



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:24 PM GMT

PDB ID : 1K32
Title : Crystal structure of the tricorn protease
Authors : Brandstetter, H.; Kim, J.-S.; Groll, M.; Huber, R.
Deposited on : 2001-10-01
Resolution : 2.00 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

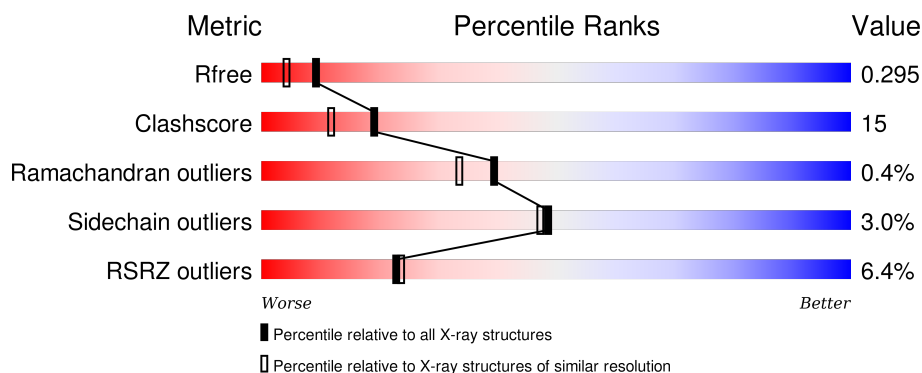
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
R_{free}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	1045	<div> <div>3%</div> <div>72%</div> <div>23%</div> <div>..</div> </div>
1	B	1045	<div> <div>3%</div> <div>71%</div> <div>24%</div> <div>..</div> </div>
1	C	1045	<div> <div>12%</div> <div>70%</div> <div>26%</div> <div>..</div> </div>
1	D	1045	<div> <div>5%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>
1	E	1045	<div> <div>4%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	1045	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment on the left labeled '11%', a green segment in the middle labeled '67%', and a yellow segment on the right labeled '28%'. The bar ends with a small grey segment and two dots '• •'.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 51456 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 tricorn protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			
1	B	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			
1	C	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			
1	D	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			
1	E	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			
1	F	1023	Total	C	N	O	S	95	0	0
			8177	5196	1402	1551	28			

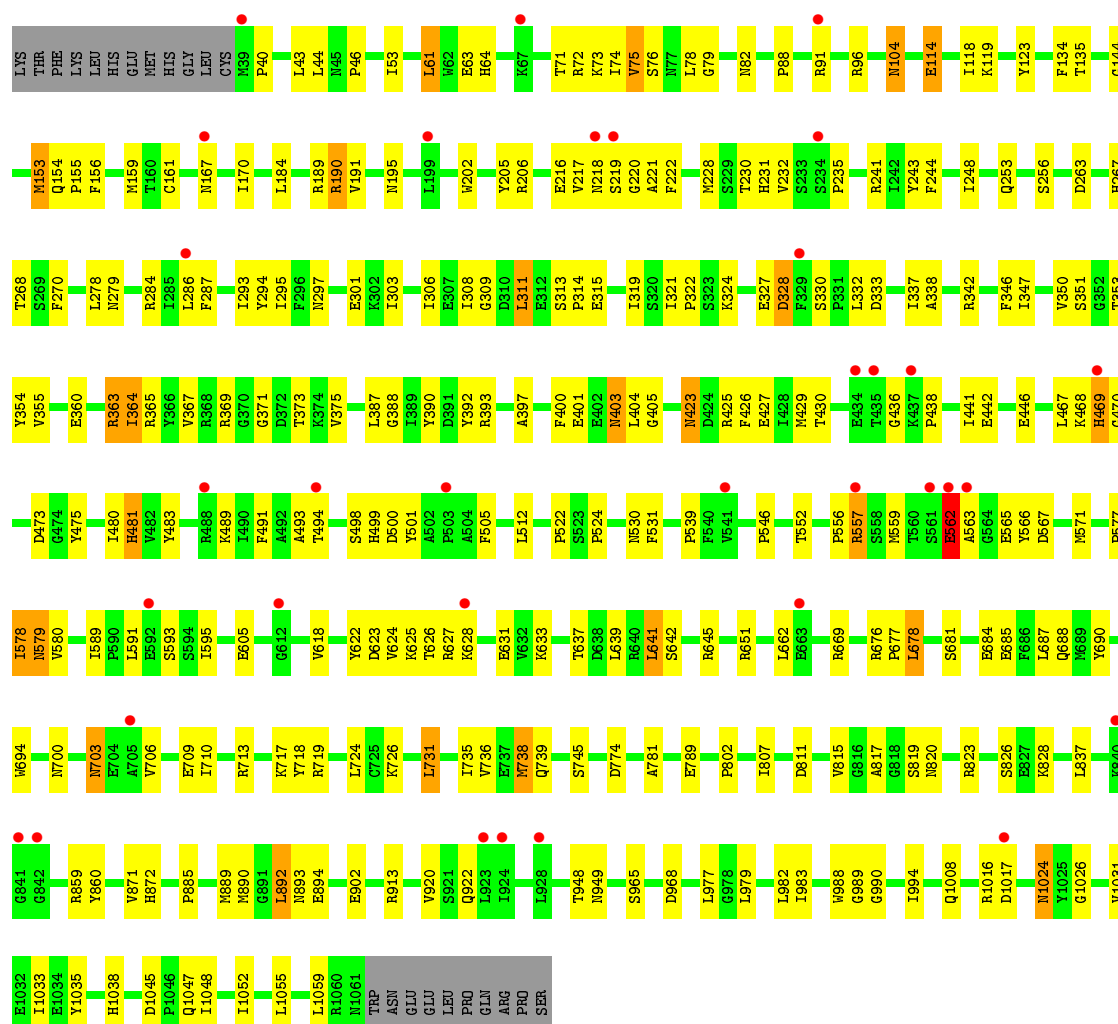
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	401	Total	O	0	0
			401	401		
2	B	395	Total	O	0	0
			395	395		
2	C	398	Total	O	0	0
			398	398		
2	D	401	Total	O	0	0
			401	401		
2	E	405	Total	O	0	0
			405	405		
2	F	394	Total	O	0	0
			394	394		

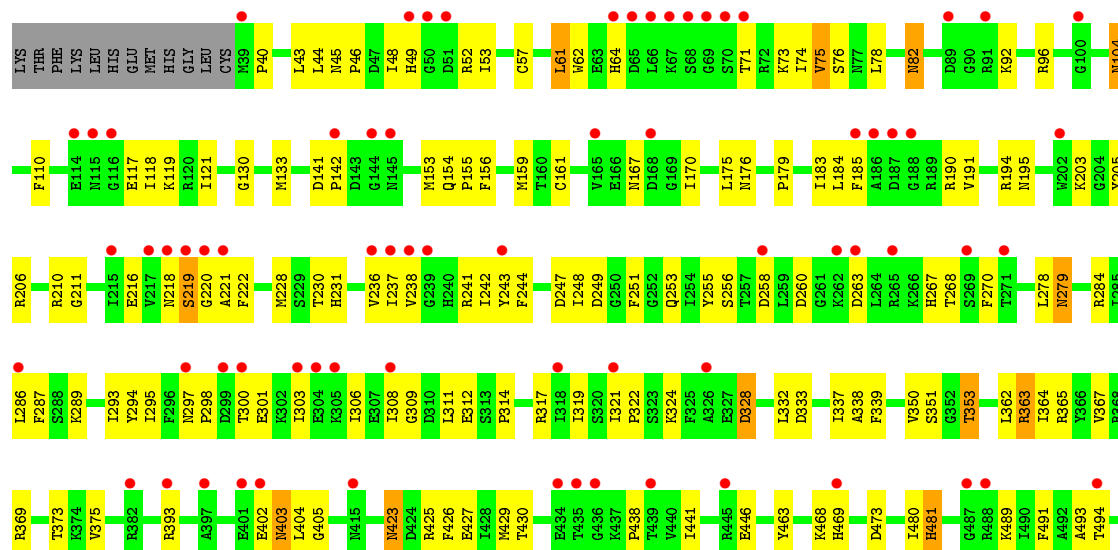
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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.

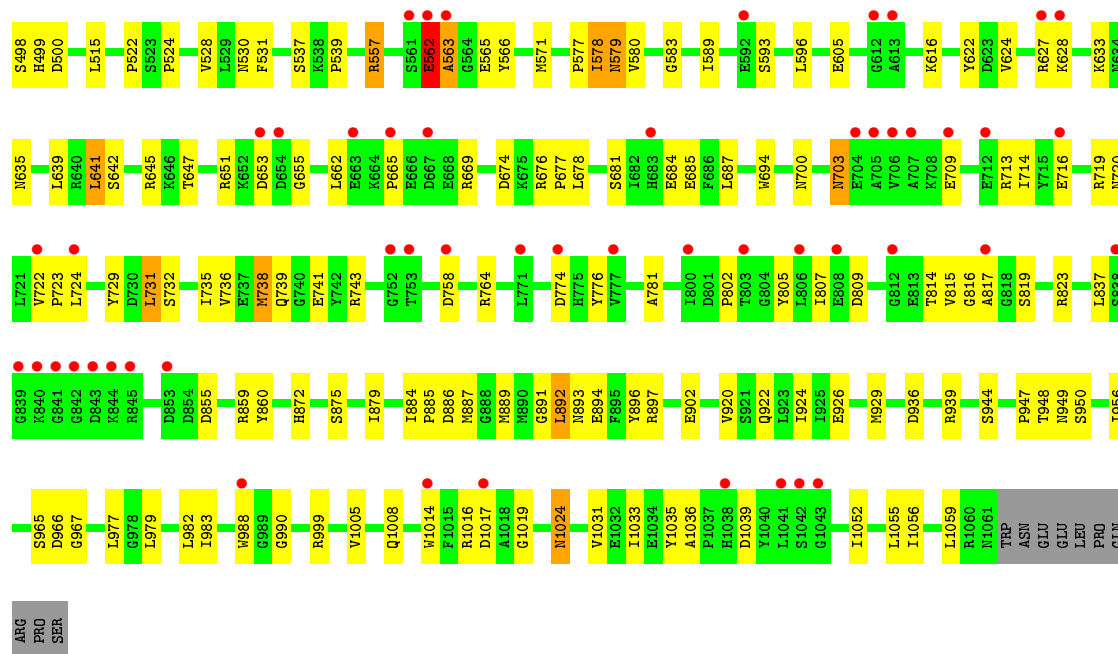
- Chain A:  3% 72% 23% ..



