b	1506	SER
2	b	1509	GLU
2	b	1521	ILE
2	b	1522	LYS
3	d	1024	LYS
3	d	1084	MET
3	d	1087	LEU
3	d	1153	ASP
3	d	1176	SER
3	d	1215	LYS
3	d	1216	LYS
3	d	1217	LEU
3	d	1387	LYS
3	d	1394	ARG
3	d	1396	SER
3	d	1397	ASN
3	d	1424	LEU
3	d	1478	SER
3	d	1518	SER
3	d	1520	SER
3	d	1531	SER
3	d	1542	ARG
4	e	1022	GLN
4	e	1023	ASP
4	e	1024	ARG
4	e	1025	LYS
4	e	1027	ARG
4	e	1048	MET
4	e	1055	ASN

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Mol	Chain	Res	Type
4	e	1118	GLU
4	e	1195	THR
4	e	1203	ASP
4	e	1383	VAL
4	e	1392	LYS
4	e	1393	MET
4	e	1426	GLU
4	e	1515	GLN
5	g	1012	GLN
5	g	1016	ARG
5	g	1023	GLN
5	g	1051	LEU
5	g	1059	MET
5	g	1064	ASN
5	g	1091	VAL
5	g	1118	HIS
5	g	1140	ILE
5	g	1158	SER
5	g	1162	THR
5	g	1170	SER
5	g	1216	ARG
5	g	1372	CYS
5	g	1397	VAL
5	g	1398	CYS
5	g	1433	GLU
5	g	1503	LEU
5	g	1518	ARG
6	h	1008	LEU
6	h	1016	SER
6	h	1019	ILE
6	h	1021	GLN
6	h	1043	ARG
6	h	1045	MET
6	h	1051	ASP
6	h	1092	ASP
6	h	1126	ARG
6	h	1186	LEU
6	h	1370	CYS
6	h	1381	PHE
6	h	1403	ASP
6	h	1425	ARG
6	h	1450	CYS

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Mol	Chain	Res	Type
6	h	1473	MET
6	h	1497	MET
6	h	1504	THR
7	q	1015	LEU
7	q	1016	LYS
7	q	1085	MET
7	q	1126	SER
7	q	1138	LYS
7	q	1156	ASP
7	q	1166	THR
7	q	1173	TYR
7	q	1205	CYS
7	q	1208	LEU
7	q	1381	THR
7	q	1399	PHE
7	q	1403	THR
7	q	1408	LEU
7	q	1456	SER
7	q	1499	ASP
7	q	1524	ILE
8	z	1007	LEU
8	z	1017	GLN
8	z	1032	ASP
8	z	1043	THR
8	z	1047	LEU
8	z	1093	THR
8	z	1104	LYS
8	z	1121	GLU
8	z	1135	GLU
8	z	1138	LYS
8	z	1146	GLU
8	z	1196	MET
8	z	1201	GLU
8	z	1208	ARG
8	z	1229	TYR
8	z	1238	GLU
8	z	1337	ASP
8	z	1342	ASP
8	z	1351	TYR
8	z	1374	LEU
8	z	1386	GLN
8	z	1460	GLN

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Mol	Chain	Res	Type
8	z	1504	LEU
8	z	1523	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (144) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	103	ASN
1	A	366	ASN
1	A	425	ASN
1	A	435	GLN
1	A	455	ASN
1	A	472	ASN
1	A	498	ASN
2	B	161	ASN
2	B	227	ASN
2	B	288	ASN
2	B	294	GLN
2	B	302	GLN
2	B	337	HIS
2	B	381	GLN
2	B	391	HIS
2	B	453	ASN
2	B	498	GLN
3	D	40	ASN
3	D	83	GLN
3	D	101	GLN
3	D	132	HIS
3	D	292	GLN
3	D	371	ASN
3	D	471	ASN
4	E	22	GLN
4	E	46	ASN
4	E	98	GLN
4	E	129	HIS
4	E	236	HIS
4	E	311	ASN
4	E	317	ASN
4	E	481	GLN
4	E	522	GLN
5	G	23	GLN
5	G	28	ASN

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Mol	Chain	Res	Type
5	G	64	ASN
5	G	73	GLN
5	G	118	HIS
5	G	154	ASN
5	G	221	ASN
5	G	321	ASN
5	G	396	GLN
5	G	400	ASN
5	G	434	GLN
5	G	454	ASN
6	H	17	GLN
6	H	21	GLN
6	H	25	ASN
6	H	73	HIS
6	H	107	GLN
6	H	134	ASN
6	H	171	GLN
6	H	241	ASN
6	H	432	GLN
6	H	448	GLN
6	H	470	GLN
6	H	487	ASN
6	H	501	ASN
7	Q	59	HIS
7	Q	93	GLN
7	Q	198	ASN
7	Q	201	ASN
7	Q	219	HIS
7	Q	346	HIS
7	Q	435	GLN
7	Q	513	ASN
8	Z	23	ASN
8	Z	71	HIS
8	Z	294	GLN
8	Z	380	ASN
8	Z	400	ASN
8	Z	438	GLN
8	Z	453	GLN
8	Z	454	ASN
8	Z	514	ASN
1	a	1021	ASN
1	a	1082	GLN

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Mol	Chain	Res	Type
1	a	1103	ASN
1	a	1110	GLN
1	a	1393	HIS
1	a	1425	ASN
1	a	1498	ASN
1	a	1500	GLN
2	b	1073	ASN
2	b	1091	GLN
2	b	1124	GLN
2	b	1161	ASN
2	b	1195	ASN
2	b	1200	HIS
2	b	1380	GLN
2	b	1502	GLN
3	d	1028	GLN
3	d	1141	GLN
3	d	1168	ASN
3	d	1175	ASN
3	d	1485	ASN
4	e	1055	ASN
4	e	1098	GLN
4	e	1184	GLN
4	e	1391	ASN
4	e	1411	ASN
4	e	1481	GLN
4	e	1522	GLN
5	g	1012	GLN
5	g	1073	GLN
5	g	1154	ASN
5	g	1434	GLN
5	g	1454	ASN
5	g	1470	HIS
5	g	1504	GLN
6	h	1021	GLN
6	h	1073	HIS
6	h	1134	ASN
6	h	1151	GLN
6	h	1191	GLN
6	h	1201	GLN
6	h	1209	GLN
6	h	1402	ASN
6	h	1431	GLN

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Mol	Chain	Res	Type
6	h	1448	GLN
6	h	1452	ASN
6	h	1487	ASN
7	q	1050	ASN
7	q	1093	GLN
7	q	1102	ASN
7	q	1165	HIS
7	q	1185	GLN
7	q	1435	GLN
7	q	1513	ASN
7	q	1523	GLN
8	z	1023	ASN
8	z	1031	GLN
8	z	1070	GLN
8	z	1234	ASN
8	z	1293	ASN
8	z	1368	ASN
8	z	1386	GLN
8	z	1400	ASN
8	z	1434	GLN
8	z	1438	GLN
8	z	1460	GLN
8	z	1497	ASN
8	z	1503	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	481/556 (86%)	1.72	145 (30%) 1 4	260, 260, 260, 260	0
1	a	359/556 (64%)	2.23	159 (44%) 0 3	282, 282, 282, 282	0
2	B	481/535 (89%)	2.76	237 (49%) 0 3	281, 281, 281, 281	0
2	b	359/535 (67%)	2.33	167 (46%) 0 3	272, 272, 272, 272	0
3	D	481/542 (88%)	1.93	168 (34%) 0 3	289, 289, 289, 289	0
3	d	359/542 (66%)	1.92	139 (38%) 0 3	266, 266, 266, 266	0
4	E	481/541 (88%)	1.35	121 (25%) 1 4	262, 262, 262, 262	0
4	e	359/541 (66%)	2.55	170 (47%) 0 3	283, 283, 283, 283	0
5	G	481/545 (88%)	2.09	192 (39%) 0 3	283, 283, 283, 283	0
5	g	359/545 (65%)	1.27	86 (23%) 1 4	275, 275, 275, 275	0
6	H	481/543 (88%)	1.82	170 (35%) 0 3	272, 272, 272, 272	0
6	h	359/543 (66%)	1.29	98 (27%) 1 4	258, 258, 258, 258	0
7	Q	481/548 (87%)	2.74	241 (50%) 0 3	308, 308, 308, 308	0
7	q	359/548 (65%)	2.15	162 (45%) 0 3	261, 261, 261, 261	0
8	Z	481/531 (90%)	2.68	232 (48%) 0 3	297, 297, 297, 297	0
8	z	481/531 (90%)	2.51	201 (41%) 0 3	276, 276, 276, 276	0
All	All	6842/8682 (78%)	2.10	2688 (39%) 0 3	258, 276, 308, 308	0

All (2688) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	Z	288	GLY	26.2
8	z	1209	GLY	22.1
6	H	224	GLY	19.0
8	z	1288	GLY	17.1
4	e	1226	LYS	16.0

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Mol	Chain	Res	Type	RSRZ
8	z	1216	ALA	15.2
2	B	219	LEU	15.2
6	H	228	GLN	15.2
8	z	1268	GLU	14.9
3	d	1170	ALA	14.9
2	B	215	ASP	14.8
2	B	218	PHE	14.7
8	Z	312	ALA	14.2
7	Q	412	GLY	13.9
7	Q	192	PRO	13.7
8	z	1312	ALA	13.4
1	A	334	LEU	13.3
1	A	333	ASN	13.2
2	B	200	HIS	13.1
8	z	1210	LEU	12.9
7	Q	197	PHE	12.8
1	A	190	TYR	12.7
1	A	331	LEU	12.7
8	z	1267	ILE	12.3
2	B	223	LYS	12.3
2	b	1406	THR	12.1
7	Q	290	VAL	12.1
8	Z	278	LYS	12.0
8	Z	267	ILE	12.0
5	G	156	ILE	11.9
8	Z	216	ALA	11.8
4	e	1224	LEU	11.8
7	Q	219	HIS	11.8
7	Q	67	ASN	11.7
2	B	220	LEU	11.7
7	Q	311	MET	11.7
8	z	1237	LEU	11.7
2	b	1407	VAL	11.7
6	H	229	PRO	11.5
3	D	236	VAL	11.5
3	D	312	LEU	11.5
3	D	327	VAL	11.5
7	Q	231	VAL	11.4
8	Z	236	SER	11.3
8	z	1311	ILE	11.2
8	Z	289	PHE	11.1
8	z	1208	ARG	11.1

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Mol	Chain	Res	Type	RSRZ
2	b	1016	ALA	11.0
2	b	1013	LYS	10.9
8	Z	209	GLY	10.9
8	Z	211	VAL	10.9
4	E	235	SER	10.8
7	Q	309	ASN	10.8
2	B	308	GLY	10.8
2	B	16	ALA	10.8
8	z	1310	ILE	10.7
8	Z	344	LEU	10.7
2	B	214	LEU	10.7
4	e	1493	CYS	10.7
7	Q	289	ASN	10.7
2	B	221	ASP	10.7
5	G	525	GLY	10.6
8	Z	210	LEU	10.6
8	z	1289	PHE	10.6
2	b	1495	GLU	10.6
2	b	1494	THR	10.6
1	A	191	PRO	10.5
8	Z	237	LEU	10.4
6	H	10	LYS	10.4
7	Q	188	VAL	10.4
2	B	224	ILE	10.3
2	b	1015	GLY	10.3
7	Q	191	PHE	10.3
7	Q	190	ILE	10.3
8	Z	296	GLY	10.3
2	b	1496	SER	10.3
8	z	1213	ASP	10.3
2	B	360	ILE	10.3
7	Q	310	ILE	10.3
1	a	1370	ARG	10.0
2	B	244	MET	10.0
1	a	1160	VAL	9.9
1	A	275	ILE	9.9
2	B	198	ALA	9.9
7	Q	189	SER	9.9
8	z	1371	SER	9.8
2	B	296	ILE	9.8
1	A	330	THR	9.8
8	Z	192	GLU	9.7

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Mol	Chain	Res	Type	RSRZ
4	e	1225	ILE	9.6
5	G	310	THR	9.6
8	z	1225	VAL	9.5
2	b	1014	ALA	9.5
4	e	1380	SER	9.5
7	q	1219	HIS	9.5
8	z	1222	LYS	9.5
8	z	1339	LEU	9.5
8	Z	232	THR	9.3
1	A	243	LYS	9.3
3	D	320	LEU	9.3
3	D	235	LYS	9.3
8	z	1313	LEU	9.3
3	D	328	VAL	9.3
3	d	1169	SER	9.2
3	D	237	ALA	9.2
2	B	313	GLU	9.2
8	z	1373	THR	9.1
2	B	309	VAL	9.1
5	G	14	THR	9.1
2	B	213	TYR	9.1
3	d	1199	ASP	9.1
3	D	232	LEU	9.0
2	b	1409	GLY	9.0
8	z	1223	LYS	9.0
6	H	215	ALA	9.0
2	B	15	GLY	9.0
2	b	1408	TYR	9.0
3	D	329	LYS	8.9
2	B	304	PHE	8.9
8	z	1352	GLU	8.9
7	Q	297	VAL	8.9
8	z	1271	VAL	8.9
2	b	1410	GLY	8.9
7	Q	196	HIS	8.9
4	e	1382	ALA	8.9
4	e	1508	GLU	8.9
2	B	236	LYS	8.8
8	Z	295	LYS	8.8
8	z	1192	GLU	8.8
1	A	194	SER	8.8
2	B	370	ALA	8.8