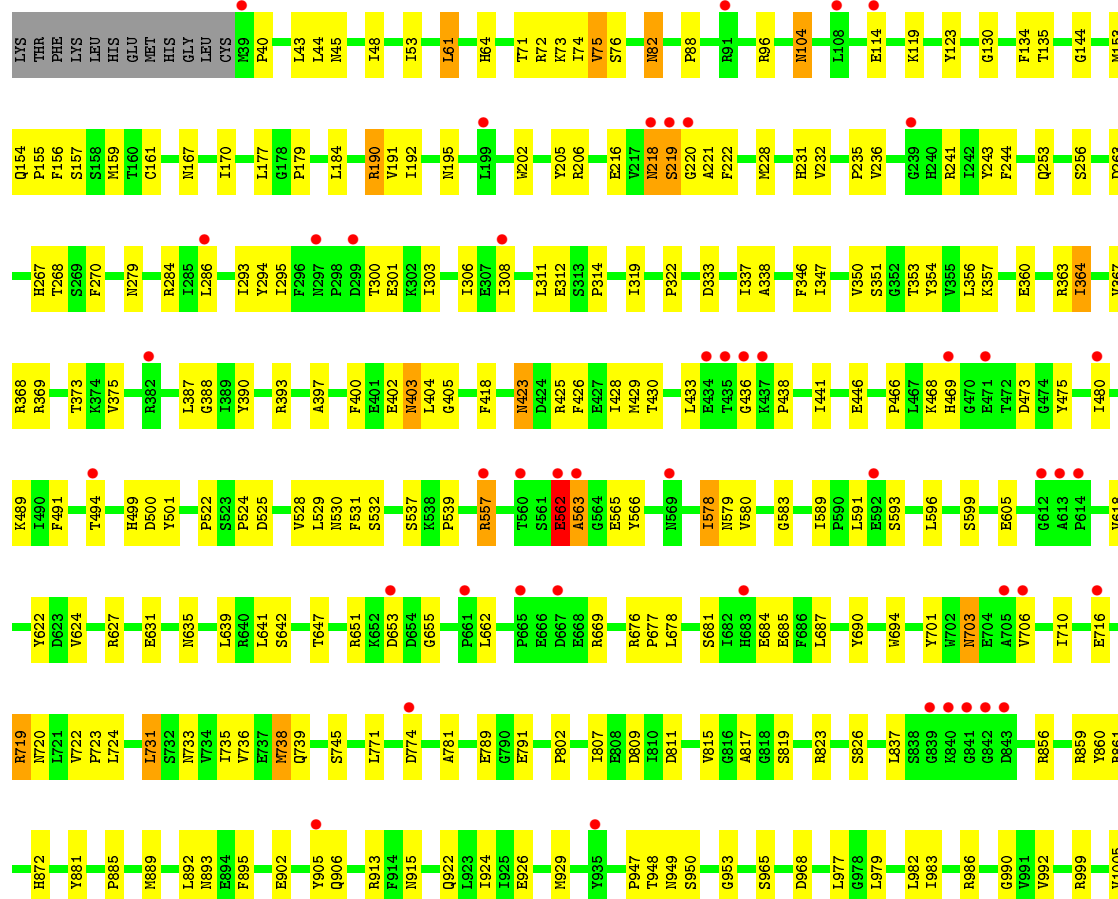


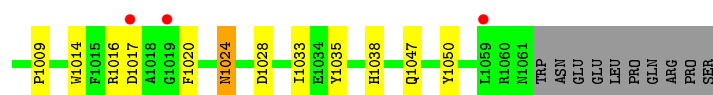
• Molecule 1: tricorn protease



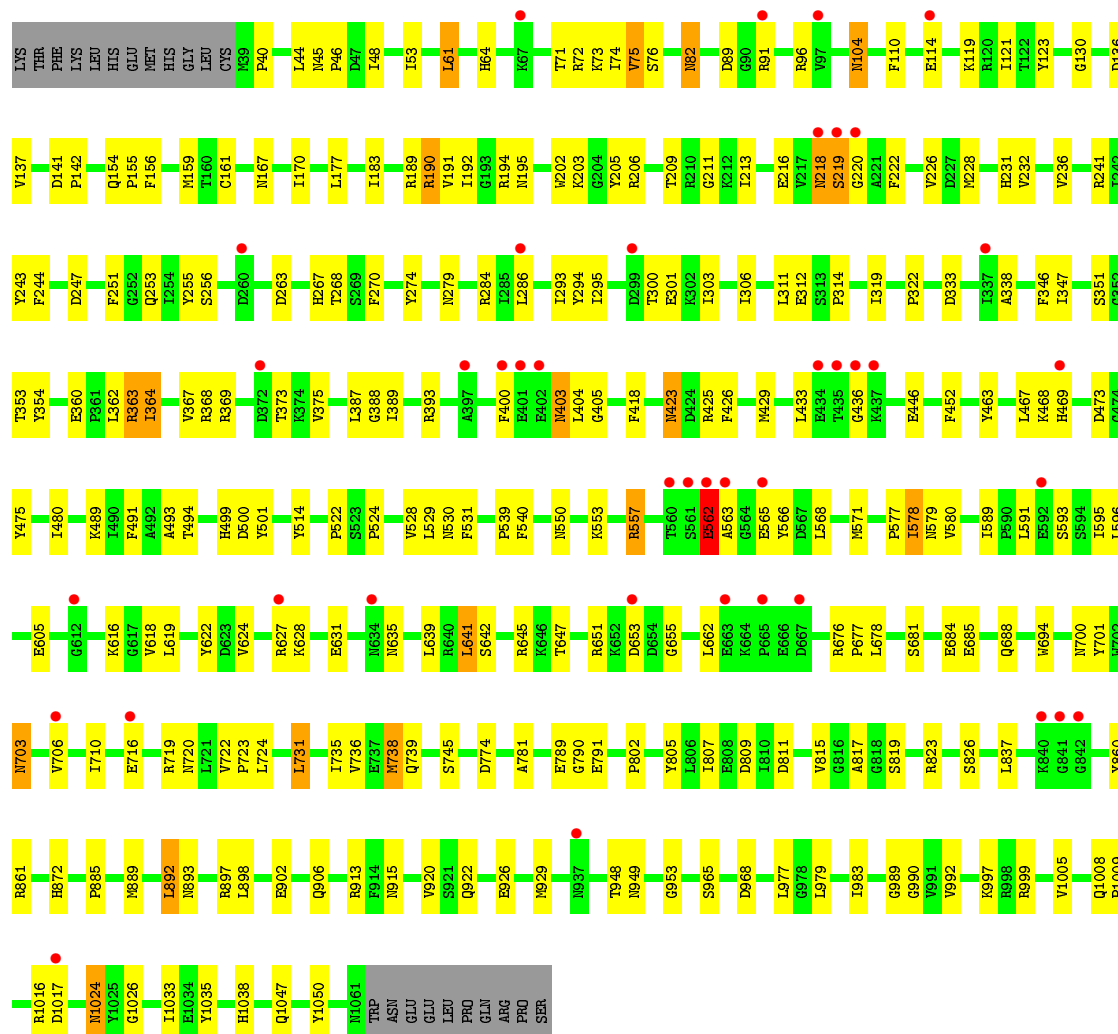
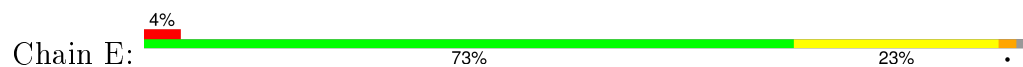


• Molecule 1: tricorn protease

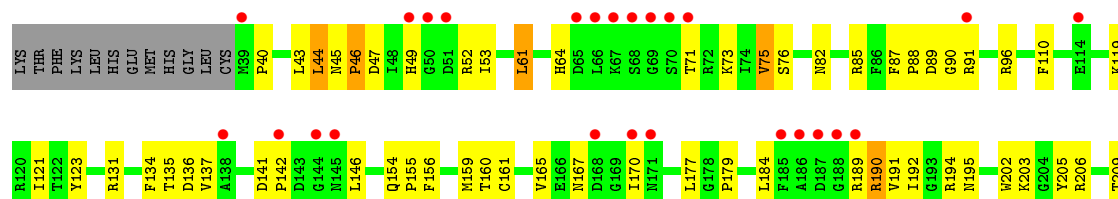


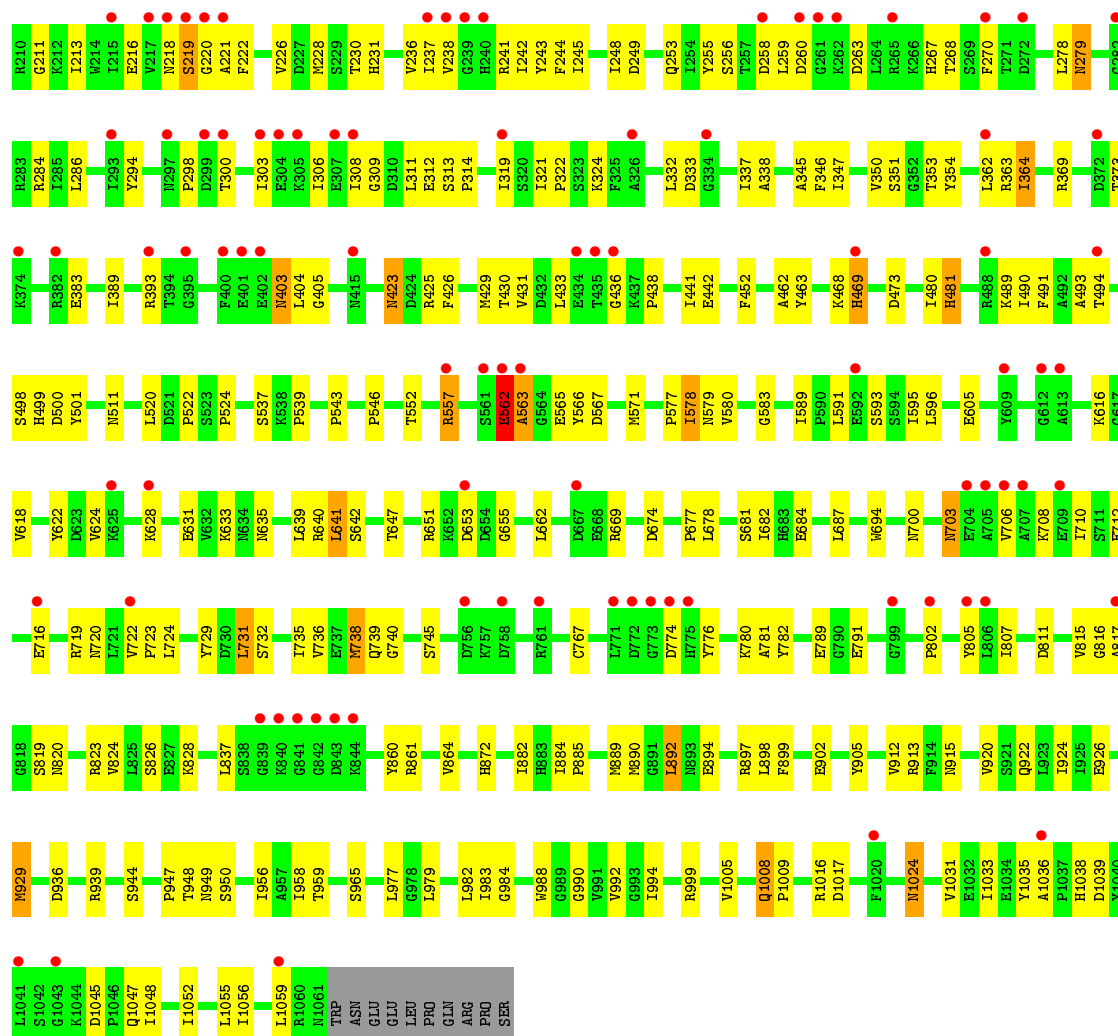


• Molecule 1: tricorn protease



• Molecule 1: tricorn protease





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.86Å 246.00Å 159.04Å 90.00° 105.30° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 37.48 – 1.98	Depositor EDS
% Data completeness (in resolution range)	78.6 (20.00-2.00) 81.6 (37.48-1.98)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.98Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.245 , 0.264 0.257 , 0.295	Depositor DCC
R_{free} test set	19825 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 54.3	EDS
Estimated twinning fraction	0.054 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	9 of 400057 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	51456	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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	0.40	0/8367	0.66	1/11311 (0.0%)
1	B	0.40	0/8367	0.66	2/11311 (0.0%)
1	C	0.36	0/8367	0.62	1/11311 (0.0%)
1	D	0.39	0/8367	0.65	1/11311 (0.0%)
1	E	0.38	0/8367	0.65	1/11311 (0.0%)
1	F	0.36	0/8367	0.62	1/11311 (0.0%)
All	All	0.38	0/50202	0.64	7/67866 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	364	ILE	N-CA-C	-6.20	94.25	111.00
1	A	364	ILE	N-CA-C	-5.63	95.81	111.00
1	E	364	ILE	N-CA-C	-5.41	96.39	111.00
1	B	79	GLY	N-CA-C	-5.28	99.89	113.10
1	D	364	ILE	N-CA-C	-5.23	96.87	111.00
1	B	364	ILE	N-CA-C	-5.15	97.10	111.00
1	F	364	ILE	N-CA-C	-5.08	97.28	111.00

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	8177	0	8003	256	0
1	B	8177	0	8003	265	0
1	C	8177	0	8003	272	0
1	D	8177	0	8003	226	0
1	E	8177	0	8003	249	0
1	F	8177	0	8003	275	0
2	A	401	0	0	12	0
2	B	395	0	0	8	0
2	C	398	0	0	18	0
2	D	401	0	0	9	0
2	E	405	0	0	10	0
2	F	394	0	0	10	0
All	All	51456	0	48018	1453	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 15.

All (1453) 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)
1:F:155:PRO:HG2	1:F:159:MET:HE1	1.33	1.09
1:B:155:PRO:HG2	1:B:159:MET:HE1	1.36	1.07
1:C:155:PRO:HG2	1:C:159:MET:HE1	1.37	1.06
1:D:155:PRO:HG2	1:D:159:MET:HE1	1.35	1.03
1:B:983:ILE:HG23	1:B:1033:ILE:HD13	1.41	1.02
1:A:983:ILE:HG23	1:A:1033:ILE:HD13	1.41	0.99
1:D:983:ILE:HG23	1:D:1033:ILE:HD12	1.43	0.97
1:A:155:PRO:HG2	1:A:159:MET:HE1	1.46	0.95
1:F:154:GLN:HB3	1:F:159:MET:HE3	1.47	0.95
1:C:983:ILE:HG23	1:C:1033:ILE:HD13	1.49	0.94
1:D:53:ILE:HG23	1:D:286:LEU:HD21	1.48	0.93
1:B:104:ASN:HD22	1:B:104:ASN:H	1.12	0.93
1:A:948:THR:H	1:B:922:GLN:HE22	1.16	0.92
1:E:155:PRO:HG2	1:E:159:MET:HE1	1.49	0.91
1:F:983:ILE:HG23	1:F:1033:ILE:HD13	1.50	0.90
1:E:53:ILE:HG23	1:E:286:LEU:HD21	1.53	0.89
1:B:253:GLN:HE22	1:B:270:PHE:H	1.20	0.89
1:C:154:GLN:HB3	1:C:159:MET:HE3	1.54	0.88
1:A:922:GLN:HE22	1:B:948:THR:H	1.21	0.88
1:A:789:GLU:HG3	1:B:577:PRO:HG3	1.55	0.87
1:D:253:GLN:HE22	1:D:270:PHE:H	1.23	0.87
1:C:922:GLN:HE22	1:D:948:THR:H	1.15	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:ILE:H	1:B:494:THR:HG22	1.38	0.87
1:B:468:LYS:HD2	1:B:473:ASP:HB2	1.58	0.86
1:F:480:ILE:H	1:F:494:THR:HG22	1.39	0.86
1:F:468:LYS:HD2	1:F:473:ASP:HB2	1.57	0.85
1:C:268:THR:HG22	1:C:303:ILE:HD11	1.56	0.85
1:E:104:ASN:H	1:E:104:ASN:HD22	1.23	0.85
1:B:539:PRO:HG2	1:B:578:ILE:HG23	1.58	0.85
1:C:104:ASN:H	1:C:104:ASN:HD22	1.22	0.85
1:E:922:GLN:HE22	1:F:948:THR:H	1.22	0.85
1:A:161:CYS:SG	2:A:2394:HOH:O	2.35	0.84
1:A:104:ASN:HD22	1:A:104:ASN:H	1.21	0.84
1:F:539:PRO:HG2	1:F:578:ILE:HG23	1.56	0.84
1:C:73:LYS:HD3	1:C:76:SER:HB3	1.60	0.84
1:A:480:ILE:H	1:A:494:THR:HG22	1.41	0.84
1:F:73:LYS:HD3	1:F:76:SER:HB3	1.59	0.83
1:F:322:PRO:HB3	1:F:678:LEU:HD13	1.59	0.83
1:E:40:PRO:HG2	1:E:724:LEU:HD22	1.59	0.83
1:E:403:ASN:ND2	1:E:405:GLY:H	1.76	0.83
1:D:104:ASN:H	1:D:104:ASN:HD22	1.26	0.82
1:A:253:GLN:HE22	1:A:270:PHE:H	1.22	0.81
1:E:983:ILE:HG23	1:E:1033:ILE:HD12	1.63	0.81
1:B:489:LYS:HG3	1:B:491:PHE:CE1	2.15	0.81
1:E:789:GLU:HG3	1:F:577:PRO:HG3	1.61	0.81
1:E:948:THR:H	1:F:922:GLN:HE22	1.29	0.81
1:C:40:PRO:HG2	1:C:724:LEU:HD22	1.61	0.80
1:F:268:THR:HG22	1:F:303:ILE:HD11	1.62	0.80
1:D:468:LYS:HD2	1:D:473:ASP:HB2	1.63	0.80
1:A:322:PRO:HG3	1:A:678:LEU:HD13	1.63	0.80
1:D:48:ILE:HB	1:D:286:LEU:HD22	1.64	0.79
1:F:404:LEU:HD22	1:F:429:MET:HE2	1.65	0.79
1:C:577:PRO:HG3	1:D:789:GLU:HG3	1.63	0.78
1:B:284:ARG:HD3	2:B:3393:HOH:O	1.81	0.78
1:E:539:PRO:HG2	1:E:578:ILE:HG23	1.65	0.78
1:A:557:ARG:NH2	1:E:393:ARG:HH12	1.80	0.78
1:B:161:CYS:SG	2:B:3394:HOH:O	2.40	0.78
1:E:154:GLN:HB3	1:E:159:MET:HE3	1.65	0.78
1:A:948:THR:H	1:B:922:GLN:NE2	1.82	0.78
1:A:404:LEU:HD22	1:A:429:MET:HE2	1.66	0.77
1:B:154:GLN:HB3	1:B:159:MET:HE3	1.67	0.77
1:F:403:ASN:ND2	1:F:405:GLY:H	1.82	0.77
1:D:662:LEU:HD23	1:D:662:LEU:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:161:CYS:SG	2:E:6394:HOH:O	2.42	0.77
1:F:694:TRP:HA	1:F:738:MET:CE	2.15	0.77
1:F:253:GLN:HE22	1:F:270:PHE:H	1.33	0.77
1:C:403:ASN:HD22	1:C:405:GLY:H	1.33	0.77
1:C:403:ASN:ND2	1:C:405:GLY:H	1.81	0.77
1:C:539:PRO:HG2	1:C:578:ILE:HG23	1.66	0.76
1:A:268:THR:HG22	1:A:303:ILE:HD11	1.67	0.76
1:C:480:ILE:H	1:C:494:THR:HG22	1.50	0.76
1:A:73:LYS:HD3	1:A:76:SER:HB3	1.67	0.76
1:C:578:ILE:HG12	1:C:580:VAL:HG23	1.67	0.76
1:A:293:ILE:HG22	1:A:306:ILE:HD12	1.68	0.76
1:A:284:ARG:HD3	2:A:2393:HOH:O	1.84	0.76
1:E:662:LEU:O	1:E:662:LEU:HD23	1.86	0.76
1:B:73:LYS:HD3	1:B:76:SER:HB3	1.68	0.76
1:B:206:ARG:H	1:B:1024:ASN:HD21	1.32	0.75
1:D:40:PRO:HG2	1:D:724:LEU:HD22	1.67	0.75
1:F:403:ASN:HD22	1:F:405:GLY:H	1.35	0.75
1:A:539:PRO:HG2	1:A:578:ILE:HG23	1.68	0.75
1:F:350:VAL:HG21	1:F:669:ARG:HH11	1.51	0.75
1:F:82:ASN:HD21	1:F:96:ARG:HH21	1.33	0.75
1:C:948:THR:H	1:D:922:GLN:HE22	1.33	0.75
1:A:154:GLN:HB3	1:A:159:MET:HE3	1.69	0.74
1:D:53:ILE:CG2	1:D:286:LEU:HD21	2.16	0.74
1:E:403:ASN:HD22	1:E:405:GLY:H	1.35	0.74
1:C:167:ASN:HB2	1:C:170:ILE:HB	1.68	0.74
1:C:286:LEU:HD12	1:C:294:TYR:O	1.87	0.74
1:A:353:THR:HG23	1:A:354:TYR:CD1	2.23	0.74
1:A:489:LYS:HG3	1:A:491:PHE:CE1	2.22	0.74
1:E:253:GLN:HE22	1:E:270:PHE:H	1.34	0.74
1:B:206:ARG:H	1:B:1024:ASN:ND2	1.85	0.74
1:D:268:THR:HG22	1:D:303:ILE:HD11	1.69	0.74
1:B:295:ILE:HG13	1:B:306:ILE:HD11	1.68	0.74
1:B:480:ILE:H	1:B:494:THR:CG2	2.00	0.73
1:D:578:ILE:HG12	1:D:580:VAL:HG23	1.70	0.73
1:A:40:PRO:HG2	1:A:724:LEU:HD22	1.69	0.73
1:F:206:ARG:H	1:F:1024:ASN:ND2	1.86	0.73
1:E:268:THR:HG22	1:E:303:ILE:HD11	1.69	0.73
1:E:480:ILE:H	1:E:494:THR:HG22	1.54	0.73
1:A:468:LYS:HD2	1:A:473:ASP:HB2	1.70	0.73
1:B:286:LEU:HD12	1:B:294:TYR:O	1.88	0.73
1:F:206:ARG:H	1:F:1024:ASN:HD21	1.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:468:LYS:HD2	1:C:473:ASP:HB2	1.70	0.72
1:B:202:TRP:CH2	1:B:745:SER:HB3	2.24	0.72
1:F:578:ILE:HG12	1:F:580:VAL:HG23	1.70	0.72
1:B:350:VAL:HG21	1:B:669:ARG:HH11	1.53	0.72
1:B:351:SER:OG	1:B:353:THR:HG22	1.88	0.72
1:C:161:CYS:SG	2:C:4394:HOH:O	2.47	0.72
1:E:922:GLN:NE2	1:F:948:THR:H	1.86	0.72
1:B:681:SER:HB3	1:B:684:GLU:HG2	1.70	0.72
1:A:350:VAL:HG21	1:A:669:ARG:HH11	1.54	0.72
1:B:40:PRO:HG2	1:B:724:LEU:HD22	1.72	0.71
1:D:161:CYS:SG	2:D:5394:HOH:O	2.48	0.71
1:F:155:PRO:CG	1:F:159:MET:HE1	2.17	0.71
1:F:286:LEU:HD12	1:F:294:TYR:O	1.90	0.71
1:C:253:GLN:HE22	1:C:270:PHE:H	1.37	0.71
1:A:351:SER:OG	1:A:353:THR:HG22	1.91	0.71
1:C:694:TRP:HA	1:C:738:MET:CE	2.21	0.71
1:D:73:LYS:HD3	1:D:76:SER:HB3	1.73	0.71
1:D:403:ASN:ND2	1:D:405:GLY:H	1.87	0.71
1:A:480:ILE:H	1:A:494:THR:CG2	2.04	0.71
1:A:922:GLN:NE2	1:B:948:THR:H	1.86	0.71
1:A:206:ARG:H	1:A:1024:ASN:ND2	1.88	0.71
1:D:404:LEU:HD22	1:D:429:MET:HE2	1.72	0.70
1:D:403:ASN:HD22	1:D:405:GLY:H	1.38	0.70
1:A:205:TYR:HA	1:A:1024:ASN:HD21	1.57	0.70
1:C:322:PRO:HB3	1:C:678:LEU:HD13	1.72	0.69
1:E:468:LYS:HD2	1:E:473:ASP:HB2	1.74	0.69
1:F:82:ASN:ND2	1:F:96:ARG:HH21	1.90	0.69
1:B:268:THR:HG22	1:B:303:ILE:HD11	1.71	0.69
1:B:82:ASN:ND2	1:B:96:ARG:HH21	1.90	0.69
1:F:40:PRO:HG2	1:F:724:LEU:CD2	2.21	0.69
1:D:206:ARG:H	1:D:1024:ASN:ND2	1.90	0.69
1:F:662:LEU:HD23	1:F:662:LEU:O	1.92	0.69