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Mol	Chain	Res	Type	RSRZ
1	a	1397	CYS	8.8
2	B	311	ALA	8.8
2	B	287	ILE	8.7
7	q	1172	GLN	8.7
2	B	216	GLU	8.7
1	a	1373	ALA	8.7
2	B	282	ILE	8.7
6	H	223	ALA	8.7
5	G	230	ARG	8.7
8	Z	274	ILE	8.7
3	d	1173	SER	8.6
3	D	189	MET	8.6
8	z	1372	VAL	8.6
7	q	1499	ASP	8.6
8	Z	313	LEU	8.6
7	Q	413	GLY	8.5
8	Z	310	ILE	8.5
8	Z	292	ILE	8.5
1	a	1086	VAL	8.5
7	Q	248	GLY	8.5
4	E	323	ARG	8.4
8	Z	221	MET	8.4
3	D	238	ASN	8.4
6	H	310	CYS	8.4
6	H	13	THR	8.4
3	D	311	ALA	8.4
8	Z	217	ARG	8.4
8	z	1217	ARG	8.4
8	z	1307	LYS	8.4
4	E	95	SER	8.4
8	z	1308	GLU	8.3
8	z	1224	ARG	8.3
8	Z	235	VAL	8.3
2	B	342	LYS	8.3
4	e	1383	VAL	8.3
8	z	1290	VAL	8.3
3	D	256	LEU	8.3
8	z	1291	VAL	8.3
8	z	1336	LEU	8.3
4	E	321	ALA	8.2
8	Z	345	GLY	8.2
8	z	1269	ASP	8.2

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Mol	Chain	Res	Type	RSRZ
2	b	1368	GLY	8.2
7	q	1018	GLY	8.2
2	B	237	ILE	8.2
3	d	1495	GLY	8.2
5	G	290	VAL	8.2
5	G	15	LYS	8.2
7	Q	225	LYS	8.2
1	a	1471	HIS	8.1
2	B	334	THR	8.1
1	a	1394	ASP	8.1
3	D	377	ILE	8.1
5	G	219	MET	8.1
8	z	1293	ASN	8.1
8	z	1212	LEU	8.1
7	Q	232	THR	8.1
7	Q	366	GLU	8.1
8	z	1226	GLU	8.1
8	Z	320	ASN	8.1
8	z	1228	ALA	8.1
8	z	1363	ILE	8.1
2	B	327	THR	8.1
8	z	1361	THR	8.0
3	d	1221	ILE	8.0
7	Q	308	TYR	8.0
4	e	1102	ILE	8.0
8	z	1304	ALA	8.0
5	G	282	ILE	8.0
5	G	203	LYS	8.0
7	Q	500	THR	8.0
7	q	1203	ARG	8.0
4	E	285	PHE	8.0
4	e	1405	ALA	8.0
7	q	1410	PRO	8.0
2	B	343	LEU	7.9
8	Z	311	ILE	7.9
4	E	306	PHE	7.9
1	a	1161	ILE	7.9
1	a	1205	GLN	7.9
5	G	289	VAL	7.9
4	E	322	VAL	7.9
1	A	195	ILE	7.9
6	H	216	PHE	7.8

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Mol	Chain	Res	Type	RSRZ
4	e	1185	MET	7.8
4	e	1409	ILE	7.8
5	G	160	ILE	7.8
2	B	362	PHE	7.8
7	Q	370	GLY	7.8
2	B	199	ILE	7.7
7	Q	288	ALA	7.7
5	G	311	ALA	7.7
4	e	1223	LYS	7.7
8	Z	497	ASN	7.7
5	g	1199	ALA	7.7
7	Q	155	ARG	7.7
2	b	1148	HIS	7.7
6	H	309	PHE	7.6
2	B	312	ILE	7.6
8	Z	230	ILE	7.6
1	A	143	LEU	7.6
7	q	1173	TYR	7.6
2	B	239	ILE	7.6
7	q	1370	GLY	7.6
4	e	1022	GLN	7.6
4	e	1509	THR	7.6
7	q	1398	THR	7.6
7	Q	193	ASP	7.6
1	A	271	THR	7.6
4	E	255	PHE	7.6
2	B	300	PRO	7.5
1	A	345	LEU	7.5
1	a	1472	ASN	7.5
2	B	372	THR	7.5
3	D	190	SER	7.5
8	Z	271	VAL	7.5
1	A	332	ALA	7.5
1	A	335	GLU	7.5
4	e	1172	THR	7.5
5	G	524	SER	7.5
2	B	279	VAL	7.5
1	a	1162	GLY	7.5
2	B	494	THR	7.5
8	Z	321	MET	7.5
8	z	1227	ASP	7.5
6	H	308	MET	7.5

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Mol	Chain	Res	Type	RSRZ
3	d	1428	GLY	7.4
2	B	338	PRO	7.4
8	z	1305	LEU	7.4
8	z	1338	ASP	7.4
3	D	231	VAL	7.4
8	Z	191	VAL	7.4
7	Q	187	CYS	7.4
7	Q	239	ILE	7.4
5	G	526	HIS	7.4
8	Z	233	CYS	7.4
7	q	1097	VAL	7.3
8	Z	223	LYS	7.3
3	D	105	ALA	7.3
4	e	1173	LEU	7.3
8	Z	293	ASN	7.3
2	B	345	SER	7.3
5	G	287	PRO	7.3
8	Z	291	VAL	7.3
2	b	1149	GLY	7.3
2	B	411	GLY	7.3
6	H	468	HIS	7.3
7	q	1099	ASP	7.3
8	z	1274	ILE	7.3
8	Z	363	ILE	7.2
4	e	1491	ILE	7.2
5	g	1201	VAL	7.2
6	H	12	GLY	7.2
8	z	1211	VAL	7.2
7	Q	287	GLY	7.2
8	Z	323	ARG	7.2
7	q	1197	PHE	7.2
7	Q	99	ASP	7.2
5	G	283	ILE	7.2
8	z	1186	ILE	7.2
2	B	297	TYR	7.2
6	H	244	LEU	7.2
8	Z	231	LEU	7.2
2	B	228	GLN	7.1
7	q	1374	THR	7.1
5	G	224	VAL	7.1
3	D	170	ALA	7.1
8	Z	411	ALA	7.1

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Mol	Chain	Res	Type	RSRZ
4	e	1387	ILE	7.1
4	e	1537	GLY	7.1
3	d	1174	LEU	7.1
8	Z	234	ASN	7.1
3	d	1107	ASP	7.1
2	B	307	ALA	7.1
3	d	1159	GLU	7.1
4	e	1084	ASP	7.0
7	Q	365	HIS	7.0
8	Z	346	HIS	7.0
3	d	1228	GLU	7.0
2	B	290	PHE	7.0
7	Q	235	LYS	7.0
7	Q	151	ALA	7.0
8	z	1297	ILE	7.0
1	a	1145	ARG	7.0
7	q	1217	VAL	7.0
2	b	1493	ILE	7.0
1	a	1144	GLY	7.0
7	Q	348	ASP	7.0
8	Z	222	LYS	7.0
3	d	1426	ALA	7.0
3	D	378	LYS	7.0
4	e	1166	ILE	7.0
4	e	1190	VAL	6.9
8	z	1179	ILE	6.9
1	a	1413	GLY	6.9
2	B	163	ALA	6.9
5	g	1372	CYS	6.9
4	E	234	PHE	6.9
1	A	372	SER	6.9
2	B	217	GLY	6.9
5	G	239	VAL	6.9
3	D	426	ALA	6.9
4	E	289	ILE	6.9
2	b	1369	GLU	6.9
4	e	1497	GLY	6.9
2	B	164	GLY	6.9
4	e	1055	ASN	6.8
5	g	1200	ARG	6.8
1	A	283	ALA	6.8
2	B	335	PHE	6.8

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Mol	Chain	Res	Type	RSRZ
4	e	1404	ASP	6.8
7	q	1204	VAL	6.8
5	G	335	PRO	6.8
7	q	1202	ILE	6.8
7	q	1373	SER	6.8
6	H	402	ASN	6.8
2	B	361	HIS	6.8
2	B	373	ILE	6.8
7	q	1048	GLY	6.8
2	b	1477	GLY	6.8
3	D	233	THR	6.8
4	e	1183	ARG	6.8
6	H	225	PHE	6.7
7	Q	479	GLY	6.7
7	Q	299	ASP	6.7
8	z	1320	ASN	6.7
1	A	214	TYR	6.7
4	e	1384	THR	6.7
7	q	1019	ALA	6.7
7	Q	202	ILE	6.7
4	e	1381	ARG	6.7
8	Z	330	GLY	6.7
4	e	1189	ALA	6.7
7	Q	371	ALA	6.7
8	Z	350	VAL	6.7
2	B	14	ALA	6.7
2	B	235	ALA	6.7
5	G	291	ILE	6.7
1	A	274	ARG	6.7
3	D	326	MET	6.6
2	B	230	LYS	6.6
7	Q	367	LYS	6.6
2	b	1411	GLY	6.6
3	D	365	ALA	6.6
4	e	1053	GLY	6.6
2	B	201	VAL	6.6
1	a	1157	SER	6.6
4	e	1054	PRO	6.6
5	G	13	ASN	6.6
7	Q	373	SER	6.6
2	B	301	GLU	6.6
4	e	1385	ILE	6.6

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Mol	Chain	Res	Type	RSRZ
4	e	1182	HIS	6.6
2	B	303	LEU	6.6
2	b	1476	ALA	6.6
7	q	1500	THR	6.6
3	d	1211	ILE	6.6
4	e	1082	ASP	6.6
4	e	1406	LEU	6.5
7	Q	501	TYR	6.5
7	Q	204	VAL	6.5
8	z	1272	LYS	6.5
8	Z	179	ILE	6.5
4	e	1422	GLY	6.5
7	Q	489	VAL	6.5
8	Z	331	ILE	6.5
7	q	1216	SER	6.5
6	H	520	ILE	6.5
7	Q	326	LYS	6.5
3	d	1389	VAL	6.5
2	B	96	GLY	6.5
4	e	1170	LYS	6.5
2	B	298	ASN	6.5
7	Q	372	ILE	6.5
8	z	1238	GLU	6.5
1	a	1177	LEU	6.5
5	G	7	VAL	6.5
7	Q	291	VAL	6.5
3	d	1161	SER	6.5
3	d	1423	ALA	6.5
7	Q	224	LYS	6.5
7	Q	327	THR	6.5
8	Z	212	LEU	6.4
7	Q	236	ASP	6.4
7	Q	414	ALA	6.4
3	D	214	VAL	6.4
6	h	1014	ASP	6.4
2	B	371	CYS	6.4
1	a	1156	MET	6.4
7	Q	324	LEU	6.4
4	E	236	HIS	6.4
1	a	1473	GLU	6.4
2	B	341	VAL	6.4
7	Q	363	PHE	6.4

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Mol	Chain	Res	Type	RSRZ
5	G	157	ASN	6.4
2	b	1474	THR	6.4
7	Q	403	THR	6.4
8	z	1316	ALA	6.4
3	D	212	LYS	6.4
3	d	1177	LYS	6.4
8	z	1236	SER	6.3
2	B	238	LEU	6.3
5	G	8	LEU	6.3
2	b	1146	VAL	6.3
8	Z	294	GLN	6.3
7	q	1212	VAL	6.3
3	D	325	ILE	6.3
7	Q	150	SER	6.3
8	z	1301	SER	6.3
6	h	1083	ALA	6.3
4	e	1496	LYS	6.3
3	d	1206	VAL	6.3
5	G	394	ALA	6.3
7	q	1412	GLY	6.3
4	e	1095	SER	6.3
6	H	494	GLU	6.3
7	Q	347	CYS	6.3
1	a	1159	LYS	6.3
8	Z	268	GLU	6.3
7	q	1395	GLY	6.3
1	a	1155	SER	6.2
3	D	322	LYS	6.2
8	z	1207	ILE	6.2
5	G	16	ARG	6.2
8	z	1231	LEU	6.2
1	a	1470	PHE	6.2
7	q	1215	SER	6.2
8	Z	361	THR	6.2
8	Z	315	ARG	6.2
8	z	1524	ALA	6.2
8	Z	180	LYS	6.2
2	B	95	VAL	6.2
5	G	296	ILE	6.2
4	e	1169	ALA	6.2
2	b	1500	LYS	6.2
6	H	311	ALA	6.2