1:B:557:ARG:NE	1:D:393:ARG:HH22	1.91	0.69
1:F:61:LEU:HB3	1:F:75:VAL:HG13	1.73	0.69
1:D:351:SER:OG	1:D:353:THR:HG22	1.93	0.69
1:F:774:ASP:HA	1:F:817:ALA:HB2	1.74	0.68
1:A:577:PRO:HG3	1:B:789:GLU:HG3	1.75	0.68
1:D:404:LEU:HD22	1:D:429:MET:CE	2.22	0.68
1:A:393:ARG:HH22	1:C:557:ARG:NE	1.91	0.68
1:B:430:THR:HG23	1:B:441:ILE:HD11	1.75	0.68
1:E:530:ASN:ND2	1:E:531:PHE:H	1.90	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:404:LEU:HD22	1:B:429:MET:HE2	1.74	0.68
1:C:350:VAL:HG21	1:C:669:ARG:HH11	1.58	0.68
1:F:480:ILE:H	1:F:494:THR:CG2	2.07	0.68
1:F:892:LEU:HD13	1:F:920:VAL:HG21	1.73	0.68
1:B:363:ARG:HG3	1:B:688:GLN:NE2	2.09	0.68
1:C:681:SER:HB3	1:C:684:GLU:HG2	1.74	0.68
1:A:53:ILE:HG23	1:A:286:LEU:HD21	1.75	0.68
1:E:73:LYS:HD3	1:E:76:SER:HB3	1.74	0.68
1:D:977:LEU:HB2	1:D:979:LEU:CD1	2.24	0.68
1:D:190:ARG:NH2	1:D:222:PHE:HZ	1.93	0.67
1:E:322:PRO:HG3	1:E:678:LEU:HD13	1.75	0.67
1:E:53:ILE:CG2	1:E:286:LEU:HD21	2.23	0.67
1:F:351:SER:OG	1:F:353:THR:HG22	1.93	0.67
1:E:205:TYR:HA	1:E:1024:ASN:HD21	1.58	0.67
1:C:922:GLN:NE2	1:D:948:THR:H	1.89	0.67
1:B:40:PRO:HG2	1:B:724:LEU:CD2	2.24	0.67
1:F:236:VAL:HG23	1:F:243:TYR:HB2	1.76	0.67
1:C:635:ASN:HB3	1:C:653:ASP:OD1	1.95	0.67
1:A:222:PHE:H	1:A:1038:HIS:HD2	1.42	0.67
1:C:190:ARG:NH2	1:C:222:PHE:HZ	1.91	0.67
1:B:404:LEU:HD22	1:B:429:MET:CE	2.24	0.67
1:D:703:ASN:HD22	1:D:703:ASN:C	1.98	0.67
1:A:350:VAL:HG21	1:A:669:ARG:NH1	2.10	0.67
1:E:190:ARG:NH2	1:E:222:PHE:HZ	1.93	0.67
1:F:53:ILE:HG23	1:F:286:LEU:HD21	1.77	0.67
1:B:72:ARG:HG3	1:E:72:ARG:HG3	1.75	0.67
1:F:982:LEU:O	1:F:983:ILE:HD12	1.95	0.66
1:A:393:ARG:HH12	1:C:557:ARG:HD2	1.59	0.66
1:D:913:ARG:HH21	1:D:1047:GLN:HE21	1.42	0.66
1:D:480:ILE:H	1:D:494:THR:HG22	1.60	0.66
1:D:681:SER:O	1:D:684:GLU:HG2	1.95	0.66
1:D:154:GLN:HB3	1:D:159:MET:HE3	1.78	0.66
1:B:489:LYS:HG3	1:B:491:PHE:HE1	1.57	0.66
1:D:286:LEU:HD12	1:D:294:TYR:O	1.96	0.66
1:A:681:SER:HB3	1:A:684:GLU:HG2	1.77	0.66
1:D:539:PRO:HG2	1:D:578:ILE:HG23	1.76	0.66
1:D:40:PRO:HG2	1:D:724:LEU:CD2	2.26	0.66
1:D:206:ARG:H	1:D:1024:ASN:HD21	1.43	0.66
1:E:284:ARG:HD3	2:E:6393:HOH:O	1.95	0.66
1:F:977:LEU:HB2	1:F:979:LEU:HD13	1.78	0.66
1:E:403:ASN:HD22	1:E:403:ASN:C	1.99	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:893:ASN:OD1	1:B:522:PRO:HD3	1.96	0.66
1:E:404:LEU:HD22	1:E:429:MET:HE2	1.77	0.65
1:A:522:PRO:HD3	1:B:893:ASN:OD1	1.95	0.65
1:E:48:ILE:HB	1:E:286:LEU:HD22	1.77	0.65
1:C:61:LEU:CB	1:C:75:VAL:HG13	2.26	0.65
1:D:61:LEU:CB	1:D:75:VAL:HG13	2.26	0.65
1:F:628:LYS:HE3	2:F:7366:HOH:O	1.95	0.65
1:D:446:GLU:OE1	1:D:468:LYS:HE2	1.97	0.65
1:C:46:PRO:HB2	1:C:286:LEU:CD2	2.26	0.65
1:E:206:ARG:H	1:E:1024:ASN:ND2	1.94	0.65
1:B:774:ASP:HA	1:B:817:ALA:HB2	1.78	0.65
1:B:593:SER:O	1:B:624:VAL:HG22	1.96	0.65
1:B:256:SER:OG	1:B:267:HIS:HE1	1.80	0.65
1:F:982:LEU:C	1:F:983:ILE:HD12	2.17	0.65
1:E:591:LEU:HD11	1:E:662:LEU:HD21	1.79	0.64
1:B:53:ILE:HG23	1:B:286:LEU:HD21	1.79	0.64
1:F:179:PRO:HG2	2:F:7045:HOH:O	1.96	0.64
1:A:552:THR:HG21	1:A:578:ILE:HD12	1.78	0.64
1:C:480:ILE:H	1:C:494:THR:CG2	2.10	0.64
1:C:74:ILE:HG13	1:C:75:VAL:HG12	1.78	0.64
1:B:61:LEU:CB	1:B:75:VAL:HG13	2.27	0.64
1:C:662:LEU:HD23	1:C:662:LEU:O	1.96	0.64
1:E:293:ILE:HG22	1:E:306:ILE:HD12	1.78	0.64
1:B:82:ASN:HD21	1:B:96:ARG:HH21	1.45	0.64
1:E:353:THR:HG23	1:E:354:TYR:CD1	2.32	0.64
1:F:694:TRP:HA	1:F:738:MET:HE1	1.78	0.64
1:F:161:CYS:SG	2:F:7394:HOH:O	2.55	0.64
1:C:322:PRO:HA	1:C:678:LEU:HD22	1.80	0.64
1:D:530:ASN:ND2	1:D:531:PHE:H	1.96	0.64
1:A:286:LEU:HD12	1:A:294:TYR:O	1.97	0.64
1:A:46:PRO:HB2	1:A:286:LEU:HD21	1.80	0.64
1:B:46:PRO:HB2	1:B:286:LEU:CD2	2.27	0.64
1:B:222:PHE:H	1:B:1038:HIS:HD2	1.46	0.64
1:A:628:LYS:HE3	2:A:2366:HOH:O	1.98	0.64
1:A:46:PRO:HB2	1:A:286:LEU:CD2	2.28	0.64
1:B:350:VAL:HG21	1:B:669:ARG:NH1	2.12	0.64
1:B:403:ASN:HD22	1:B:405:GLY:H	1.46	0.64
1:A:774:ASP:HA	1:A:817:ALA:HB2	1.78	0.64
1:F:872:HIS:HE1	1:F:902:GLU:OE1	1.81	0.64
1:C:948:THR:H	1:D:922:GLN:NE2	1.95	0.63
1:B:403:ASN:ND2	1:B:405:GLY:H	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:ASN:H	1:C:104:ASN:ND2	1.94	0.63
1:C:694:TRP:HA	1:C:738:MET:HE1	1.79	0.63
1:A:206:ARG:H	1:A:1024:ASN:HD21	1.44	0.63
1:C:155:PRO:CG	1:C:159:MET:HE1	2.21	0.63
1:C:40:PRO:HG2	1:C:724:LEU:CD2	2.28	0.63
1:A:815:VAL:HA	1:A:819:SER:HB3	1.81	0.63
1:A:493:ALA:HA	1:A:571:MET:HG3	1.79	0.63
1:A:789:GLU:OE2	2:A:2230:HOH:O	2.15	0.63
1:D:53:ILE:HG23	1:D:286:LEU:CD2	2.27	0.63
1:F:350:VAL:HG21	1:F:669:ARG:NH1	2.12	0.63
1:D:977:LEU:HB2	1:D:979:LEU:HD13	1.80	0.63
1:A:684:GLU:HG3	1:A:685:GLU:N	2.14	0.63
1:B:618:VAL:HG23	1:B:633:LYS:O	1.99	0.63
1:F:681:SER:O	1:F:684:GLU:HG2	1.99	0.63
1:B:353:THR:HG23	1:B:354:TYR:CD1	2.34	0.63
1:D:403:ASN:HD22	1:D:403:ASN:C	2.01	0.63
1:A:889:MET:SD	1:B:522:PRO:HG2	2.38	0.63
1:E:312:GLU:HG2	1:E:314:PRO:HD3	1.80	0.63
1:A:522:PRO:HG2	1:B:889:MET:SD	2.39	0.62
1:A:61:LEU:HB2	1:A:75:VAL:HG13	1.81	0.62
1:B:578:ILE:HG12	1:B:580:VAL:HG23	1.81	0.62
1:F:195:ASN:O	1:F:231:HIS:HE1	1.83	0.62
1:D:155:PRO:HG2	1:D:159:MET:CE	2.22	0.62
1:F:40:PRO:HG2	1:F:724:LEU:HD22	1.82	0.62
1:D:494:THR:HG21	1:D:500:ASP:OD1	1.99	0.62
1:A:40:PRO:HG2	1:A:724:LEU:CD2	2.29	0.62
1:B:241:ARG:NH1	1:B:263:ASP:OD1	2.33	0.62
1:B:319:ILE:HG23	1:B:677:PRO:HB3	1.80	0.62
1:C:403:ASN:HD22	1:C:403:ASN:C	2.03	0.62
1:F:61:LEU:CB	1:F:75:VAL:HG13	2.30	0.62
1:C:628:LYS:HE3	2:C:4366:HOH:O	1.99	0.62
1:B:64:HIS:HD2	1:B:71:THR:OG1	1.82	0.62
1:F:404:LEU:HD22	1:F:429:MET:CE	2.28	0.62
1:E:446:GLU:OE1	1:E:468:LYS:HE2	2.00	0.62
1:B:363:ARG:HD2	1:B:365:ARG:NH2	2.15	0.62
1:E:489:LYS:HG3	1:E:491:PHE:CE1	2.35	0.62
1:D:815:VAL:HA	1:D:819:SER:HB3	1.82	0.62
1:D:716:GLU:HG2	1:D:720:ASN:HD21	1.64	0.62
1:F:716:GLU:HG2	1:F:720:ASN:HD21	1.64	0.62
1:E:53:ILE:HD11	1:E:295:ILE:HD11	1.82	0.62
1:F:999:ARG:HG2	1:F:1005:VAL:HG22	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:ASN:HD21	1:D:96:ARG:HH21	1.48	0.62
1:A:489:LYS:HG3	1:A:491:PHE:HE1	1.65	0.61
1:F:736:VAL:HA	1:F:739:GLN:HE21	1.64	0.61
1:A:189:ARG:HD2	1:A:216:GLU:O	1.99	0.61
1:B:913:ARG:HH21	1:B:1047:GLN:HE21	1.47	0.61
1:A:387:LEU:HD13	1:A:388:GLY:N	2.15	0.61
1:F:489:LYS:HG3	1:F:491:PHE:CE1	2.36	0.61
1:E:130:GLY:HA3	2:E:6163:HOH:O	2.00	0.61
1:B:480:ILE:N	1:B:494:THR:HG22	2.12	0.61
1:E:716:GLU:HG2	1:E:720:ASN:ND2	2.16	0.61
1:C:256:SER:OG	1:C:267:HIS:HE1	1.84	0.61
1:A:403:ASN:ND2	1:A:405:GLY:H	1.97	0.61
1:F:46:PRO:HB2	1:F:286:LEU:CD2	2.30	0.61
1:D:716:GLU:HG2	1:D:720:ASN:ND2	2.14	0.61
1:D:694:TRP:HA	1:D:738:MET:CE	2.31	0.61
1:D:489:LYS:HG3	1:D:491:PHE:CE1	2.35	0.61
1:F:423:ASN:C	1:F:423:ASN:HD22	2.04	0.61
1:B:190:ARG:NH2	1:B:222:PHE:HZ	1.98	0.61
1:B:393:ARG:HH12	1:F:557:ARG:HD2	1.66	0.61
1:A:1031:VAL:HG12	1:A:1033:ILE:HD11	1.83	0.61
1:F:167:ASN:HB2	1:F:170:ILE:HB	1.83	0.61
1:F:253:GLN:HB2	1:F:255:TYR:CE1	2.36	0.61
1:A:241:ARG:NH1	1:A:263:ASP:OD1	2.33	0.61
1:E:53:ILE:HG23	1:E:286:LEU:CD2	2.29	0.60
1:E:635:ASN:HB3	1:E:653:ASP:OD1	2.01	0.60
1:C:236:VAL:HG23	1:C:243:TYR:HB2	1.82	0.60
1:E:404:LEU:HD22	1:E:429:MET:CE	2.31	0.60
1:B:393:ARG:HH12	1:F:557:ARG:CZ	2.13	0.60
1:A:662:LEU:HD23	1:A:662:LEU:O	2.02	0.60
1:D:190:ARG:HH21	1:D:190:ARG:HB2	1.66	0.60
1:C:279:ASN:ND2	2:C:4071:HOH:O	2.32	0.60
1:F:694:TRP:HA	1:F:738:MET:HE2	1.84	0.60
1:D:61:LEU:HB2	1:D:75:VAL:HG13	1.82	0.60
1:C:593:SER:O	1:C:624:VAL:HG22	2.00	0.60
1:E:40:PRO:HG2	1:E:724:LEU:CD2	2.32	0.60
1:B:155:PRO:CG	1:B:159:MET:HE1	2.22	0.60
1:A:498:SER:HB2	2:A:3192:HOH:O	2.01	0.60
1:E:977:LEU:HB2	1:E:979:LEU:HD13	1.84	0.60
1:B:684:GLU:HG3	1:B:685:GLU:N	2.16	0.60
1:C:681:SER:O	1:C:684:GLU:HG2	2.01	0.60
1:C:195:ASN:O	1:C:231:HIS:HE1	1.85	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:SER:OG	1:A:267:HIS:HE1	1.84	0.60
1:C:423:ASN:HD22	1:C:423:ASN:C	2.04	0.60
1:E:622:TYR:OH	1:E:627:ARG:HG2	2.01	0.59
1:E:206:ARG:H	1:E:1024:ASN:HD21	1.50	0.59
1:B:322:PRO:HB3	1:B:678:LEU:HD13	1.83	0.59
1:A:480:ILE:N	1:A:494:THR:HG22	2.14	0.59
1:B:206:ARG:N	1:B:1024:ASN:HD21	2.00	0.59
1:E:716:GLU:HG2	1:E:720:ASN:HD21	1.66	0.59
1:A:230:THR:HG21	1:A:248:ILE:HA	1.84	0.59
1:C:872:HIS:HE1	1:C:902:GLU:OE1	1.85	0.59
1:E:367:VAL:CG1	1:E:375:VAL:HG21	2.32	0.59
1:C:309:GLY:O	1:C:311:LEU:HD13	2.03	0.59
1:A:489:LYS:HE2	1:A:491:PHE:HZ	1.67	0.59
1:A:222:PHE:H	1:A:1038:HIS:CD2	2.19	0.59
1:B:61:LEU:HB2	1:B:75:VAL:HG13	1.83	0.59
1:E:489:LYS:HE2	1:E:491:PHE:HZ	1.66	0.59
1:D:82:ASN:ND2	1:D:96:ARG:HH21	2.00	0.59
1:A:393:ARG:HH12	1:C:557:ARG:NH2	2.01	0.59
1:C:61:LEU:HB3	1:C:75:VAL:HG13	1.83	0.59
1:D:642:SER:HB2	1:D:647:THR:HB	1.83	0.59
1:B:872:HIS:HE1	1:B:902:GLU:OE1	1.85	0.59
1:E:155:PRO:HD2	1:E:159:MET:HE3	1.85	0.59
1:B:662:LEU:O	1:B:662:LEU:HD23	2.02	0.59
1:F:988:TRP:CZ3	1:F:990:GLY:HA3	2.38	0.59
1:C:322:PRO:HG2	1:C:674:ASP:OD1	2.02	0.59
1:A:202:TRP:CH2	1:A:745:SER:HB3	2.38	0.59
1:E:676:ARG:HD2	2:E:6370:HOH:O	2.02	0.59
1:C:404:LEU:HD22	1:C:429:MET:HE2	1.85	0.59
1:B:46:PRO:HB2	1:B:286:LEU:HD21	1.85	0.59
1:F:256:SER:OG	1:F:267:HIS:HE1	1.86	0.59
1:E:913:ARG:HH21	1:E:1047:GLN:HE21	1.49	0.59
1:F:1045:ASP:HB3	1:F:1048:ILE:HG22	1.85	0.59
1:A:64:HIS:HD2	1:A:71:THR:OG1	1.85	0.59
1:F:52:ARG:HG3	1:F:52:ARG:HH21	1.68	0.59
1:C:999:ARG:HG2	1:C:1005:VAL:HG22	1.84	0.59
1:E:61:LEU:CB	1:E:75:VAL:HG13	2.33	0.58
1:E:82:ASN:HD21	1:E:96:ARG:HH21	1.51	0.58
1:E:681:SER:O	1:E:684:GLU:HG2	2.03	0.58
1:B:589:ILE:HD13	1:B:641:LEU:HD12	1.85	0.58
1:D:190:ARG:NH2	1:D:222:PHE:CZ	2.71	0.58
1:D:190:ARG:NH2	1:D:216:GLU:OE2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:681:SER:HB3	1:E:684:GLU:HG2	1.85	0.58
1:D:256:SER:OG	1:D:267:HIS:HE1	1.86	0.58
1:E:82:ASN:ND2	1:E:96:ARG:HH21	2.01	0.58
1:D:622:TYR:OH	1:D:627:ARG:HG2	2.03	0.58
1:A:82:ASN:ND2	1:A:96:ARG:HH21	2.01	0.58
1:B:119:LYS:NZ	1:B:823:ARG:HH22	2.01	0.58
1:E:333:ASP:CG	1:E:369:ARG:HE	2.06	0.58
1:B:628:LYS:HE3	2:B:3366:HOH:O	2.03	0.58
1:B:293:ILE:HG22	1:B:306:ILE:HD12	1.86	0.58
1:E:61:LEU:HB3	1:E:75:VAL:HG13	1.84	0.58
1:C:947:PRO:HD2	1:C:950:SER:HB3	1.86	0.58
1:C:889:MET:SD	1:D:522:PRO:HG2	2.44	0.58
1:F:403:ASN:C	1:F:403:ASN:HD22	2.07	0.58
1:C:43:LEU:O	1:C:44:LEU:HG	2.04	0.58
1:D:872:HIS:HE1	1:D:902:GLU:OE1	1.86	0.58
1:E:190:ARG:NH2	1:E:222:PHE:CZ	2.72	0.58
1:B:781:ALA:HB2	1:B:802:PRO:HG2	1.86	0.58
1:B:104:ASN:ND2	1:B:104:ASN:H	1.89	0.57
1:F:319:ILE:HG23	1:F:677:PRO:HB3	1.85	0.57
1:F:815:VAL:HA	1:F:819:SER:HB3	1.85	0.57
1:E:64:HIS:HD2	1:E:71:THR:OG1	1.87	0.57
1:E:104:ASN:ND2	1:E:104:ASN:H	1.99	0.57
1:E:104:ASN:N	1:E:104:ASN:HD22	1.91	0.57
1:A:872:HIS:HE1	1:A:902:GLU:OE1	1.87	0.57
1:D:322:PRO:HB3	1:D:678:LEU:HD13	1.85	0.57
1:E:694:TRP:HA	1:E:738:MET:CE	2.34	0.57
1:C:530:ASN:ND2	1:C:531:PHE:H	2.02	0.57
1:F:884:ILE:HD13	1:F:924:ILE:HD13	1.86	0.57
1:F:735:ILE:O	1:F:739:GLN:HG3	2.04	0.57
1:F:618:VAL:HG23	1:F:633:LYS:O	2.03	0.57
1:D:635:ASN:HB3	1:D:653:ASP:OD1	2.04	0.57
1:E:202:TRP:CH2	1:E:745:SER:HB3	2.39	0.57
1:F:947:PRO:HD2	1:F:950:SER:HB3	1.85	0.57
1:F:218:ASN:O	1:F:219:SER:C	2.43	0.57
1:F:350:VAL:CG2	1:F:669:ARG:HH11	2.15	0.57
1:B:557:ARG:CZ	1:D:393:ARG:HH12	2.18	0.57
1:C:524:PRO:HD3	1:D:605:GLU:HG2	1.87	0.57
1:B:390:TYR:HD1	1:B:397:ALA:HB2	1.69	0.57
1:D:965:SER:HA	1:D:990:GLY:O	2.03	0.57
1:A:319:ILE:HG23	1:A:677:PRO:HB3	1.87	0.57
1:E:815:VAL:HA	1:E:819:SER:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:684:GLU:HG3	1:D:685:GLU:N	2.19	0.57
1:C:230:THR:HG21	1:C:248:ILE:HA	1.87	0.57
1:C:319:ILE:HG23	1:C:677:PRO:HB3	1.86	0.56
1:D:489:LYS:HG3	1:D:491:PHE:HE1	1.70	0.56
1:A:346:PHE:C	1:A:347:ILE:HD12	2.25	0.56
1:F:642:SER:HB2	1:F:647:THR:HB	1.87	0.56
1:D:241:ARG:NH1	1:D:263:ASP:OD1	2.37	0.56
1:C:350:VAL:HG21	1:C:669:ARG:NH1	2.19	0.56
1:E:351:SER:OG	1:E:353:THR:HG22	2.05	0.56
1:D:694:TRP:HA	1:D:738:MET:HE1	1.87	0.56
1:F:216:GLU:OE1	1:F:219:SER:HA	2.05	0.56
1:E:807:ILE:HG12	1:E:837:LEU:CD2	2.35	0.56
1:E:232:VAL:HG13	1:E:244:PHE:CD1	2.41	0.56
1:D:360:GLU:HB2	1:D:364:ILE:HD11	1.86	0.56
1:F:202:TRP:CH2	1:F:745:SER:HB3	2.40	0.56
1:F:308:ILE:HG22	1:F:311:LEU:HD11	1.87	0.56
1:A:104:ASN:ND2	1:A:104:ASN:H	1.98	0.56
1:B:489:LYS:HE2	1:B:491:PHE:HZ	1.71	0.56
1:D:205:TYR:HA	1:D:1024:ASN:HD21	1.70	0.56
1:B:811:ASP:OD1	1:E:676:ARG:NH1	2.39	0.56
1:F:562:GLU:O	1:F:563:ALA:HB3	2.06	0.56