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Mol	Chain	Res	Type	RSRZ
2	B	365	VAL	6.2
1	a	1174	ASP	6.1
6	H	14	ASP	6.1
7	q	1414	ALA	6.1
4	e	1174	GLY	6.1
7	Q	227	THR	6.1
1	A	210	LEU	6.1
8	z	1364	GLU	6.1
2	B	374	VAL	6.1
4	E	102	ILE	6.1
6	H	214	VAL	6.1
1	A	278	ILE	6.1
4	e	1408	VAL	6.1
2	B	310	MET	6.1
8	z	1522	MET	6.1
4	e	1402	LEU	6.1
1	A	66	GLU	6.1
4	e	1209	ILE	6.1
5	G	319	ASP	6.1
7	Q	364	LYS	6.1
7	Q	201	ASN	6.0
4	E	256	GLU	6.0
5	G	58	VAL	6.0
3	d	1386	GLY	6.0
5	G	355	ILE	6.0
8	Z	229	TYR	6.0
8	Z	277	LEU	6.0
1	a	1208	SER	6.0
8	Z	218	HIS	6.0
2	B	13	LYS	6.0
8	z	1089	GLY	6.0
3	D	239	SER	6.0
8	Z	301	SER	6.0
1	A	145	ARG	6.0
3	D	85	GLN	6.0
4	e	1165	LEU	6.0
1	a	1488	LEU	6.0
8	Z	316	ALA	6.0
4	e	1178	VAL	6.0
3	d	1493	THR	6.0
3	D	376	LEU	6.0
5	G	91	VAL	6.0

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Mol	Chain	Res	Type	RSRZ
7	q	1378	ARG	6.0
5	G	244	SER	6.0
1	a	1212	ASN	5.9
7	Q	237	ALA	5.9
7	Q	198	ASN	5.9
3	D	321	ASN	5.9
3	D	313	SER	5.9
6	H	9	LEU	5.9
8	Z	366	CYS	5.9
7	q	1375	ILE	5.9
3	d	1213	ILE	5.9
5	G	308	ASN	5.9
3	D	318	HIS	5.9
8	Z	336	LEU	5.9
8	Z	225	VAL	5.9
8	Z	10	LYS	5.9
7	Q	240	ALA	5.9
2	B	225	GLY	5.9
4	E	22	GLN	5.9
3	D	185	LEU	5.9
4	e	1191	ASN	5.9
1	A	373	ALA	5.8
8	z	1309	GLY	5.8
4	e	1176	LYS	5.8
7	q	1150	SER	5.8
4	e	1025	LYS	5.8
8	Z	496	ASP	5.8
8	Z	373	THR	5.8
2	B	329	GLY	5.8
8	Z	328	CYS	5.8
8	z	1229	TYR	5.8
7	Q	416	GLU	5.8
8	Z	371	SER	5.8
8	Z	347	ALA	5.8
5	G	17	GLU	5.8
7	Q	480	LEU	5.8
1	a	1401	ARG	5.8
1	A	212	ASN	5.8
8	Z	275	ILE	5.8
2	b	1154	LYS	5.8
7	Q	411	GLY	5.8
3	d	1496	ILE	5.8

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Mol	Chain	Res	Type	RSRZ
2	b	1466	ARG	5.8
2	B	286	GLY	5.8
6	H	410	GLY	5.8
3	D	215	LYS	5.8
7	Q	499	ASP	5.8
3	D	224	CYS	5.7
7	Q	307	LYS	5.7
5	G	218	VAL	5.7
3	D	366	GLU	5.7
1	A	281	THR	5.7
2	b	1199	ILE	5.7
5	g	1216	ARG	5.7
8	Z	213	ASP	5.7
5	G	245	LEU	5.7
2	b	1478	LEU	5.7
2	B	278	LYS	5.7
2	B	366	ALA	5.7
5	G	390	ASN	5.7
2	b	1497	PHE	5.7
4	E	292	ILE	5.7
3	d	1388	THR	5.7
2	B	344	GLY	5.7
4	e	1168	THR	5.7
8	Z	314	ARG	5.7
2	B	478	LEU	5.7
2	B	229	PRO	5.7
1	A	342	ALA	5.6
5	G	384	LEU	5.6
8	Z	332	ALA	5.6
2	B	421	VAL	5.6
8	z	1323	ARG	5.6
8	Z	90	ASP	5.6
7	Q	180	ALA	5.6
2	B	337	HIS	5.6
4	E	98	GLN	5.6
8	Z	364	GLU	5.6
8	z	1230	ILE	5.6
8	z	1221	MET	5.6
4	e	1024	ARG	5.6
2	b	1043	LEU	5.6
2	B	288	ASN	5.6
6	H	519	THR	5.6

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Mol	Chain	Res	Type	RSRZ
1	a	1204	SER	5.6
5	G	363	ILE	5.6
8	z	1292	ILE	5.6
7	Q	147	VAL	5.6
4	E	311	ASN	5.6
7	Q	220	GLY	5.6
8	Z	88	THR	5.6
3	D	173	SER	5.6
5	G	159	SER	5.6
3	D	324	LYS	5.6
6	h	1407	ALA	5.5
2	b	1415	MET	5.5
8	z	1350	VAL	5.5
1	a	1372	SER	5.5
5	G	152	MET	5.5
5	G	165	ILE	5.5
8	z	1321	MET	5.5
5	G	338	LEU	5.5
3	D	367	GLU	5.5
1	a	1210	LEU	5.5
2	B	331	ILE	5.5
5	G	304	LEU	5.5
8	z	1278	LYS	5.5
4	e	1175	SER	5.5
2	b	1165	THR	5.5
5	g	1433	GLU	5.5
2	B	392	ASP	5.5
4	e	1056	GLY	5.5
5	G	361	THR	5.5
6	H	11	GLU	5.5
6	H	348	PHE	5.5
8	z	1158	THR	5.5
8	z	1181	LYS	5.4
2	B	92	ASP	5.4
3	D	310	ASP	5.4
7	q	1411	GLY	5.4
4	e	1161	ASN	5.4
2	b	1499	VAL	5.4
7	Q	47	TYR	5.4
8	Z	239	TYR	5.4
2	B	289	CYS	5.4
7	Q	298	ALA	5.4

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Mol	Chain	Res	Type	RSRZ
7	Q	218	LEU	5.4
2	B	280	GLU	5.4
2	b	1184	VAL	5.4
8	z	1088	THR	5.4
7	q	1049	PRO	5.4
7	Q	368	GLU	5.4
4	e	1192	ALA	5.4
1	a	1163	ILE	5.4
8	Z	305	LEU	5.4
5	G	202	GLU	5.4
7	Q	55	MET	5.4
1	a	1164	ASN	5.4
8	Z	148	LEU	5.4
5	g	1203	LYS	5.4
6	H	476	GLY	5.4
8	z	1525	GLY	5.4
7	Q	215	SER	5.4
4	e	1386	PHE	5.4
7	q	1478	VAL	5.4
8	Z	238	GLU	5.4
6	H	465	ARG	5.4
2	B	17	ASP	5.4
3	d	1171	ALA	5.3
4	e	1388	ARG	5.3
7	q	1047	TYR	5.3
4	E	288	MET	5.3
6	H	347	VAL	5.3
7	Q	407	ARG	5.3
8	Z	334	ASN	5.3
8	Z	11	ALA	5.3
3	D	330	ASP	5.3
4	E	26	SER	5.3
8	z	1039	GLY	5.3
5	G	155	ILE	5.3
3	D	298	CYS	5.3
6	h	1091	GLY	5.3
7	q	1196	HIS	5.3
5	G	312	ILE	5.3
4	e	1532	ASP	5.3
4	e	1459	PRO	5.3
2	B	485	ILE	5.3
4	E	254	PRO	5.3

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Mol	Chain	Res	Type	RSRZ
5	G	315	VAL	5.3
2	b	1465	LEU	5.3
4	e	1186	ALA	5.3
5	G	523	VAL	5.3
2	b	1145	ALA	5.3
7	Q	223	PHE	5.3
3	D	368	VAL	5.3
2	B	332	ALA	5.3
3	D	56	GLY	5.3
1	A	404	GLU	5.2
5	G	11	SER	5.2
3	d	1178	VAL	5.2
8	z	1239	TYR	5.2
5	G	221	ASN	5.2
6	h	1495	PRO	5.2
7	q	1164	LEU	5.2
5	G	59	MET	5.2
6	H	401	LYS	5.2
2	B	169	SER	5.2
2	B	322	ARG	5.2
3	D	213	ILE	5.2
2	B	336	ASP	5.2
2	b	1414	GLU	5.2
2	B	166	THR	5.2
7	Q	415	THR	5.2
2	b	1485	ILE	5.2
3	D	336	ILE	5.2
8	Z	297	ILE	5.2
2	B	430	GLY	5.2
2	b	1405	ARG	5.2
6	H	409	GLY	5.2
7	Q	399	PHE	5.2
4	E	373	VAL	5.2
2	B	393	ALA	5.2
6	H	140	ALA	5.2
2	b	1166	THR	5.2
7	Q	296	ARG	5.2
7	q	1184	ALA	5.2
6	H	369	THR	5.2
7	Q	66	THR	5.2
2	B	170	LYS	5.2
4	E	104	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
2	B	291	ILE	5.2
2	B	315	ALA	5.2
4	E	364	PHE	5.2
5	g	1432	VAL	5.2
7	Q	305	ALA	5.2
2	B	196	LEU	5.2
1	a	1047	ASP	5.1
7	q	1371	ALA	5.1
7	q	1498	LEU	5.1
1	a	1391	SER	5.1
8	Z	402	ILE	5.1
2	b	1164	GLY	5.1
1	A	344	MET	5.1
2	b	1012	PHE	5.1
3	D	206	VAL	5.1
5	g	1087	GLN	5.1
1	a	1044	MET	5.1
7	Q	179	LEU	5.1
8	Z	193	ILE	5.1
3	d	1422	ARG	5.1
1	a	1211	ILE	5.1
5	G	309	ILE	5.1
7	Q	146	LEU	5.1
2	B	319	GLY	5.1
6	H	400	ILE	5.1
1	a	1051	ASP	5.1
2	B	167	LEU	5.1
8	Z	398	VAL	5.1
8	Z	394	GLY	5.1
4	E	307	ASP	5.1
6	h	1212	ALA	5.1
6	h	1187	ASP	5.1
7	Q	286	THR	5.1
8	z	1195	GLU	5.1
1	a	1203	ARG	5.1
7	q	1067	ASN	5.1
7	q	1191	PHE	5.1
2	b	1163	ALA	5.1
7	q	1201	ASN	5.1
1	A	215	ALA	5.1
8	Z	187	ASP	5.1
8	z	1206	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
3	d	1198	ILE	5.0
1	A	192	VAL	5.0
7	q	1050	ASN	5.0
4	e	1531	ASP	5.0
3	d	1226	LEU	5.0
6	H	230	LYS	5.0
3	d	1140	PHE	5.0
5	G	281	ASP	5.0
7	Q	230	ASP	5.0
6	H	467	ARG	5.0
1	a	1375	VAL	5.0
1	a	1398	VAL	5.0
3	d	1506	ILE	5.0
7	Q	234	VAL	5.0
7	Q	284	ALA	5.0
1	a	1393	HIS	5.0
5	g	1431	GLY	5.0
4	e	1222	THR	5.0
7	q	1390	ARG	5.0
1	a	1374	SER	5.0
7	Q	476	LYS	5.0
7	q	1188	VAL	4.9
8	Z	324	LEU	4.9
3	D	188	PRO	4.9
8	Z	372	VAL	4.9
7	Q	312	LEU	4.9
1	a	1006	SER	4.9
1	a	1484	LYS	4.9
4	e	1104	ASP	4.9
5	G	247	TYR	4.9
8	Z	300	PHE	4.9
8	z	1275	ILE	4.9
7	q	1476	LYS	4.9
4	E	286	GLU	4.9
3	d	1393	VAL	4.9
6	H	286	ALA	4.9
5	G	9	VAL	4.9
7	Q	302	LEU	4.9
4	E	253	CYS	4.9
2	b	1095	VAL	4.9
2	b	1206	GLY	4.9
2	b	1469	HIS	4.9

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Mol	Chain	Res	Type	RSRZ
5	G	288	ASP	4.9
8	z	1479	VAL	4.9
2	b	1010	ASN	4.9
3	D	364	LEU	4.9
4	e	1052	LEU	4.9
3	d	1212	LYS	4.9
5	G	391	LEU	4.9
1	a	1158	SER	4.9
7	q	1167	SER	4.9
8	Z	270	ARG	4.9
6	H	367	ALA	4.9
7	q	1376	VAL	4.9
2	B	429	PRO	4.9
4	e	1421	GLY	4.8
3	D	361	SER	4.8
7	q	1394	ASP	4.8
1	a	1416	GLU	4.8
2	B	339	GLU	4.8
4	E	72	ASN	4.8
7	Q	185	GLN	4.8
3	d	1166	LEU	4.8
3	D	384	SER	4.8
6	H	493	TRP	4.8
3	d	1158	VAL	4.8
5	g	1202	GLU	4.8
8	z	1004	VAL	4.8
2	B	88	SER	4.8
1	A	241	LEU	4.8
5	G	87	GLN	4.8
2	B	240	ALA	4.8
4	e	1536	PRO	4.8
4	e	1023	ASP	4.8
7	Q	503	GLY	4.8
8	z	1194	MET	4.8
2	b	1492	GLY	4.8
4	e	1187	GLU	4.8
2	b	1045	PRO	4.8
8	Z	341	PRO	4.8
7	q	1377	LEU	4.8
6	H	477	VAL	4.8
5	G	383	ILE	4.8
7	q	1415	THR	4.8

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Mol	Chain	Res	Type	RSRZ
6	H	364	CYS	4.8
3	D	303	ILE	4.8
3	D	301	LEU	4.8
7	Q	184	ALA	4.8
6	H	361	PHE	4.8
3	d	1417	CYS	4.8
6	H	141	VAL	4.8
1	A	235	ALA	4.8
4	e	1072	ASN	4.8
1	a	1192	VAL	4.8
4	e	1389	GLY	4.8
7	q	1413	GLY	4.8
2	B	48	MET	4.8
8	z	1180	LYS	4.8
2	B	305	GLY	4.7
7	q	1171	LYS	4.7
2	B	320	VAL	4.7
7	Q	79	GLN	4.7
5	G	60	THR	4.7
8	Z	169	THR	4.7
8	Z	343	CYS	4.7
8	z	1185	PRO	4.7
4	E	491	ILE	4.7
1	A	328	LEU	4.7
4	e	1535	LYS	4.7
7	Q	325	CYS	4.7
5	g	1088	ASP	4.7
8	Z	348	GLY	4.7
4	e	1091	MET	4.7
7	Q	478	VAL	4.7
1	a	1505	GLU	4.7
1	A	179	ILE	4.7
2	B	160	MET	4.7
1	a	1087	GLY	4.7
6	H	232	TYR	4.7
5	G	12	GLN	4.7
3	d	1492	LYS	4.7
7	Q	206	LYS	4.7
5	G	376	LEU	4.7
8	z	1273	LYS	4.7
3	d	1194	VAL	4.7
7	q	1403	THR	4.7

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Mol	Chain	Res	Type	RSRZ
5	G	226	HIS	4.7
1	a	1175	ALA	4.7
1	a	1178	ALA	4.7
4	e	1193	VAL	4.7
6	H	196	GLY	4.7
3	D	230	LEU	4.7
6	H	405	VAL	4.7
2	b	1159	LEU	4.7
6	h	1168	ILE	4.7
6	H	458	THR	4.7
6	H	186	LEU	4.7
7	Q	408	LEU	4.7
2	B	306	ALA	4.7
5	G	173	CYS	4.7
1	A	144	GLY	4.7
5	G	169	SER	4.7
5	G	241	LEU	4.7
5	G	411	GLY	4.7
7	Q	461	ASN	4.7
8	Z	290	VAL	4.7
3	d	1189	MET	4.6
3	d	1167	LEU	4.6
8	z	1277	LEU	4.6
1	A	196	ASN	4.6
2	b	1400	THR	4.6
2	b	1488	MET	4.6
5	G	294	LYS	4.6
3	d	1208	LEU	4.6
1	a	1387	GLU	4.6
5	g	1214	VAL	4.6
3	D	171	ALA	4.6
4	e	1533	ILE	4.6
7	Q	246	PHE	4.6
1	A	280	ALA	4.6
7	q	1372	ILE	4.6
4	E	421	GLY	4.6
6	H	406	VAL	4.6
6	h	1094	THR	4.6
2	B	91	GLN	4.6
2	B	299	TYR	4.6
2	b	1401	VAL	4.6
8	Z	304	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
2	B	162	ILE	4.6
6	H	287	LYS	4.6
8	Z	395	LEU	4.6
7	q	1218	LEU	4.6
8	Z	335	SER	4.6
2	B	326	VAL	4.6
7	Q	149	CYS	4.6
2	b	1138	ARG	4.6
2	b	1162	ILE	4.6
8	z	1335	SER	4.6
3	D	316	ALA	4.6
5	G	292	THR	4.6
7	q	1180	ALA	4.6
3	D	323	MET	4.6
5	G	323	ILE	4.6
4	E	359	VAL	4.5
5	G	88	ASP	4.5
5	G	362	PHE	4.5
6	H	86	GLN	4.5
3	d	1193	ALA	4.5
2	b	1447	PRO	4.5
3	D	405	GLU	4.5
7	Q	148	CYS	4.5
3	D	242	THR	4.5
5	G	356	GLY	4.5
8	z	1478	GLY	4.5
1	a	1071	ALA	4.5
5	g	1398	CYS	4.5
7	Q	217	VAL	4.5
7	Q	301	ALA	4.5
6	H	350	GLU	4.5
8	z	1411	ALA	4.5
2	B	172	LEU	4.5
2	b	1017	ASP	4.5
8	Z	524	ALA	4.5
4	e	1177	VAL	4.5
8	Z	342	ASP	4.5
2	b	1183	ALA	4.5
7	Q	228	GLU	4.5
1	A	209	MET	4.5
1	a	1415	VAL	4.5
7	Q	304	TYR	4.5

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Mol	Chain	Res	Type	RSRZ
4	e	1051	SER	4.5
2	B	323	LEU	4.5
5	g	1506	TYR	4.5
8	z	1367	ASN	4.5
5	G	480	VAL	4.4
5	G	10	LEU	4.4
7	Q	164	LEU	4.4
5	G	387	VAL	4.4
1	A	193	ASN	4.4
3	D	23	GLY	4.4
1	a	1434	GLU	4.4
6	h	1013	THR	4.4
7	Q	362	VAL	4.4
5	G	388	GLU	4.4
6	H	411	ALA	4.4
5	G	204	ILE	4.4
8	z	1314	ARG	4.4
5	g	1371	ALA	4.4
6	h	1438	TYR	4.4
2	b	1524	ALA	4.4
1	a	1449	PRO	4.4
4	E	257	PRO	4.4
6	h	1150	GLU	4.4
2	B	523	ALA	4.4
7	Q	221	MET	4.4
2	B	364	GLY	4.4
6	h	1092	ASP	4.4
8	Z	498	TYR	4.4
5	g	1522	ILE	4.4
3	D	339	ILE	4.4
7	Q	410	PRO	4.4
1	a	1414	ALA	4.4
8	Z	208	ARG	4.4
2	B	65	ASN	4.4
7	Q	212	VAL	4.4
1	a	1412	GLY	4.4
2	b	1160	MET	4.4
3	D	186	LEU	4.4
4	e	1083	VAL	4.4
8	Z	412	GLY	4.4
2	B	474	THR	4.4
5	G	295	GLY	4.4

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Mol	Chain	Res	Type	RSRZ
7	q	1471	HIS	4.4
3	D	169	SER	4.4
3	d	1227	VAL	4.4
7	q	1187	CYS	4.4
5	G	302	HIS	4.4
6	H	325	ALA	4.4
8	Z	188	LEU	4.4
7	Q	482	ILE	4.4
1	A	374	SER	4.4
7	Q	238	LYS	4.4
8	Z	355	LEU	4.4
3	D	335	ASP	4.4
2	B	165	THR	4.3
8	Z	181	LYS	4.3
1	a	1469	ALA	4.3
7	Q	303	HIS	4.3
7	q	1185	GLN	4.3
8	z	1369	PRO	4.3
3	D	104	GLU	4.3
8	Z	143	MET	4.3
3	D	107	ASP	4.3
8	Z	39	GLY	4.3
6	h	1205	LEU	4.3
7	Q	471	HIS	4.3
1	A	86	VAL	4.3
1	A	375	VAL	4.3
5	g	1198	TYR	4.3
7	q	1409	VAL	4.3
5	g	1402	LEU	4.3
1	a	1395	ALA	4.3
6	H	484	ILE	4.3
2	b	1198	ALA	4.3
6	H	362	THR	4.3
8	Z	352	GLU	4.3
7	Q	143	LEU	4.3
4	e	1217	GLY	4.3
2	B	363	SER	4.3
8	Z	152	ALA	4.3
1	a	1121	TYR	4.3
5	G	316	ARG	4.3
7	q	1423	ILE	4.3
4	e	1219	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
8	Z	170	GLU	4.3
8	Z	220	ASP	4.3
3	D	211	ILE	4.3
7	q	1024	GLY	4.3
5	g	1434	GLN	4.3
6	H	412	ILE	4.3
7	q	1051	GLY	4.3
1	A	208	SER	4.3
8	Z	176	ILE	4.3
2	B	64	THR	4.2
4	e	1492	ASP	4.2
8	Z	327	ALA	4.2
1	A	364	ILE	4.2
3	d	1105	ALA	4.2
4	e	1208	LEU	4.2
6	H	198	LYS	4.2
4	e	1188	ILE	4.2
8	Z	410	GLY	4.2
3	D	343	ILE	4.2
6	H	285	GLY	4.2
7	Q	64	PHE	4.2
8	z	1349	LEU	4.2
4	e	1160	LYS	4.2
2	B	283	LEU	4.2
8	z	1412	GLY	4.2
6	h	1070	ASP	4.2
3	d	1141	GLN	4.2
6	H	282	HIS	4.2
7	Q	135	ALA	4.2
7	Q	203	ARG	4.2
2	b	1047	GLY	4.2
6	H	359	ASN	4.2
3	D	380	THR	4.2
6	H	15	SER	4.2
2	B	275	MET	4.2
3	d	1215	LYS	4.2
3	d	1414	VAL	4.2
3	d	1415	ILE	4.2
5	G	313	ARG	4.2
4	e	1395	ILE	4.2
1	A	4	PRO	4.2
3	D	393	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
7	q	1069	ALA	4.2
8	Z	303	ASP	4.2
1	A	396	LEU	4.2
7	q	1163	LEU	4.2
8	Z	408	VAL	4.2
1	a	1468	ARG	4.2
8	z	1374	LEU	4.2
4	E	490	GLY	4.2
2	B	439	TYR	4.2
7	q	1397	ASN	4.2
3	D	379	ILE	4.2
1	a	1495	PRO	4.2
4	E	420	TYR	4.2
5	g	1437	TYR	4.2
3	D	187	SER	4.2
8	z	1270	ARG	4.2
1	A	233	LYS	4.2
1	A	367	THR	4.2
3	D	317	LEU	4.2
2	B	493	ILE	4.2
1	A	36	LEU	4.2
1	a	1419	LEU	4.2
2	B	410	GLY	4.1
6	h	1494	GLU	4.1
4	E	325	VAL	4.1
5	G	228	ARG	4.1
6	H	371	THR	4.1
7	Q	285	ASP	4.1
8	Z	309	GLY	4.1
4	e	1507	ILE	4.1
8	z	1324	LEU	4.1
2	b	1096	GLY	4.1
3	D	225	GLU	4.1
8	Z	367	ASN	4.1
6	h	1521	LYS	4.1
1	A	371	THR	4.1
2	B	333	SER	4.1
5	G	220	ILE	4.1
2	b	1412	CYS	4.1
8	z	1303	ASP	4.1
1	A	303	ALA	4.1
7	Q	229	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
5	G	238	ILE	4.1
3	D	362	ALA	4.1
6	H	197	ILE	4.1
3	d	1387	LYS	4.1
5	G	301	GLN	4.1
1	a	1417	ALA	4.1
7	q	1399	PHE	4.1
3	D	240	GLY	4.1
5	g	1376	LEU	4.1
8	Z	190	MET	4.1
7	q	1176	GLU	4.1
3	D	342	THR	4.1
8	Z	325	THR	4.1
4	e	1181	CYS	4.1
2	B	168	SER	4.1
5	G	92	GLY	4.1
7	Q	56	VAL	4.1
7	q	1391	ALA	4.1
1	A	234	ILE	4.1
2	B	81	ALA	4.1
2	b	1397	LEU	4.1
7	Q	442	ALA	4.1
1	a	1005	LEU	4.1
4	e	1164	PRO	4.1
7	Q	222	VAL	4.1
6	h	1406	VAL	4.0
8	Z	393	ASP	4.0
3	d	1416	ARG	4.0
5	G	209	ILE	4.0
8	z	1232	THR	4.0
4	E	360	LYS	4.0
7	q	1420	ALA	4.0
7	Q	226	GLU	4.0
2	b	1468	ALA	4.0
3	d	1391	ILE	4.0
2	B	195	ASN	4.0
1	A	207	GLU	4.0
3	d	1195	MET	4.0
6	H	403	ASP	4.0
6	h	1183	VAL	4.0
1	a	1486	ILE	4.0
6	h	1184	MET	4.0