1:A:605:GLU:CG	1:B:524:PRO:HD3	2.36	0.56
1:B:153:MET:HG3	1:B:859:ARG:CZ	2.35	0.56
1:F:312:GLU:HG2	1:F:314:PRO:HD3	1.87	0.56
1:F:965:SER:HA	1:F:990:GLY:O	2.06	0.56
1:D:999:ARG:HG2	1:D:1005:VAL:HG22	1.86	0.56
1:F:353:THR:HG23	1:F:354:TYR:CD1	2.40	0.56
1:D:284:ARG:HD3	2:D:5393:HOH:O	2.05	0.56
1:A:423:ASN:HD22	1:A:423:ASN:C	2.09	0.56
1:A:429:MET:HE3	1:A:438:PRO:HB2	1.87	0.56
1:A:965:SER:HA	1:A:990:GLY:O	2.06	0.56
1:B:499:HIS:HD2	2:B:3176:HOH:O	1.89	0.56
1:E:872:HIS:HE1	1:E:902:GLU:OE1	1.89	0.56
1:E:568:LEU:HB3	1:E:571:MET:HE2	1.87	0.56
1:D:312:GLU:HG2	1:D:314:PRO:HD3	1.86	0.56
1:E:1016:ARG:O	1:E:1017:ASP:HB2	2.06	0.56
1:A:403:ASN:HD22	1:A:405:GLY:H	1.54	0.55
1:E:499:HIS:HE1	2:E:6239:HOH:O	1.89	0.55
1:C:53:ILE:HG23	1:C:286:LEU:HD21	1.87	0.55
1:D:353:THR:HG23	1:D:354:TYR:CD1	2.41	0.55
1:B:493:ALA:HA	1:B:571:MET:HG3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:977:LEU:HB2	1:B:979:LEU:HD13	1.88	0.55
1:E:605:GLU:HG2	1:F:524:PRO:HD3	1.88	0.55
1:C:929:MET:HA	1:C:929:MET:CE	2.36	0.55
1:A:293:ILE:CG2	1:A:306:ILE:HD12	2.36	0.55
1:E:190:ARG:NH2	1:E:216:GLU:OE2	2.40	0.55
1:E:593:SER:O	1:E:624:VAL:HG22	2.05	0.55
1:B:167:ASN:HB2	1:B:170:ILE:HB	1.87	0.55
1:C:565:GLU:HG2	1:C:566:TYR:N	2.21	0.55
1:B:494:THR:HG21	1:B:500:ASP:OD1	2.06	0.55
1:A:681:SER:O	1:A:684:GLU:HG2	2.06	0.55
1:F:635:ASN:HB3	1:F:653:ASP:OD1	2.07	0.55
1:D:929:MET:HA	1:D:929:MET:CE	2.36	0.55
1:F:236:VAL:CG2	1:F:243:TYR:HB2	2.36	0.55
1:D:184:LEU:HB2	1:D:191:VAL:HB	1.88	0.55
1:F:431:VAL:HG22	1:F:438:PRO:HB3	1.88	0.55
1:E:731:LEU:HD22	1:E:735:ILE:HG13	1.88	0.55
1:E:480:ILE:H	1:E:494:THR:CG2	2.18	0.55
1:B:228:MET:HE3	1:B:232:VAL:CG2	2.36	0.55
1:B:423:ASN:HD22	1:B:423:ASN:C	2.09	0.55
1:F:565:GLU:HG2	1:F:566:TYR:N	2.21	0.55
1:C:522:PRO:HD3	1:D:893:ASN:OD1	2.05	0.55
1:E:494:THR:HG21	1:E:500:ASP:OD1	2.07	0.55
1:F:258:ASP:C	1:F:260:ASP:H	2.10	0.55
1:D:346:PHE:C	1:D:347:ILE:HD12	2.27	0.55
1:A:155:PRO:HD2	1:A:159:MET:HE3	1.88	0.55
1:E:286:LEU:CD1	1:E:295:ILE:HG12	2.36	0.55
1:B:189:ARG:HD2	1:B:216:GLU:O	2.07	0.55
1:F:913:ARG:HH21	1:F:1047:GLN:HE21	1.55	0.55
1:B:155:PRO:HG2	1:B:159:MET:CE	2.25	0.55
1:B:88:PRO:HG3	1:B:144:GLY:HA2	1.89	0.55
1:D:295:ILE:HG13	1:D:306:ILE:HD11	1.87	0.54
1:C:694:TRP:HA	1:C:738:MET:HE2	1.87	0.54
1:B:892:LEU:HD13	1:B:920:VAL:HG21	1.89	0.54
1:A:119:LYS:NZ	1:A:823:ARG:HH22	2.05	0.54
1:D:565:GLU:HG2	1:D:566:TYR:N	2.22	0.54
1:C:965:SER:HA	1:C:990:GLY:O	2.08	0.54
1:D:681:SER:HB3	1:D:684:GLU:HG2	1.88	0.54
1:F:618:VAL:HG21	1:F:631:GLU:HG3	1.89	0.54
1:F:43:LEU:O	1:F:44:LEU:HG	2.08	0.54
1:C:321:ILE:HB	1:C:324:LYS:HG3	1.89	0.54
1:C:61:LEU:HB2	1:C:75:VAL:HG13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:872:HIS:CE1	1:F:902:GLU:OE1	2.61	0.54
1:F:489:LYS:HG3	1:F:491:PHE:HE1	1.71	0.54
1:C:241:ARG:HB2	1:C:243:TYR:CE1	2.42	0.54
1:C:774:ASP:HA	1:C:817:ALA:HB2	1.88	0.54
1:E:155:PRO:CD	1:E:159:MET:HE3	2.38	0.54
1:E:530:ASN:ND2	1:E:531:PHE:N	2.55	0.54
1:A:220:GLY:O	1:A:1038:HIS:HB3	2.08	0.54
1:D:591:LEU:HD11	1:D:662:LEU:HD21	1.89	0.54
1:E:167:ASN:HB2	1:E:170:ILE:HB	1.90	0.54
1:D:104:ASN:H	1:D:104:ASN:ND2	2.00	0.54
1:E:948:THR:H	1:F:922:GLN:NE2	2.03	0.54
1:D:480:ILE:H	1:D:494:THR:CG2	2.19	0.54
1:F:332:LEU:HD11	1:F:338:ALA:HB2	1.90	0.54
1:A:524:PRO:HD3	1:B:605:GLU:CG	2.36	0.54
1:A:736:VAL:HA	1:A:739:GLN:HE21	1.72	0.54
1:D:983:ILE:CG2	1:D:1033:ILE:HD12	2.28	0.54
1:E:156:PHE:CD1	1:E:159:MET:HE1	2.43	0.54
1:C:351:SER:OG	1:C:353:THR:HG22	2.07	0.54
1:B:676:ARG:NH1	1:E:811:ASP:OD1	2.41	0.54
1:C:589:ILE:HG21	1:C:641:LEU:HD11	1.89	0.54
1:A:706:VAL:HG12	1:A:710:ILE:HD12	1.89	0.54
1:F:184:LEU:HD13	1:F:237:ILE:HG13	1.90	0.54
1:F:49:HIS:CD2	1:F:90:GLY:HA3	2.43	0.54
1:F:498:SER:OG	1:F:499:HIS:N	2.40	0.54
1:C:700:ASN:HD22	1:C:1008:GLN:NE2	2.06	0.54
1:B:546:PRO:CG	1:B:567:ASP:HB3	2.38	0.54
1:C:562:GLU:O	1:C:563:ALA:HB3	2.08	0.54
1:D:807:ILE:HG12	1:D:837:LEU:CD2	2.38	0.54
1:C:206:ARG:H	1:C:1024:ASN:ND2	2.06	0.54
1:D:64:HIS:HD2	1:D:71:THR:OG1	1.91	0.54
1:F:1036:ALA:O	1:F:1039:ASP:HB2	2.08	0.54
1:B:703:ASN:C	1:B:703:ASN:HD22	2.12	0.54
1:E:286:LEU:HD12	1:E:294:TYR:O	2.07	0.53
1:F:87:PHE:HB3	1:F:88:PRO:HD2	1.90	0.53
1:A:494:THR:HG21	1:A:500:ASP:OD1	2.08	0.53
1:B:393:ARG:HH22	1:F:557:ARG:NE	2.06	0.53
1:F:222:PHE:H	1:F:1038:HIS:HD2	1.53	0.53
1:B:355:VAL:HG12	1:B:676:ARG:HH21	1.74	0.53
1:B:218:ASN:HB3	1:B:221:ALA:HB3	1.90	0.53
1:A:363:ARG:HG3	1:A:688:GLN:NE2	2.23	0.53
1:F:253:GLN:NE2	1:F:268:THR:OG1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:681:SER:CB	1:B:684:GLU:HG2	2.37	0.53
1:C:522:PRO:HG2	1:D:889:MET:SD	2.47	0.53
1:A:913:ARG:HH21	1:A:1047:GLN:HE21	1.55	0.53
1:B:789:GLU:OE2	2:B:3230:HOH:O	2.19	0.53
1:E:241:ARG:NH1	1:E:263:ASP:OD1	2.41	0.53
1:E:475:TYR:OH	1:F:949:ASN:ND2	2.37	0.53
1:A:703:ASN:C	1:A:703:ASN:HD22	2.11	0.53
1:E:220:GLY:O	1:E:1038:HIS:HB3	2.09	0.53
1:B:61:LEU:HB3	1:B:75:VAL:HG13	1.91	0.53
1:A:319:ILE:CG2	1:A:677:PRO:HB3	2.39	0.53
1:C:1036:ALA:O	1:C:1039:ASP:HB2	2.09	0.53
1:F:206:ARG:N	1:F:1024:ASN:HD21	2.04	0.53
1:C:190:ARG:NH2	1:C:222:PHE:CZ	2.75	0.53
1:A:676:ARG:NH1	1:D:811:ASP:OD1	2.42	0.53
1:E:568:LEU:HB3	1:E:571:MET:CE	2.39	0.53
1:F:190:ARG:NH2	1:F:222:PHE:HZ	2.07	0.53
1:A:156:PHE:HB2	1:A:159:MET:HE2	1.91	0.53
1:C:524:PRO:HD3	1:D:605:GLU:CG	2.39	0.53
1:B:546:PRO:HG2	1:B:567:ASP:HB3	1.91	0.53
1:C:82:ASN:HD21	1:C:96:ARG:HD3	1.71	0.53
1:F:64:HIS:HD2	1:F:71:THR:OG1	1.91	0.53
1:A:562:GLU:O	1:A:563:ALA:HB3	2.09	0.53
1:F:253:GLN:HB2	1:F:255:TYR:HE1	1.74	0.53
1:C:46:PRO:HB2	1:C:286:LEU:HD21	1.90	0.53
1:F:618:VAL:CG2	1:F:631:GLU:HG3	2.39	0.53
1:A:167:ASN:HB2	1:A:170:ILE:HB	1.90	0.53
1:D:418:PHE:HA	1:D:433:LEU:HG	1.89	0.53
1:C:722:VAL:N	1:C:723:PRO:HD2	2.24	0.53
1:F:977:LEU:HB2	1:F:979:LEU:CD1	2.39	0.53
1:D:61:LEU:HB3	1:D:75:VAL:HG13	1.90	0.53
1:C:241:ARG:NH1	1:C:263:ASP:HB3	2.24	0.53
1:A:82:ASN:HD21	1:A:96:ARG:HH21	1.56	0.53
1:D:319:ILE:HG23	1:D:677:PRO:HB3	1.91	0.53
1:C:393:ARG:HH22	1:E:557:ARG:NE	2.07	0.53
1:F:700:ASN:HD22	1:F:1008:GLN:NE2	2.07	0.53
1:F:134:PHE:O	1:F:135:THR:HB	2.09	0.53