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Mol	Chain	Res	Type	RSRZ
7	Q	498	LEU	4.0
8	Z	186	ILE	4.0
7	q	1017	GLU	4.0
6	H	195	ILE	4.0
1	a	1392	LEU	4.0
8	z	1347	ALA	4.0
7	Q	168	VAL	4.0
3	D	404	ALA	4.0
5	g	1137	LEU	4.0
8	z	1395	LEU	4.0
4	e	1481	GLN	4.0
4	e	1167	GLN	4.0
4	e	1057	LEU	4.0
5	G	350	LEU	4.0
3	D	106	GLY	4.0
4	E	21	ASP	4.0
4	e	1162	THR	4.0
3	D	226	LEU	4.0
6	H	199	LYS	4.0
3	D	370	LEU	4.0
4	e	1194	LEU	4.0
5	G	278	LEU	4.0
5	g	1374	ILE	4.0
5	G	381	LYS	4.0
3	d	1066	ASP	4.0
8	z	1008	ASN	4.0
2	b	1214	LEU	4.0
3	d	1192	ASP	4.0
7	q	1056	VAL	4.0
8	Z	269	ASP	4.0
8	z	1365	LYS	4.0
7	q	1527	ALA	4.0
3	D	331	ILE	4.0
5	G	336	GLU	4.0
7	q	1477	ASN	4.0
8	Z	478	GLY	4.0
5	G	382	GLU	4.0
6	h	1197	ILE	3.9
6	H	284	SER	3.9
8	Z	391	ILE	3.9
2	b	1097	ASP	3.9
4	e	1221	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
8	Z	523	ARG	3.9
4	E	456	GLU	3.9
2	b	1046	LYS	3.9
1	A	296	CYS	3.9
4	e	1184	GLN	3.9
7	q	1183	ILE	3.9
3	d	1197	VAL	3.9
5	G	42	GLY	3.9
7	Q	349	SER	3.9
4	E	314	LEU	3.9
7	q	1392	VAL	3.9
7	Q	173	TYR	3.9
1	A	211	ILE	3.9
1	a	1402	VAL	3.9
2	B	346	CYS	3.9
7	Q	233	SER	3.9
7	q	1211	GLY	3.9
1	A	47	ASP	3.9
8	z	1344	LEU	3.9
1	A	6	SER	3.9
2	b	1413	SER	3.9
3	D	471	ASN	3.9
7	Q	375	ILE	3.9
2	b	1486	GLY	3.9
2	B	49	ASP	3.9
8	Z	155	SER	3.9
7	Q	452	LEU	3.9
4	e	1419	VAL	3.9
3	d	1424	LEU	3.9
2	b	1428	THR	3.9
3	D	387	LYS	3.9
1	A	315	ASP	3.9
5	G	229	MET	3.9
1	a	1467	LEU	3.9
7	Q	441	PHE	3.9
2	b	1463	ALA	3.9
4	e	1048	MET	3.9
4	e	1218	ARG	3.9
7	q	1416	GLU	3.9
3	D	193	ALA	3.9
3	d	1390	THR	3.9
6	h	1098	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	300	PHE	3.9
7	Q	65	VAL	3.9
3	d	1144	LEU	3.9
1	a	1207	GLU	3.8
2	B	277	GLU	3.8
4	e	1216	GLY	3.8
4	E	324	TRP	3.8
1	a	1518	THR	3.8
6	H	90	VAL	3.8
5	G	225	THR	3.8
7	Q	423	ILE	3.8
6	H	523	PRO	3.8
5	g	1212	SER	3.8
7	Q	404	ARG	3.8
1	a	1190	TYR	3.8
5	g	1388	GLU	3.8
7	Q	445	PHE	3.8
7	Q	328	VAL	3.8
6	H	495	PRO	3.8
7	Q	292	VAL	3.8
1	A	504	PHE	3.8
2	B	12	PHE	3.8
7	Q	409	VAL	3.8
2	B	285	HIS	3.8
4	E	310	ALA	3.8
3	D	391	ILE	3.8
4	E	240	PRO	3.8
1	a	1085	GLU	3.8
2	B	197	GLU	3.8
7	q	1389	GLU	3.8
4	e	1171	THR	3.8
2	b	1156	ARG	3.8
4	E	241	LYS	3.8
3	d	1504	SER	3.8
5	G	521	ASP	3.8
3	D	299	ASN	3.8
8	Z	276	GLU	3.8
4	E	320	PRO	3.8
4	E	448	MET	3.8
8	z	1366	CYS	3.8
2	B	431	LYS	3.8
6	H	217	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
7	Q	245	PRO	3.8
1	A	37	GLY	3.8
4	e	1462	LEU	3.8
1	a	1506	PRO	3.8
7	q	1206	LYS	3.8
6	h	1090	VAL	3.8
8	Z	172	VAL	3.8
7	Q	59	HIS	3.8
5	G	352	ILE	3.8
7	q	1155	ARG	3.8
8	z	1190	MET	3.8
2	b	1185	GLU	3.8
7	q	1504	LYS	3.8
3	D	257	SER	3.8
6	H	407	ALA	3.8
7	q	1149	CYS	3.8
5	G	395	MET	3.8
8	z	1362	PHE	3.8
4	E	239	MET	3.7
6	H	346	GLN	3.7
4	e	1466	SER	3.7
3	D	194	VAL	3.7
3	d	1143	ALA	3.7
8	Z	156	LEU	3.7
2	B	389	SER	3.7
7	Q	183	ILE	3.7
3	D	191	VAL	3.7
7	Q	418	GLU	3.7
8	z	1084	GLN	3.7
4	E	345	PHE	3.7
4	e	1478	ARG	3.7
2	B	476	ALA	3.7
6	H	457	ALA	3.7
1	A	318	ARG	3.7
2	B	97	ASP	3.7
2	B	180	THR	3.7
4	E	71	THR	3.7
5	G	41	LEU	3.7
4	e	1103	GLY	3.7
5	G	56	GLY	3.7
8	Z	89	GLY	3.7
2	b	1443	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
5	G	50	LEU	3.7
7	Q	97	VAL	3.7
1	A	189	ARG	3.7
2	b	1498	GLN	3.7
4	e	1489	LEU	3.7
8	z	1191	VAL	3.7
5	G	161	THR	3.7
5	G	522	ILE	3.7
2	B	302	GLN	3.7
7	q	1526	MET	3.7
8	z	1409	PRO	3.7
4	E	478	ARG	3.7
7	Q	456	SER	3.7
8	z	1337	ASP	3.7
2	B	242	THR	3.7
5	G	280	GLU	3.7
2	b	1161	ASN	3.7
6	h	1372	ILE	3.7
7	q	1146	LEU	3.7
8	z	1050	GLY	3.7
3	d	1418	LEU	3.7
3	d	1179	VAL	3.7
8	z	1159	LYS	3.7
1	A	282	GLY	3.7
1	a	1191	PRO	3.7
2	b	1429	PRO	3.7
1	a	1378	ARG	3.7
2	B	42	THR	3.7
3	d	1191	VAL	3.7
3	d	1058	LYS	3.7
5	G	307	ALA	3.7
2	B	369	GLU	3.6
6	h	1473	MET	3.6
5	g	1401	VAL	3.6
8	z	1175	SER	3.6
7	q	1103	PHE	3.6
1	a	1050	GLY	3.6
3	d	1210	ASP	3.6
7	Q	241	VAL	3.6
7	q	1147	VAL	3.6
8	Z	443	ALA	3.6
6	H	290	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
7	Q	165	HIS	3.6
6	H	183	VAL	3.6
8	Z	406	CYS	3.6
4	e	1059	LYS	3.6
8	Z	479	VAL	3.6
5	G	37	ILE	3.6
2	B	234	ASN	3.6
2	B	477	GLY	3.6
3	D	319	PHE	3.6
3	D	300	VAL	3.6
7	q	1448	ILE	3.6
8	Z	319	ARG	3.6
1	A	197	VAL	3.6
1	a	1171	LEU	3.6
8	Z	173	VAL	3.6
1	A	293	ASP	3.6
5	g	1521	ASP	3.6
8	z	1495	TRP	3.6
2	B	50	LYS	3.6
2	b	1446	LEU	3.6
3	D	390	THR	3.6
5	G	179	ALA	3.6
4	E	372	LEU	3.6
1	a	1400	LYS	3.6
2	B	386	ALA	3.6
8	Z	8	ASN	3.6
1	a	1428	THR	3.6
8	Z	495	TRP	3.6
8	Z	409	PRO	3.6
8	Z	444	LEU	3.6
1	a	1048	ASP	3.6
7	Q	346	HIS	3.6
1	A	279	LEU	3.6
1	a	1143	LEU	3.6
6	H	190	LEU	3.6
4	E	375	GLU	3.6
2	b	1182	LEU	3.6
8	z	1497	ASN	3.6
6	H	413	GLU	3.6
7	q	1386	ASP	3.6
5	g	1092	GLY	3.6
2	B	179	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
7	Q	247	ASP	3.6
8	z	1085	ASP	3.6
8	z	1193	ILE	3.6
8	z	1306	ALA	3.6
1	A	277	LYS	3.6
1	a	1390	ARG	3.6
5	G	380	SER	3.6
4	E	433	VAL	3.6
1	A	326	THR	3.5
2	B	19	GLU	3.5
1	A	176	VAL	3.5
6	H	358	TYR	3.5
2	b	1158	ASP	3.5
5	G	57	ILE	3.5
7	q	1170	SER	3.5
8	z	1523	ARG	3.5
3	d	1168	ASN	3.5
3	d	1214	VAL	3.5
3	d	1190	SER	3.5
1	A	148	LEU	3.5
7	Q	406	LYS	3.5
2	B	469	HIS	3.5
3	D	101	GLN	3.5
3	D	221	ILE	3.5
3	d	1425	ILE	3.5
8	z	1041	LYS	3.5
1	A	495	PRO	3.5
4	E	166	ILE	3.5
6	H	245	GLU	3.5
6	H	91	GLY	3.5
6	h	1119	GLN	3.5
3	d	1503	ILE	3.5
5	G	298	ASP	3.5
2	B	314	HIS	3.5
7	Q	205	CYS	3.5
6	h	1015	SER	3.5
7	Q	283	ILE	3.5
2	B	330	GLU	3.5
2	B	159	LEU	3.5
5	G	506	TYR	3.5
8	z	1370	ARG	3.5
1	a	1504	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
2	b	1196	LEU	3.5
2	b	1201	VAL	3.5
3	d	1205	SER	3.5
4	e	1049	LYS	3.5
8	Z	501	LYS	3.5
2	B	77	ASP	3.5
1	a	1007	VAL	3.5
2	B	161	ASN	3.5
2	b	1141	LEU	3.5
5	G	158	SER	3.5
5	G	170	SER	3.5
6	h	1413	GLU	3.5
6	H	303	PHE	3.5
6	H	357	ARG	3.5
6	H	446	PRO	3.5
6	h	1442	LEU	3.5
8	Z	362	PHE	3.5
2	b	1370	ALA	3.5
5	G	172	ALA	3.5
4	E	498	THR	3.5
8	Z	302	LEU	3.5
5	G	199	ALA	3.5
7	Q	139	ALA	3.5
8	z	1070	GLN	3.5
3	d	1106	GLY	3.5
6	h	1186	LEU	3.5
6	h	1132	ALA	3.5
8	z	1332	ALA	3.5
1	A	366	ASN	3.5
4	E	59	LYS	3.5
4	e	1534	ARG	3.5
2	B	367	LEU	3.4
2	b	1501	ARG	3.4
3	D	416	ARG	3.4
7	q	1385	MET	3.4
1	a	1181	TYR	3.4
3	d	1514	PRO	3.4
6	h	1211	VAL	3.4
8	z	1040	PRO	3.4
3	D	382	CYS	3.4
2	B	276	LYS	3.4
7	Q	504	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
6	H	473	MET	3.4
1	a	1410	PRO	3.4
6	h	1195	ILE	3.4
8	Z	494	ILE	3.4
5	G	314	ARG	3.4
6	H	239	LEU	3.4
7	q	1449	PRO	3.4
1	A	343	SER	3.4
8	Z	224	ARG	3.4
3	D	258	ALA	3.4
4	E	18	ILE	3.4
7	q	1068	ASP	3.4
6	H	150	GLU	3.4
6	h	1180	VAL	3.4
7	Q	167	SER	3.4
2	B	492	GLY	3.4
1	a	1209	MET	3.4
5	G	379	ALA	3.4
4	e	1444	GLU	3.4
1	A	48	ASP	3.4
1	A	228	ARG	3.4
2	b	1187	VAL	3.4
5	G	231	ARG	3.4
5	G	346	GLY	3.4
8	Z	388	LYS	3.4
2	B	45	PRO	3.4
4	e	1027	ARG	3.4
8	z	1276	GLU	3.4
4	e	1215	VAL	3.4
7	q	1408	LEU	3.4
8	Z	396	ARG	3.4
8	z	1298	ASP	3.4
2	B	292	ASN	3.4
2	B	351	GLU	3.4
5	G	63	GLY	3.4
5	G	378	GLY	3.4
1	a	1049	ILE	3.4
3	d	1406	ARG	3.4
8	z	1331	ILE	3.4
1	A	365	LYS	3.4
3	D	427	GLY	3.4
6	h	1369	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	351	VAL	3.4
1	a	1038	PRO	3.4
4	e	1087	ILE	3.4
5	G	176	ALA	3.4
6	H	187	ASP	3.4
7	Q	502	LEU	3.4
1	A	292	ILE	3.4
8	z	1376	ILE	3.4
2	b	1399	GLN	3.4
4	E	103	GLY	3.4
4	E	308	ASP	3.4
1	A	51	ASP	3.3
7	q	1168	VAL	3.3
5	G	276	GLN	3.3
6	H	79	LEU	3.3
7	Q	419	LEU	3.3
8	Z	525	GLY	3.3
1	A	325	ALA	3.3
1	A	91	THR	3.3
7	q	1388	ILE	3.3
8	Z	368	ASN	3.3
2	b	1134	THR	3.3
5	g	1519	ILE	3.3
6	h	1520	ILE	3.3
8	Z	207	ILE	3.3
6	h	1472	GLY	3.3
7	q	1159	GLU	3.3
4	e	1058	ASP	3.3
8	Z	415	GLU	3.3
6	h	1010	LYS	3.3
8	Z	397	ALA	3.3
1	A	276	GLN	3.3
4	E	348	LEU	3.3
2	B	44	GLY	3.3
3	d	1431	PRO	3.3
3	D	302	LEU	3.3
1	a	1409	VAL	3.3
5	g	1133	MET	3.3
2	B	184	VAL	3.3
5	G	386	GLU	3.3
3	D	57	PRO	3.3
6	H	353	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
7	Q	98	GLY	3.3
1	a	1072	ALA	3.3
5	G	305	MET	3.3
2	b	1450	ILE	3.3
7	q	1192	PRO	3.3
2	b	1211	ASP	3.3
2	B	202	ILE	3.3
7	Q	163	LEU	3.3
8	Z	226	GLU	3.3
7	Q	276	MET	3.3
7	Q	300	MET	3.3
2	B	394	LEU	3.3
5	g	1159	SER	3.3
7	Q	103	PHE	3.3
8	Z	370	ARG	3.3
2	b	1431	LYS	3.3
4	e	1458	ILE	3.3
2	b	1467	ALA	3.3
3	D	172	THR	3.3
1	a	1075	LEU	3.3
5	g	1391	LEU	3.3
4	e	1180	SER	3.3
1	A	352	VAL	3.3
2	b	1475	THR	3.3
6	h	1190	LEU	3.3
1	A	284	ASN	3.3
8	Z	219	PRO	3.3
3	D	293	ILE	3.3
3	d	1427	GLY	3.3
5	g	1390	ASN	3.3
7	Q	314	ARG	3.2
1	a	1438	ILE	3.2
4	e	1037	HIS	3.2
8	z	1296	GLY	3.2
6	h	1063	ALA	3.2
1	A	62	LEU	3.2
5	G	233	ILE	3.2
7	Q	330	ALA	3.2
3	d	1515	LEU	3.2
4	E	23	ASP	3.2
6	H	398	ARG	3.2
4	e	1021	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
8	Z	298	ASP	3.2
1	A	242	GLN	3.2
1	a	1435	GLN	3.2
4	e	1407	CYS	3.2
8	z	1152	ALA	3.2
2	B	368	GLY	3.2
2	b	1515	LEU	3.2
3	d	1435	LEU	3.2
8	Z	9	PRO	3.2
8	z	1351	TYR	3.2
4	E	60	MET	3.2
1	a	1003	GLY	3.2
8	Z	374	LEU	3.2
3	D	351	VAL	3.2
3	D	415	ILE	3.2
5	g	1017	GLU	3.2
7	Q	361	VAL	3.2
2	B	328	GLY	3.2
2	b	1439	TYR	3.2
6	H	363	GLY	3.2
7	Q	323	ARG	3.2
2	b	1018	GLU	3.2
1	A	69	HIS	3.2
6	H	231	LYS	3.2
8	Z	6	THR	3.2
1	a	1206	MET	3.2
5	G	303	TYR	3.2
1	a	1004	PRO	3.2
2	B	316	ASP	3.2
3	D	388	THR	3.2
7	Q	374	THR	3.2
2	B	80	ALA	3.2
2	B	156	ARG	3.2
2	b	1378	ALA	3.2
4	E	344	ARG	3.2
4	e	1498	THR	3.2
5	G	240	LEU	3.2
7	q	1023	SER	3.2
8	z	1014	ALA	3.2
3	d	1439	LEU	3.2
5	G	393	ASP	3.2
8	z	1090	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	a	1431	GLY	3.2
2	B	390	LEU	3.2
3	d	1172	THR	3.2
8	Z	93	THR	3.2
3	D	249	ILE	3.2
4	E	497	GLY	3.2
5	G	279	CYS	3.2
1	A	410	PRO	3.2
5	G	53	PRO	3.2
6	H	435	ILE	3.2
7	Q	181	LYS	3.2
5	g	1072	VAL	3.2
7	q	1501	TYR	3.2
8	z	1340	ASN	3.2
2	B	465	LEU	3.2
3	D	199	ASP	3.2
2	B	447	PRO	3.2
2	b	1402	LYS	3.2
5	G	153	LEU	3.2
6	H	306	ARG	3.2
2	b	1209	LEU	3.1
4	e	1026	SER	3.1
5	g	1523	VAL	3.1
2	B	480	MET	3.1
8	z	1359	LYS	3.1
3	d	1067	GLY	3.1
2	B	415	MET	3.1
4	e	1071	THR	3.1
6	h	1370	CYS	3.1
3	D	228	GLU	3.1
8	Z	369	PRO	3.1
7	q	1199	VAL	3.1
4	e	1490	GLY	3.1
7	q	1479	GLY	3.1
4	E	422	GLY	3.1
6	h	1012	GLY	3.1
4	E	319	LEU	3.1
6	h	1396	VAL	3.1
4	E	25	LYS	3.1
4	E	474	MET	3.1
5	G	55	GLY	3.1
7	Q	350	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	213	GLY	3.1
1	A	236	CYS	3.1
8	z	1475	GLN	3.1
1	A	322	ALA	3.1
1	a	1418	ALA	3.1
7	q	1467	LEU	3.1
8	Z	306	ALA	3.1
7	Q	400	LYS	3.1
2	b	1396	VAL	3.1
3	d	1069	GLY	3.1
7	Q	186	ALA	3.1
6	h	1125	PHE	3.1
7	Q	178	PHE	3.1
5	G	277	GLN	3.1
6	H	521	LYS	3.1
6	h	1410	GLY	3.1
8	Z	64	LEU	3.1
1	A	329	SER	3.1
3	d	1162	ASP	3.1
1	A	409	VAL	3.1
2	B	295	LEU	3.1
4	e	1454	ALA	3.1
6	h	1163	LEU	3.1
8	z	1481	LEU	3.1
1	a	1045	LEU	3.1
2	B	76	VAL	3.1
2	b	1009	VAL	3.1
2	b	1193	SER	3.1
6	H	89	GLU	3.1
8	z	1360	PHE	3.1
1	A	203	ARG	3.1
4	e	1468	MET	3.1
3	d	1196	LYS	3.1
3	d	1419	VAL	3.1
6	H	92	ASP	3.1
7	q	1402	LEU	3.1
5	g	1126	TYR	3.1
5	g	1209	ILE	3.1
5	g	1394	ALA	3.1
2	B	387	GLU	3.0
1	A	175	ALA	3.0
2	B	318	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
2	b	1011	ILE	3.0
3	d	1165	THR	3.0
6	h	1086	GLN	3.0
8	z	1155	SER	3.0
1	A	152	ALA	3.0
4	E	169	ALA	3.0
5	G	357	ASP	3.0
5	g	1037	ILE	3.0
3	d	1421	LYS	3.0
8	Z	376	ILE	3.0
8	z	1218	HIS	3.0
2	b	1212	SER	3.0
6	H	289	VAL	3.0
7	Q	417	ILE	3.0
2	B	103	THR	3.0
2	b	1418	ALA	3.0
7	q	1401	VAL	3.0
6	H	368	LYS	3.0
2	B	186	ALA	3.0
7	q	1445	PHE	3.0
8	Z	360	PHE	3.0
3	D	355	THR	3.0
1	A	3	GLY	3.0
1	A	405	SER	3.0
1	A	505	GLU	3.0
3	d	1025	SER	3.0
6	H	158	CYS	3.0
1	a	1053	THR	3.0
3	d	1175	ASN	3.0
3	D	363	GLU	3.0
1	A	400	LYS	3.0
4	e	1398	ALA	3.0
1	A	323	SER	3.0
2	b	1063	VAL	3.0
4	E	318	ASP	3.0
5	G	398	CYS	3.0
6	H	464	LEU	3.0
8	z	1341	PRO	3.0
3	D	241	ILE	3.0
8	z	1034	LEU	3.0
3	d	1494	THR	3.0
7	Q	43	THR	3.0

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Mol	Chain	Res	Type	RSRZ
6	H	414	MET	3.0
6	H	420	LEU	3.0
4	e	1420	TYR	3.0
1	a	1079	ALA	3.0
2	b	1398	ALA	3.0
4	e	1220	GLU	3.0
5	G	320	ASN	3.0
1	A	488	LEU	3.0
4	E	204	VAL	3.0
4	e	1390	GLY	3.0
5	g	1152	MET	3.0
5	g	1395	MET	3.0
8	z	1302	LEU	3.0
1	A	305	ALA	3.0
4	e	1099	ASP	3.0
6	H	295	ILE	3.0
8	Z	392	ARG	3.0
3	D	386	GLY	3.0
1	a	1062	LEU	3.0
2	B	43	LEU	3.0
3	d	1186	LEU	3.0
6	H	399	ALA	3.0
7	Q	378	ARG	3.0
7	q	1151	ALA	3.0
8	z	1038	LEU	3.0
7	Q	216	SER	3.0
8	Z	475	GLN	3.0
2	B	245	ASP	3.0
7	q	1198	ASN	3.0
4	E	252	THR	3.0
5	G	180	VAL	3.0
7	q	1046	ALA	3.0
8	z	1317	LYS	3.0
6	H	328	GLY	3.0
2	b	1504	LEU	3.0
6	h	1367	ALA	3.0
6	h	1414	MET	3.0
7	q	1055	MET	3.0
7	Q	497	VAL	3.0
5	G	96	THR	3.0
4	E	251	LEU	3.0
6	h	1475	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
7	Q	48	GLY	3.0
7	Q	200	ASP	3.0
1	A	370	ARG	2.9
6	H	415	GLU	2.9
2	B	183	ALA	2.9
4	e	1400	ARG	2.9
3	D	354	PHE	2.9
7	Q	242	TYR	2.9
2	b	1517	VAL	2.9
6	H	326	CYS	2.9
8	Z	228	ALA	2.9
6	h	1386	GLU	2.9
1	a	1490	LEU	2.9
7	q	1419	LEU	2.9
7	Q	402	LEU	2.9
8	Z	63	LEU	2.9
6	H	370	CYS	2.9
5	G	171	LEU	2.9
6	H	355	GLY	2.9
8	Z	322	GLU	2.9
3	d	1472	ALA	2.9
2	b	1147	ASP	2.9
3	d	1207	ASP	2.9
7	Q	160	VAL	2.9
7	q	1480	LEU	2.9
8	Z	329	GLY	2.9
7	Q	145	ASP	2.9
4	E	374	ILE	2.9
8	Z	401	ALA	2.9
3	D	24	LYS	2.9
1	A	319	ILE	2.9
2	b	1523	ALA	2.9
7	Q	172	GLN	2.9
7	q	1393	ASP	2.9
1	a	1120	GLY	2.9
6	H	312	GLY	2.9
6	H	425	ARG	2.9
3	d	1225	GLU	2.9
2	b	1167	LEU	2.9
4	E	55	ASN	2.9
1	A	304	GLY	2.9
2	b	1025	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
2	b	1444	ARG	2.9
6	h	1493	TRP	2.9
7	Q	339	PRO	2.9
1	A	67	VAL	2.9
1	A	299	TYR	2.9
4	E	101	GLU	2.9
5	G	243	SER	2.9
3	D	58	LYS	2.9
2	B	18	GLU	2.9
7	Q	446	GLU	2.9
2	b	1480	MET	2.9
3	d	1407	SER	2.9
7	q	1175	ASN	2.9
4	E	144	ALA	2.9
4	e	1041	ALA	2.9
1	a	1131	TYR	2.9
3	d	1413	CYS	2.9
4	e	1210	LYS	2.9
7	Q	329	GLY	2.9
1	a	1139	ASN	2.9
4	e	1506	VAL	2.9
8	z	1160	VAL	2.9
3	D	392	VAL	2.8
6	H	322	THR	2.8
8	z	1346	HIS	2.8
5	G	61	ASN	2.8
6	H	419	TYR	2.8
6	H	235	PRO	2.8
1	a	1189	ARG	2.8
3	d	1429	GLY	2.8
2	b	1514	ILE	2.8
7	Q	388	ILE	2.8
7	q	1193	ASP	2.8
3	d	1405	GLU	2.8
7	q	1090	SER	2.8
3	d	1163	ARG	2.8
4	E	449	ARG	2.8
4	e	1195	THR	2.8
1	A	401	ARG	2.8
2	B	47	GLY	2.8
6	H	83	ALA	2.8
8	Z	407	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	363	LEU	2.8
2	B	397	LEU	2.8
4	e	1050	THR	2.8
3	d	1224	CYS	2.8
8	z	1328	CYS	2.8
1	A	5	LEU	2.8
6	H	321	ARG	2.8
7	q	1482	ILE	2.8
4	E	512	GLY	2.8
7	Q	58	ASN	2.8
8	Z	339	LEU	2.8
2	B	396	VAL	2.8
8	Z	356	GLY	2.8
4	e	1427	ILE	2.8
1	A	327	VAL	2.8
4	E	66	GLY	2.8
3	D	484	ARG	2.8
3	D	109	THR	2.8
6	h	1412	ILE	2.8
3	d	1410	ASP	2.8
8	Z	448	PRO	2.8
3	D	84	MET	2.8
8	Z	77	ILE	2.8
2	b	1168	SER	2.8
6	h	1011	GLU	2.8
7	Q	77	GLU	2.8
2	B	391	HIS	2.8
3	d	1507	LEU	2.8
6	h	1188	ASP	2.8
1	a	1388	MET	2.8
5	G	84	SER	2.8
5	G	476	GLU	2.8
4	E	515	GLN	2.8
5	g	1093	ASP	2.8
8	z	1233	CYS	2.8
4	E	509	THR	2.8
2	b	1172	LEU	2.8
5	G	385	SER	2.8
8	z	1377	LYS	2.8
3	d	1449	MET	2.8
6	H	450	CYS	2.8
2	B	182	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
3	d	1151	LEU	2.8
3	D	205	SER	2.8
4	E	237	PRO	2.8
7	Q	483	GLU	2.8
2	B	464	GLN	2.8
2	b	1207	GLY	2.8
6	h	1087	ASP	2.8
8	z	1161	HIS	2.8
2	b	1462	VAL	2.8
5	G	201	VAL	2.8
5	g	1130	LEU	2.8
4	E	309	GLU	2.8
6	h	1170	GLN	2.8
1	a	1046	VAL	2.8
8	z	1151	VAL	2.8
8	z	1333	LEU	2.8
4	e	1086	GLN	2.8
8	z	1187	ASP	2.8
4	e	1163	GLU	2.8
6	H	281	ILE	2.8
7	q	1396	VAL	2.8
5	G	36	ILE	2.8
2	b	1394	LEU	2.7
2	b	1430	GLY	2.7
8	Z	81	ALA	2.7
6	H	421	ARG	2.7
1	a	1088	ASP	2.7
4	E	78	LEU	2.7
6	h	1519	THR	2.7
6	H	466	ALA	2.7
1	A	354	GLU	2.7
2	b	1028	SER	2.7
5	g	1524	SER	2.7
8	Z	147	THR	2.7
8	z	1013	VAL	2.7
1	a	1441	PHE	2.7
1	a	1380	ALA	2.7
3	d	1516	LEU	2.7
2	B	284	LYS	2.7
2	b	1044	GLY	2.7
4	e	1463	ALA	2.7
2	B	436	MET	2.7