1:A:88:PRO:HG3	1:A:144:GLY:HA2	1.91	0.53
1:B:982:LEU:C	1:B:983:ILE:HD12	2.29	0.52
1:E:295:ILE:HG13	1:E:306:ILE:HD11	1.90	0.52
1:F:735:ILE:O	1:F:738:MET:HG3	2.09	0.52
1:C:404:LEU:HD22	1:C:429:MET:CE	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:LEU:CB	1:A:75:VAL:HG13	2.39	0.52
1:A:423:ASN:ND2	1:A:425:ARG:HB2	2.24	0.52
1:F:249:ASP:HB2	2:F:7014:HOH:O	2.09	0.52
1:B:337:ILE:HG22	1:B:338:ALA:N	2.24	0.52
1:B:706:VAL:HG12	1:B:710:ILE:HD12	1.91	0.52
1:C:53:ILE:HD11	1:C:295:ILE:HD11	1.92	0.52
1:A:393:ARG:NH1	1:C:557:ARG:HD2	2.24	0.52
1:F:1052:ILE:O	1:F:1056:ILE:HG13	2.10	0.52
1:D:333:ASP:CG	1:D:369:ARG:HE	2.12	0.52
1:D:913:ARG:HH21	1:D:1047:GLN:NE2	2.07	0.52
1:D:179:PRO:HG2	2:D:5045:HOH:O	2.09	0.52
1:E:524:PRO:HD3	1:F:605:GLU:CG	2.39	0.52
1:C:716:GLU:HG2	1:C:720:ASN:ND2	2.24	0.52
1:E:403:ASN:HD22	1:E:404:LEU:N	2.06	0.52
1:B:319:ILE:CG2	1:B:677:PRO:HB3	2.39	0.52
1:E:642:SER:HB2	1:E:647:THR:HB	1.91	0.52
1:F:729:TYR:O	1:F:732:SER:HB3	2.09	0.52
1:B:155:PRO:HD2	1:B:159:MET:HE3	1.90	0.52
1:D:155:PRO:CG	1:D:159:MET:HE1	2.23	0.52
1:C:249:ASP:HB2	2:C:4014:HOH:O	2.08	0.52
1:C:308:ILE:HG22	1:C:311:LEU:HD11	1.91	0.52
1:C:676:ARG:HD2	2:C:4370:HOH:O	2.08	0.52
1:F:123:TYR:OH	1:F:823:ARG:HD3	2.10	0.52
1:F:123:TYR:HB3	1:F:826:SER:OG	2.09	0.52
1:C:333:ASP:CG	1:C:369:ARG:HE	2.13	0.52
1:B:815:VAL:HA	1:B:819:SER:HB3	1.91	0.52
1:F:593:SER:O	1:F:624:VAL:HG22	2.10	0.52
1:E:781:ALA:HB2	1:E:802:PRO:HG2	1.91	0.52
1:A:982:LEU:C	1:A:983:ILE:HD12	2.30	0.52
1:A:190:ARG:NH2	1:A:222:PHE:HZ	2.07	0.52
1:D:557:ARG:HD2	1:F:393:ARG:HH12	1.75	0.52
1:B:467:LEU:C	1:B:467:LEU:HD12	2.29	0.52
1:B:156:PHE:HB2	1:B:159:MET:HE2	1.92	0.52
1:A:580:VAL:HG22	1:A:622:TYR:CD2	2.44	0.52
1:E:216:GLU:OE1	1:E:219:SER:HA	2.10	0.52
1:B:913:ARG:HH21	1:B:1047:GLN:NE2	2.08	0.52
1:C:807:ILE:HG12	1:C:837:LEU:CD2	2.40	0.52
1:C:184:LEU:HD13	1:C:237:ILE:HG13	1.90	0.52
1:C:52:ARG:HH21	1:C:52:ARG:HG3	1.75	0.52
1:C:350:VAL:CG2	1:C:669:ARG:HH11	2.23	0.52
1:A:781:ALA:HB2	1:A:802:PRO:HG2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ARG:N	1:A:1024:ASN:HD21	2.07	0.52
1:B:190:ARG:NH2	1:B:222:PHE:CZ	2.77	0.52
1:A:363:ARG:HD2	1:A:365:ARG:NH2	2.25	0.52
1:D:885:PRO:O	1:D:915:ASN:HA	2.09	0.52
1:B:387:LEU:HD13	1:B:388:GLY:N	2.24	0.52
1:D:156:PHE:HD1	1:D:159:MET:CE	2.23	0.51
1:C:684:GLU:HG3	1:C:685:GLU:N	2.24	0.51
1:E:684:GLU:HG3	1:E:685:GLU:N	2.24	0.51
1:F:222:PHE:H	1:F:1038:HIS:CD2	2.28	0.51
1:B:314:PRO:HD2	1:B:726:LYS:HG2	1.92	0.51
1:F:651:ARG:NH2	1:F:655:GLY:O	2.42	0.51
1:A:475:TYR:OH	1:B:949:ASN:ND2	2.43	0.51
1:E:156:PHE:HD1	1:E:159:MET:HE1	1.76	0.51
1:E:578:ILE:CD1	1:E:595:ILE:HD12	2.41	0.51
1:A:681:SER:CB	1:A:684:GLU:HG2	2.39	0.51
1:D:202:TRP:CH2	1:D:745:SER:HB3	2.45	0.51
1:D:562:GLU:O	1:D:563:ALA:HB3	2.10	0.51
1:D:1016:ARG:O	1:D:1017:ASP:HB2	2.10	0.51
1:B:965:SER:HA	1:B:990:GLY:O	2.10	0.51
1:F:1055:LEU:O	1:F:1059:LEU:HD13	2.10	0.51
1:C:776:TYR:CD1	1:C:816:GLY:HA2	2.45	0.51
1:F:241:ARG:NH1	1:F:263:ASP:OD1	2.44	0.51
1:F:430:THR:HG23	1:F:441:ILE:HD11	1.92	0.51
1:E:889:MET:SD	1:F:522:PRO:HG2	2.50	0.51
1:E:155:PRO:HG2	1:E:159:MET:CE	2.32	0.51
1:E:222:PHE:H	1:E:1038:HIS:CD2	2.28	0.51
1:B:222:PHE:H	1:B:1038:HIS:CD2	2.28	0.51
1:C:489:LYS:HG3	1:C:491:PHE:CE1	2.45	0.51
1:C:703:ASN:HD22	1:C:703:ASN:C	2.13	0.51
1:C:893:ASN:OD1	1:D:522:PRO:HD3	2.11	0.51
1:D:130:GLY:HA3	2:D:5163:HOH:O	2.10	0.51
1:E:522:PRO:HG2	1:F:889:MET:SD	2.50	0.51
1:C:242:ILE:O	1:C:256:SER:HA	2.10	0.51
1:B:393:ARG:HH12	1:F:557:ARG:CD	2.23	0.51
1:B:589:ILE:HD13	1:B:641:LEU:CD1	2.41	0.51
1:F:589:ILE:HG21	1:F:641:LEU:HD11	1.91	0.51
1:C:802:PRO:O	1:C:805:TYR:HB2	2.11	0.51
1:C:494:THR:HG21	1:C:500:ASP:OD1	2.11	0.51
1:F:238:VAL:HG11	1:F:298:PRO:HG2	1.93	0.51
1:B:205:TYR:HA	1:B:1024:ASN:HD21	1.76	0.51
1:C:736:VAL:HA	1:C:739:GLN:HE21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:TYR:HB3	1:D:826:SER:OG	2.11	0.51
1:B:315:GLU:OE2	1:E:119:LYS:HD2	2.11	0.51
1:C:278:LEU:HD23	1:C:287:PHE:HB3	1.92	0.51
1:A:1031:VAL:HG12	1:A:1033:ILE:CD1	2.40	0.51
1:F:205:TYR:HA	1:F:1024:ASN:HD21	1.76	0.51
1:E:530:ASN:HD22	1:E:531:PHE:H	1.55	0.51
1:D:593:SER:O	1:D:624:VAL:HG22	2.11	0.51
1:E:156:PHE:HD1	1:E:159:MET:CE	2.24	0.50
1:B:446:GLU:OE1	1:B:468:LYS:HE2	2.11	0.50
1:C:350:VAL:HG23	1:C:351:SER:N	2.26	0.50
1:E:700:ASN:HD22	1:E:1008:GLN:NE2	2.09	0.50
1:F:245:ILE:HD11	1:F:278:LEU:HG	1.92	0.50
1:F:156:PHE:H	1:F:159:MET:CE	2.24	0.50
1:B:373:THR:HG21	1:B:393:ARG:HD2	1.92	0.50
1:A:134:PHE:O	1:A:135:THR:HB	2.12	0.50
1:A:43:LEU:HD13	1:A:308:ILE:HD12	1.92	0.50
1:C:153:MET:HG3	1:C:859:ARG:NH1	2.26	0.50
1:E:703:ASN:HD22	1:E:703:ASN:C	2.13	0.50
1:F:53:ILE:HG23	1:F:286:LEU:CD2	2.39	0.50
1:D:676:ARG:HD2	2:D:5370:HOH:O	2.11	0.50
1:F:493:ALA:HA	1:F:571:MET:HG3	1.92	0.50
1:E:46:PRO:HB2	1:E:286:LEU:CD2	2.41	0.50
1:E:578:ILE:HG12	1:E:580:VAL:HG23	1.94	0.50
1:C:709:GLU:OE2	1:C:713:ARG:HD3	2.11	0.50
1:D:236:VAL:HG23	1:D:243:TYR:HB2	1.93	0.50
1:A:156:PHE:CD1	1:A:159:MET:HE1	2.47	0.50
1:F:552:THR:HG21	1:F:578:ILE:HD12	1.94	0.50
1:B:363:ARG:HG3	1:B:688:GLN:HE22	1.76	0.50
1:D:190:ARG:HH21	1:D:190:ARG:CG	2.24	0.50
1:B:393:ARG:HH12	1:F:557:ARG:NH2	2.10	0.50
1:A:48:ILE:HB	1:A:286:LEU:HD22	1.94	0.50
1:B:286:LEU:HD11	1:B:293:ILE:CG2	2.42	0.50
1:C:256:SER:OG	1:C:267:HIS:CE1	2.65	0.50
1:C:317:ARG:HD3	1:F:823:ARG:HD2	1.93	0.50
1:E:913:ARG:HH21	1:E:1047:GLN:NE2	2.09	0.50
1:C:206:ARG:H	1:C:1024:ASN:HD21	1.59	0.50
1:C:716:GLU:HG2	1:C:720:ASN:HD21	1.77	0.50
1:C:332:LEU:HD11	1:C:338:ALA:HB2	1.94	0.50
1:F:46:PRO:HB2	1:F:286:LEU:HD21	1.92	0.50
1:E:977:LEU:HB2	1:E:979:LEU:CD1	2.40	0.50
1:B:872:HIS:CE1	1:B:902:GLU:OE1	2.65	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:694:TRP:HA	1:E:738:MET:HE2	1.93	0.50
1:E:618:VAL:HG21	1:E:631:GLU:HG3	1.94	0.50
1:D:557:ARG:NE	1:F:393:ARG:HH22	2.10	0.50
1:A:317:ARG:HD3	1:D:823:ARG:HD2	1.92	0.50
1:F:452:PHE:HB3	1:F:463:TYR:HB3	1.94	0.50
1:C:815:VAL:HA	1:C:819:SER:HB3	1.92	0.50
1:E:286:LEU:HD13	1:E:295:ILE:HG12	1.94	0.49
1:B:681:SER:O	1:B:684:GLU:HG2	2.12	0.49
1:B:403:ASN:HD22	1:B:403:ASN:C	2.16	0.49