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Mol	Chain	Res	Type	RSRZ
5	g	1053	PRO	2.7
3	D	102	ASP	2.7
4	e	1443	LEU	2.7
5	g	1026	ASN	2.7
7	Q	331	THR	2.7
8	z	1188	LEU	2.7
1	A	506	PRO	2.7
6	h	1198	LYS	2.7
8	Z	432	ARG	2.7
2	B	9	VAL	2.7
5	G	286	LYS	2.7
6	h	1047	LYS	2.7
2	b	1186	ALA	2.7
5	g	1386	GLU	2.7
7	Q	481	ASP	2.7
8	z	1343	CYS	2.7
2	b	1483	GLY	2.7
6	H	438	TYR	2.7
8	Z	151	VAL	2.7
1	a	1058	GLY	2.7
5	G	214	VAL	2.7
6	H	143	VAL	2.7
8	z	1007	LEU	2.7
2	b	1464	GLN	2.7
6	H	159	ALA	2.7
8	z	1173	VAL	2.7
7	Q	468	TYR	2.7
1	a	1176	VAL	2.7
2	b	1179	PHE	2.7
2	B	349	ILE	2.7
7	q	1066	THR	2.7
3	D	462	GLU	2.7
6	H	396	VAL	2.7
7	q	1418	GLU	2.7
3	D	425	ILE	2.7
5	g	1373	THR	2.7
6	h	1390	HIS	2.7
5	g	1185	PHE	2.7
6	H	430	LYS	2.7
5	g	1436	PRO	2.7
5	G	397	VAL	2.7
1	A	79	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
2	b	1417	MET	2.7
4	E	430	ALA	2.7
4	E	455	LEU	2.7
1	A	378	ARG	2.7
3	D	402	GLU	2.7
8	z	1322	GLU	2.7
1	A	90	THR	2.7
1	A	402	VAL	2.7
4	e	1204	VAL	2.7
4	E	341	ILE	2.7
4	e	1065	ASP	2.7
5	g	1387	VAL	2.7
3	D	375	LYS	2.6
4	E	250	ILE	2.6
2	b	1049	ASP	2.6
7	q	1205	CYS	2.6
4	e	1401	SER	2.6
6	H	291	SER	2.6
5	G	66	ILE	2.6
6	h	1474	TRP	2.6
7	q	1417	ILE	2.6
8	Z	171	ALA	2.6
8	z	1174	ASP	2.6
7	q	1148	CYS	2.6
8	Z	84	GLN	2.6
8	Z	500	VAL	2.6
6	H	125	PHE	2.6
7	q	1502	LEU	2.6
3	D	461	MET	2.6
3	d	1471	ASN	2.6
4	E	317	ASN	2.6
7	Q	526	MET	2.6
6	H	360	PHE	2.6
6	h	1399	ALA	2.6
8	Z	38	LEU	2.6
8	z	1172	VAL	2.6
3	d	1412	LEU	2.6
6	H	462	ASN	2.6
3	D	417	CYS	2.6
3	D	243	ARG	2.6
5	G	401	VAL	2.6
1	a	1194	SER	2.6

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Mol	Chain	Res	Type	RSRZ
7	q	1143	LEU	2.6
7	q	1379	GLY	2.6
7	Q	53	ASN	2.6
1	A	357	CYS	2.6
7	Q	355	VAL	2.6
2	b	1205	LEU	2.6
5	G	293	GLU	2.6
8	z	1140	SER	2.6
4	E	300	ALA	2.6
4	e	1179	ASN	2.6
7	Q	136	CYS	2.6
7	Q	177	VAL	2.6
7	Q	144	PRO	2.6
2	b	1502	GLN	2.6
2	B	450	ILE	2.6
2	b	1155	PHE	2.6
2	b	1079	PRO	2.6
2	b	1520	ILE	2.6
1	A	65	LEU	2.6
8	Z	7	LEU	2.6
4	E	172	THR	2.6
5	g	1369	PRO	2.6
8	z	1493	GLY	2.6
7	q	1064	PHE	2.6
1	a	1487	GLY	2.6
3	D	55	LEU	2.6
2	B	78	ASN	2.6
8	Z	138	LYS	2.6
8	z	1235	VAL	2.6
1	A	75	LEU	2.6
3	D	208	LEU	2.6
4	e	1530	ILE	2.6
6	h	1465	ARG	2.6
8	Z	272	LYS	2.6
8	Z	472	GLU	2.6
7	q	1422	GLN	2.6
2	B	187	VAL	2.6
6	H	479	ILE	2.6
5	G	194	ASP	2.6
7	Q	455	ASN	2.6
3	D	184	SER	2.6
3	d	1457	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
6	H	73	HIS	2.6
3	d	1541	THR	2.6
6	H	98	THR	2.6
1	a	1052	VAL	2.6
2	B	130	TRP	2.6
4	e	1098	GLN	2.6
3	D	496	ILE	2.6
8	z	1353	TYR	2.6
2	b	1518	ASP	2.6
6	H	240	LEU	2.5
7	Q	199	VAL	2.5
7	Q	313	VAL	2.5
5	g	1502	LYS	2.5
7	q	1503	GLY	2.5
3	D	223	ASP	2.5
7	q	1086	ILE	2.5
1	A	58	GLY	2.5
1	a	1423	LEU	2.5
1	A	353	GLN	2.5
5	G	62	ASP	2.5
7	Q	525	ILE	2.5
8	z	1069	ILE	2.5
2	b	1194	GLY	2.5
6	H	42	PRO	2.5
2	B	340	LEU	2.5
4	e	1111	VAL	2.5
5	G	374	ILE	2.5
6	h	1062	GLY	2.5
2	b	1080	ALA	2.5
3	D	227	VAL	2.5
4	e	1110	VAL	2.5
3	d	1072	THR	2.5
4	e	1107	THR	2.5
3	D	371	ASN	2.5
3	d	1222	ASP	2.5
6	H	456	ASP	2.5
1	a	1124	ALA	2.5
6	H	139	ILE	2.5
3	D	255	CYS	2.5
6	H	206	GLU	2.5
8	Z	499	CYS	2.5
6	h	1069	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
8	Z	168	LEU	2.5
1	A	356	ILE	2.5
1	a	1377	LEU	2.5
2	b	1180	THR	2.5
3	D	449	MET	2.5
4	E	303	GLN	2.5
4	e	1423	GLY	2.5
7	Q	68	ASP	2.5
8	z	1398	VAL	2.5
7	q	1020	LYS	2.5
8	Z	308	GLU	2.5
3	D	72	THR	2.5
2	B	194	GLY	2.5
7	Q	377	LEU	2.5
7	q	1073	LEU	2.5
6	h	1082	ILE	2.5
8	Z	387	ILE	2.5
8	Z	515	ILE	2.5
4	E	48	MET	2.5
4	E	160	LYS	2.5
5	G	40	CYS	2.5
8	z	1012	GLU	2.5
1	A	399	VAL	2.5
2	b	1421	VAL	2.5
4	e	1418	VAL	2.5
3	D	411	ALA	2.5
1	a	1422	TYR	2.5
1	A	156	MET	2.5
2	B	171	LEU	2.5
3	D	140	PHE	2.5
2	B	350	GLU	2.5
3	D	389	VAL	2.5
4	E	471	ILE	2.5
1	a	1115	THR	2.5
5	g	1071	GLN	2.5
8	Z	67	MET	2.5
8	z	1176	ILE	2.5
1	a	1122	ARG	2.5
6	H	8	LEU	2.5
8	Z	349	LEU	2.5
1	A	321	LYS	2.5
7	Q	398	THR	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	519	ASN	2.5
4	E	82	ASP	2.5
4	E	305	GLY	2.5
3	d	1411	ALA	2.5
5	g	1147	SER	2.5
7	Q	351	TYR	2.5
1	a	1404	GLU	2.5
2	b	1142	LEU	2.5
6	h	1066	LEU	2.5
3	d	1180	SER	2.5
7	q	1166	THR	2.5
2	b	1376	ARG	2.5
8	Z	134	LEU	2.5
6	h	1175	PHE	2.5
4	e	1394	ILE	2.5
1	a	1376	ILE	2.5
7	Q	90	SER	2.5
1	A	403	LEU	2.5
6	H	213	GLY	2.5
4	E	501	MET	2.5
6	H	136	ILE	2.4
6	H	318	ASP	2.4
5	G	162	THR	2.4
2	b	1516	ARG	2.4
6	H	227	MET	2.4
7	q	1450	ARG	2.4
2	B	375	LEU	2.4
3	d	1057	PRO	2.4
2	b	1403	ASP	2.4
4	E	537	GLY	2.4
1	a	1112	ILE	2.4
3	D	216	LYS	2.4
3	d	1392	VAL	2.4
7	q	1181	LYS	2.4
7	q	1208	LEU	2.4
2	B	317	PHE	2.4
5	G	166	SER	2.4
1	a	1448	ILE	2.4
5	G	236	PRO	2.4
7	Q	78	VAL	2.4
3	d	1155	SER	2.4
4	e	1426	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
6	H	226	GLU	2.4
1	a	1196	ASN	2.4
3	d	1408	ILE	2.4
6	H	319	LEU	2.4
6	H	337	LEU	2.4
8	Z	178	ALA	2.4
8	Z	365	LYS	2.4
2	b	1200	HIS	2.4
4	E	406	LEU	2.4
8	Z	447	ILE	2.4
2	B	243	GLY	2.4
1	a	1180	LYS	2.4
8	z	1058	LYS	2.4
1	a	1076	CYS	2.4
8	Z	47	LEU	2.4
2	B	522	LYS	2.4
2	b	1175	HIS	2.4
1	a	1426	TYR	2.4
4	E	242	GLN	2.4
2	b	1074	ILE	2.4
3	D	66	ASP	2.4
6	h	1371	THR	2.4
7	q	1054	LYS	2.4
1	a	1195	ILE	2.4
5	g	1156	ILE	2.4
5	g	1517	LEU	2.4
6	h	1009	LEU	2.4
8	Z	445	LEU	2.4
1	a	1114	PRO	2.4
5	G	392	GLN	2.4
3	D	498	VAL	2.4
7	Q	86	ILE	2.4
8	Z	418	MET	2.4
8	z	1358	GLU	2.4
2	B	428	THR	2.4
5	g	1070	ILE	2.4
7	q	1382	ASP	2.4
7	q	1444	ALA	2.4
8	Z	340	ASN	2.4
2	B	231	ARG	2.4
5	G	322	ARG	2.4
6	h	1499	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
8	z	1141	LYS	2.4
3	D	381	GLY	2.4
7	q	1446	GLU	2.4
3	d	1187	SER	2.4
1	a	1117	VAL	2.4
1	a	1437	ALA	2.4
7	Q	337	ASN	2.4
4	e	1483	LYS	2.4
8	Z	326	LEU	2.4
8	z	1396	ARG	2.4
7	Q	420	ALA	2.4
7	Q	394	ASP	2.4
3	d	1182	TYR	2.4
1	a	1389	GLU	2.4
2	B	495	GLU	2.4
3	d	1462	GLU	2.4
7	Q	356	GLY	2.4
4	E	67	ASP	2.4
5	G	359	TYR	2.4
2	b	1029	PHE	2.4
7	q	1139	ALA	2.4
2	B	246	THR	2.4
5	G	67	LEU	2.4
8	Z	34	LEU	2.4
8	z	1327	ALA	2.4
2	b	1377	GLY	2.4
3	d	1542	ARG	2.4
5	G	18	SER	2.4
5	G	354	LYS	2.4
7	Q	438	ILE	2.4
1	a	1128	ALA	2.4
5	G	178	ASP	2.4
8	z	1156	LEU	2.4
5	G	487	LEU	2.4
8	z	1330	GLY	2.3
3	D	314	ASP	2.3
6	h	1144	LYS	2.3
8	Z	511	ILE	2.3
5	g	1127	ARG	2.3
7	Q	488	ALA	2.3
8	z	1178	ALA	2.3
1	A	306	MET	2.3

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Mol	Chain	Res	Type	RSRZ
3	D	179	VAL	2.3
8	Z	60	GLY	2.3
2	B	99	THR	2.3
5	g	1095	THR	2.3
2	b	1019	GLU	2.3
1	a	1430	MET	2.3
2	b	1189	ARG	2.3
6	H	469	ALA	2.3
7	q	1424	THR	2.3
4	e	1403	HIS	2.3
5	g	1091	VAL	2.3
2	B	87	MET	2.3
3	D	500	LYS	2.3
4	e	1094	LEU	2.3
3	d	1401	ILE	2.3
5	G	227	PRO	2.3
4	e	1474	MET	2.3
6	h	1166	LYS	2.3
2	B	414	GLU	2.3
4	E	477	VAL	2.3
7	Q	439	LYS	2.3
1	A	376	ILE	2.3
1	a	1148	LEU	2.3
6	H	237	ILE	2.3
3	d	1104	GLU	2.3
5	G	284	GLN	2.3
8	z	1030	LEU	2.3
2	b	1050	LYS	2.3
7	Q	107	PHE	2.3
2	B	71	LEU	2.3
3	d	1458	ALA	2.3
6	h	1522	ASN	2.3
4	E	91	MET	2.3
4	e	1464	GLU	2.3
6	H	76	ALA	2.3
5	G	482	GLY	2.3
7	Q	472	GLN	2.3
2	b	1416	LEU	2.3
8	z	1391	ILE	2.3
6	h	1133	VAL	2.3
2	b	1022	GLU	2.3
5	G	149	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	a	1517	ALA	2.3
1	a	1179	ILE	2.3
5	g	1393	ASP	2.3
2	b	1419	HIS	2.3
8	z	1408	VAL	2.3
1	A	499	LYS	2.3
3	D	315	LEU	2.3
4	E	293	LYS	2.3
5	G	93	ASP	2.3
8	z	1480	ASP	2.3
4	e	1467	GLY	2.3
5	g	1444	LEU	2.3
1	A	172	VAL	2.3
5	G	151	THR	2.3
6	h	1185	MET	2.3
1	a	1427	ALA	2.3
5	g	1076	ALA	2.3
6	H	471	GLY	2.3
8	z	1494	ILE	2.3
4	E	506	VAL	2.3
5	g	1397	VAL	2.3
5	g	1510	VAL	2.3
2	B	408	TYR	2.3
2	b	1456	TYR	2.3
3	d	1131	ILE	2.3
3	d	1430	ALA	2.3
6	H	423	TYR	2.3
7	Q	467	LEU	2.3
7	q	1057	ILE	2.3
8	Z	141	LYS	2.3
7	q	1209	GLY	2.3
1	A	113	HIS	2.3
3	d	1440	THR	2.3
5	G	215	LEU	2.3
6	H	29	CYS	2.3
1	A	128	ALA	2.3
7	Q	69	ALA	2.3
8	Z	159	LYS	2.3
8	Z	520	GLU	2.3
8	z	1410	GLY	2.3
1	A	216	LEU	2.2
2	B	100	THR	2.2

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Mol	Chain	Res	Type	RSRZ
5	G	168	TRP	2.2
2	B	419	HIS	2.2
5	G	481	ASN	2.2
7	q	1421	LYS	2.2
8	Z	317	LYS	2.2
3	D	120	LEU	2.2
6	h	1136	ILE	2.2
7	q	1190	ILE	2.2
2	b	1386	ALA	2.2
8	Z	204	THR	2.2
8	Z	400	ASN	2.2
8	z	1204	THR	2.2
1	A	297	LEU	2.2
1	a	1063	LYS	2.2
4	E	63	ASP	2.2
5	g	1098	VAL	2.2
7	q	1179	LEU	2.2
6	h	1084	LYS	2.2
6	h	1477	VAL	2.2
1	a	1396	LEU	2.2
6	H	175	PHE	2.2
4	e	1060	MET	2.2
6	H	184	MET	2.2
7	Q	295	GLY	2.2
3	d	1185	LEU	2.2
3	d	1498	VAL	2.2
1	a	1154	THR	2.2
1	a	1502	GLY	2.2
8	Z	390	ALA	2.2
2	B	422	THR	2.2
3	d	1454	ILE	2.2
3	d	1505	ASN	2.2
4	e	1465	ASN	2.2
7	q	1461	ASN	2.2
7	q	1098	GLY	2.2
2	b	1077	ASP	2.2
5	g	1476	GLU	2.2
6	H	288	VAL	2.2
8	Z	126	ALA	2.2
4	E	230	VAL	2.2
5	g	1194	ASP	2.2
5	g	1403	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
7	Q	443	GLU	2.2
7	q	1094	GLU	2.2
2	B	388	ARG	2.2
2	b	1101	SER	2.2
8	z	1393	ASP	2.2
3	d	1436	ALA	2.2
7	q	1442	ALA	2.2
8	z	1345	GLY	2.2
8	z	1348	GLY	2.2
1	A	237	LEU	2.2
2	B	39	VAL	2.2
7	Q	401	VAL	2.2
3	d	1028	GLN	2.2
4	E	77	ILE	2.2
4	E	297	ALA	2.2
5	G	242	ASP	2.2
6	h	1398	ARG	2.2
5	g	1123	ILE	2.2
2	B	46	LYS	2.2
5	g	1096	THR	2.2
8	z	1168	LEU	2.2
2	B	281	ARG	2.2
8	Z	195	GLU	2.2
2	B	74	ILE	2.2
3	D	472	ALA	2.2
6	h	1446	PRO	2.2
3	D	178	VAL	2.2
1	a	1025	ALA	2.2
6	H	182	ALA	2.2
3	D	394	ARG	2.2
5	g	1129	ALA	2.2
4	E	301	ILE	2.2
2	B	461	LEU	2.2
3	D	69	GLY	2.2
3	d	1448	GLY	2.2
6	H	299	ALA	2.2
3	D	304	GLN	2.2
6	h	1400	ILE	2.2
7	Q	159	GLU	2.2
1	A	46	VAL	2.2
5	G	43	PRO	2.2
2	b	1491	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
5	G	175	ILE	2.2
6	h	1445	ILE	2.2
1	a	1119	SER	2.2
2	B	468	ALA	2.2
2	b	1137	ALA	2.2
7	Q	70	ALA	2.2
7	q	1441	PHE	2.2
8	z	1466	VAL	2.2
4	E	516	GLN	2.2
8	Z	404	ASP	2.2
1	A	68	GLU	2.2
6	H	385	THR	2.2
6	h	1523	PRO	2.2
8	Z	333	LEU	2.2
6	H	212	ALA	2.2
6	h	1128	ALA	2.2
5	g	1141	SER	2.2
4	E	94	LEU	2.2
1	A	173	VAL	2.1
7	q	1043	THR	2.1
1	a	1123	LEU	2.1
3	D	533	LEU	2.1
6	H	404	SER	2.1
6	h	1045	MET	2.1
7	q	1400	LYS	2.1
8	z	1315	ARG	2.1
3	D	64	ILE	2.1
6	H	374	LEU	2.1
6	h	1210	LEU	2.1
6	h	1458	THR	2.1
7	q	1105	LEU	2.1
5	G	200	ARG	2.1
6	h	1189	LEU	2.1
7	Q	322	ARG	2.1
2	B	173	THR	2.1
4	e	1456	GLU	2.1
7	q	1447	ALA	2.1
8	z	1416	VAL	2.1
8	z	1294	GLN	2.1
4	E	229	ILE	2.1
8	Z	446	ILE	2.1
8	z	1334	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
7	Q	389	GLU	2.1
8	Z	307	LYS	2.1
1	A	346	GLY	2.1
2	B	444	ARG	2.1
6	h	1374	LEU	2.1
5	g	1483	GLU	2.1
6	H	185	MET	2.1
3	D	167	LEU	2.1
5	g	1145	ASP	2.1
5	G	48	LYS	2.1
6	h	1453	ALA	2.1
4	e	1101	GLU	2.1
8	z	1448	PRO	2.1
3	D	25	SER	2.1
3	d	1176	SER	2.1
6	h	1049	ILE	2.1
7	Q	244	CYS	2.1
8	Z	69	ILE	2.1
7	q	1384	LEU	2.1
2	b	1190	LEU	2.1
3	D	514	PRO	2.1
6	H	155	LEU	2.1
3	D	408	ILE	2.1
3	D	457	PHE	2.1
7	Q	306	ASN	2.1
7	q	1102	ASN	2.1
3	D	222	ASP	2.1
3	d	1156	ARG	2.1
5	g	1077	ALA	2.1
6	H	246	LEU	2.1
8	Z	273	LYS	2.1
8	Z	95	ASN	2.1
4	E	99	ASP	2.1
8	z	1477	VAL	2.1
3	d	1434	GLU	2.1
8	Z	99	ILE	2.1
3	d	1484	ARG	2.1
6	h	1123	ARG	2.1
8	z	1422	LEU	2.1
4	e	1505	HIS	2.1
6	H	455	PHE	2.1
8	Z	142	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	a	1009	GLY	2.1
4	e	1088	ALA	2.1
4	e	1513	LYS	2.1
5	g	1080	MET	2.1
8	Z	94	SER	2.1
3	d	1070	ASP	2.1
1	A	206	MET	2.1
1	a	1496	ARG	2.1
6	h	1199	LYS	2.1
6	h	1118	PRO	2.1
7	q	1475	ASN	2.1
4	E	351	GLU	2.1
4	E	508	GLU	2.1
8	Z	505	LEU	2.1
4	e	1446	TYR	2.1
2	b	1210	ALA	2.1
4	E	189	ALA	2.1
8	z	1157	ARG	2.1
8	z	1006	THR	2.1
4	E	489	LEU	2.1
6	H	298	VAL	2.1
7	q	1489	VAL	2.1
7	q	1135	ALA	2.1
1	a	1445	LEU	2.1
7	Q	132	TYR	2.1
7	q	1387	ASP	2.1
7	Q	338	PRO	2.0
2	B	227	ASN	2.0
4	e	1457	VAL	2.0
8	z	1407	VAL	2.0
2	B	432	GLU	2.0
5	g	1469	LYS	2.0
7	Q	54	LYS	2.0
2	B	209	LEU	2.0
3	d	1540	ASN	2.0
4	e	1499	ASN	2.0
2	B	185	GLU	2.0
1	a	1456	ALA	2.0
5	g	1125	ALA	2.0
6	H	43	ARG	2.0
8	z	1205	SER	2.0
7	Q	87	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
5	G	64	ASN	2.0
5	g	1099	ILE	2.0
6	H	168	ILE	2.0
1	a	1200	ALA	2.0
4	E	452	ALA	2.0
5	g	1050	LEU	2.0
6	h	1140	ALA	2.0
7	Q	475	ASN	2.0
5	G	52	ASP	2.0
7	Q	156	ASP	2.0
1	A	468	ARG	2.0
4	E	493	CYS	2.0
3	D	207	ASP	2.0
1	a	1140	THR	2.0
6	h	1368	LYS	2.0
8	Z	130	ALA	2.0
2	B	446	LEU	2.0
1	a	1202	GLY	2.0
4	e	1214	LYS	2.0
8	Z	206	LEU	2.0
3	D	383	ALA	2.0
5	G	347	ALA	2.0
8	Z	413	ALA	2.0
8	Z	419	ALA	2.0
5	g	1067	LEU	2.0
2	b	1040	LYS	2.0
1	a	1066	GLU	2.0
2	B	520	ILE	2.0
5	G	246	GLU	2.0
3	D	412	LEU	2.0
5	G	327	CYS	2.0
5	g	1430	THR	2.0
2	b	1071	LEU	2.0
2	b	1390	LEU	2.0
4	E	315	LEU	2.0
5	G	422	LEU	2.0
8	z	1299	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.