1:F:616:LYS:HE2	1:F:653:ASP:CB	2.42	0.49
1:E:618:VAL:CG2	1:E:631:GLU:HG3	2.41	0.49
1:F:333:ASP:CG	1:F:369:ARG:HE	2.14	0.49
1:A:992:VAL:HG11	1:A:1009:PRO:HB2	1.93	0.49
1:E:965:SER:HA	1:E:990:GLY:O	2.12	0.49
1:C:731:LEU:HD22	1:C:735:ILE:HG13	1.95	0.49
1:C:732:SER:O	1:C:736:VAL:HG23	2.12	0.49
1:E:123:TYR:HB3	1:E:826:SER:OG	2.10	0.49
1:D:350:VAL:HG21	1:D:669:ARG:HH11	1.76	0.49
1:C:228:MET:HE1	1:C:244:PHE:CE1	2.47	0.49
1:F:177:LEU:HD13	1:F:192:ILE:HD11	1.94	0.49
1:F:639:LEU:HD23	1:F:639:LEU:C	2.33	0.49
1:A:498:SER:OG	1:A:499:HIS:N	2.44	0.49
1:C:988:TRP:CZ3	1:C:990:GLY:HA3	2.47	0.49
1:F:346:PHE:C	1:F:347:ILE:HD12	2.32	0.49
1:A:236:VAL:HG23	1:A:243:TYR:HB2	1.93	0.49
1:C:218:ASN:O	1:C:221:ALA:N	2.45	0.49
1:E:300:THR:O	1:E:301:GLU:HB3	2.12	0.49
1:E:46:PRO:HB2	1:E:286:LEU:HD23	1.94	0.49
1:A:605:GLU:HG2	1:B:524:PRO:HD3	1.93	0.49
1:E:256:SER:OG	1:E:267:HIS:HE1	1.95	0.49
1:C:363:ARG:NH2	1:C:365:ARG:HH22	2.11	0.49
1:C:155:PRO:HB3	1:C:860:TYR:HA	1.94	0.49
1:A:626:THR:O	1:A:627:ARG:HB2	2.12	0.49
1:A:205:TYR:CE1	1:A:207:GLY:HA3	2.48	0.49
1:E:736:VAL:HA	1:E:739:GLN:HE21	1.77	0.49
1:B:134:PHE:O	1:B:135:THR:HB	2.12	0.49
1:C:156:PHE:HD1	1:C:159:MET:CE	2.26	0.49
1:A:155:PRO:CD	1:A:159:MET:HE3	2.43	0.49
1:B:104:ASN:N	1:B:104:ASN:HD22	1.93	0.49
1:D:706:VAL:HG12	1:D:710:ILE:CD1	2.43	0.49
1:D:774:ASP:HA	1:D:817:ALA:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:LEU:HD11	1:B:293:ILE:HG22	1.94	0.49
1:F:716:GLU:HG2	1:F:720:ASN:ND2	2.27	0.49
1:C:641:LEU:HD22	1:C:645:ARG:HA	1.94	0.49
1:E:524:PRO:HD3	1:F:605:GLU:HG2	1.94	0.49
1:C:218:ASN:O	1:C:219:SER:C	2.50	0.49
1:E:346:PHE:C	1:E:347:ILE:HD12	2.33	0.49
1:D:206:ARG:N	1:D:1024:ASN:HD21	2.09	0.49
1:C:884:ILE:HD13	1:C:924:ILE:HD13	1.94	0.49
1:D:618:VAL:CG2	1:D:631:GLU:HG3	2.42	0.49
1:D:268:THR:CG2	1:D:303:ILE:HD11	2.40	0.49
1:B:350:VAL:CG2	1:B:669:ARG:HH11	2.23	0.49
1:F:189:ARG:HD2	1:F:216:GLU:O	2.13	0.49
1:F:994:ILE:HG22	1:F:1008:GLN:O	2.13	0.49
1:C:141:ASP:HB2	1:C:142:PRO:HD2	1.93	0.49
1:E:589:ILE:HG21	1:E:641:LEU:HD11	1.95	0.49
1:D:167:ASN:HB2	1:D:170:ILE:HB	1.94	0.49
1:B:156:PHE:HD1	1:B:159:MET:CE	2.26	0.49
1:D:1033:ILE:HD11	1:D:1050:TYR:CD2	2.48	0.49
1:A:589:ILE:HD13	1:A:641:LEU:HD12	1.95	0.49
1:F:256:SER:OG	1:F:267:HIS:CE1	2.65	0.48
1:E:400:PHE:CD2	1:E:436:GLY:HA3	2.48	0.48
1:B:580:VAL:HG22	1:B:622:TYR:CD2	2.48	0.48
1:A:286:LEU:HD11	1:A:293:ILE:CG2	2.42	0.48
1:E:965:SER:N	1:E:968:ASP:OD2	2.43	0.48
1:D:367:VAL:CG1	1:D:375:VAL:HG21	2.43	0.48
1:E:499:HIS:HD2	2:E:6176:HOH:O	1.95	0.48
1:C:337:ILE:HG22	1:C:338:ALA:N	2.28	0.48
1:F:890:MET:O	1:F:894:GLU:HG2	2.12	0.48
1:A:882:ILE:HD11	1:A:899:PHE:HA	1.94	0.48
1:F:722:VAL:N	1:F:723:PRO:HD2	2.29	0.48
1:E:577:PRO:HG3	1:F:789:GLU:HG3	1.95	0.48
1:C:639:LEU:HD23	1:C:639:LEU:C	2.33	0.48
1:D:468:LYS:CD	1:D:473:ASP:HB2	2.38	0.48
1:A:578:ILE:HG12	1:A:580:VAL:HG23	1.94	0.48
1:A:676:ARG:HD2	2:A:2370:HOH:O	2.13	0.48
1:F:706:VAL:HG12	1:F:710:ILE:CD1	2.42	0.48
1:B:709:GLU:OE2	1:B:713:ARG:HD3	2.14	0.48
1:F:213:ILE:HB	1:F:226:VAL:HB	1.95	0.48
1:A:155:PRO:CG	1:A:159:MET:HE1	2.31	0.48
1:B:53:ILE:CD1	1:B:306:ILE:HD13	2.42	0.48
1:F:897:ARG:HG2	1:F:898:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:LEU:HB2	1:A:979:LEU:HD13	1.96	0.48
1:C:977:LEU:HB2	1:C:979:LEU:HD13	1.95	0.48
1:A:1016:ARG:O	1:A:1017:ASP:HB2	2.13	0.48
1:B:524:PRO:HB3	1:B:531:PHE:CE2	2.49	0.48
1:C:929:MET:HA	1:C:929:MET:HE3	1.95	0.48
1:C:205:TYR:HA	1:C:1024:ASN:HD21	1.77	0.48
1:C:119:LYS:NZ	1:C:823:ARG:HH22	2.12	0.48
1:A:499:HIS:HD2	2:A:2176:HOH:O	1.95	0.48
1:F:309:GLY:O	1:F:311:LEU:HD13	2.14	0.48
1:E:167:ASN:O	1:E:170:ILE:HG12	2.13	0.48
1:E:802:PRO:O	1:E:805:TYR:HB2	2.13	0.48
1:F:284:ARG:HD3	2:F:7393:HOH:O	2.13	0.48
1:B:639:LEU:HD23	1:B:639:LEU:C	2.34	0.48
1:C:735:ILE:O	1:C:739:GLN:HG3	2.13	0.48
1:C:241:ARG:HB2	1:C:243:TYR:HE1	1.79	0.48
1:A:791:GLU:CD	1:A:861:ARG:HE	2.16	0.48
1:D:430:THR:HG23	1:D:441:ILE:HD11	1.96	0.48
1:C:78:LEU:HB2	2:C:4254:HOH:O	2.13	0.48
1:B:505:PHE:CE2	1:B:512:LEU:HD13	2.48	0.48
1:C:238:VAL:HG11	1:C:298:PRO:HG2	1.94	0.48
1:E:999:ARG:HG2	1:E:1005:VAL:HG22	1.95	0.48
1:A:218:ASN:HB3	1:A:221:ALA:HB3	1.95	0.48
1:E:53:ILE:CD1	1:E:306:ILE:HD13	2.44	0.48
1:E:983:ILE:HG23	1:E:1033:ILE:CD1	2.38	0.48
1:A:556:PRO:HD3	1:E:354:TYR:CD1	2.49	0.48
1:B:425:ARG:O	1:B:426:PHE:HB2	2.14	0.48
1:B:230:THR:HG21	1:B:248:ILE:HA	1.95	0.48
1:C:605:GLU:HG2	1:D:524:PRO:HD3	1.95	0.48
1:B:562:GLU:O	1:B:563:ALA:HB3	2.14	0.48
1:F:403:ASN:HD22	1:F:404:LEU:N	2.12	0.47
1:C:681:SER:CB	1:C:684:GLU:HG2	2.42	0.47
1:D:913:ARG:NH2	1:D:1047:GLN:HE21	2.10	0.47
1:B:498:SER:HB2	2:B:2192:HOH:O	2.13	0.47
1:C:48:ILE:HG12	1:C:49:HIS:N	2.28	0.47
1:D:425:ARG:O	1:D:426:PHE:HB2	2.13	0.47
1:C:297:ASN:O	1:C:301:GLU:N	2.44	0.47
1:E:155:PRO:CG	1:E:159:MET:HE1	2.35	0.47
1:E:578:ILE:HD12	1:E:595:ILE:HD12	1.96	0.47
1:A:53:ILE:CD1	1:A:306:ILE:HD13	2.45	0.47
1:E:194:ARG:O	1:E:211:GLY:HA2	2.14	0.47
1:D:228:MET:HE1	1:D:232:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:GLU:HB2	1:B:364:ILE:HD11	1.97	0.47
1:F:681:SER:HB3	1:F:684:GLU:HG2	1.97	0.47
1:A:314:PRO:HD2	1:A:726:LYS:HG2	1.94	0.47
1:A:270:PHE:CD2	1:A:289:LYS:HE2	2.50	0.47
1:A:337:ILE:HD11	1:A:350:VAL:HG12	1.95	0.47
1:B:355:VAL:CG1	1:B:676:ARG:HH21	2.26	0.47
1:F:218:ASN:O	1:F:221:ALA:N	2.48	0.47
1:C:64:HIS:HD2	1:C:71:THR:OG1	1.97	0.47
1:C:956:ILE:HG22	1:C:1055:LEU:HD11	1.96	0.47
1:E:565:GLU:HG2	1:E:566:TYR:N	2.28	0.47
1:A:63:GLU:OE1	1:A:72:ARG:NH1	2.48	0.47
1:C:253:GLN:HB2	1:C:255:TYR:CE1	2.49	0.47
1:F:319:ILE:CG2	1:F:677:PRO:HB3	2.44	0.47
1:A:393:ARG:HH12	1:C:557:ARG:CD	2.25	0.47
1:C:236:VAL:CG2	1:C:243:TYR:HB2	2.44	0.47
1:C:231:HIS:HD2	2:C:4052:HOH:O	1.97	0.47
1:D:872:HIS:CE1	1:D:902:GLU:OE1	2.66	0.47
1:C:110:PHE:CD2	1:C:121:ILE:HG13	2.50	0.47
1:A:349:ASP:OD2	1:A:353:THR:HG22	2.15	0.47
1:C:425:ARG:O	1:C:426:PHE:HB2	2.15	0.47
1:E:493:ALA:HA	1:E:571:MET:HG3	1.96	0.47
1:D:350:VAL:CG2	1:D:669:ARG:HH11	2.27	0.47
1:B:43:LEU:HD13	1:B:308:ILE:HD12	1.96	0.47
1:B:1016:ARG:O	1:B:1017:ASP:HB2	2.13	0.47
1:C:949:ASN:ND2	1:D:475:TYR:OH	2.40	0.47
1:E:701:TYR:O	1:F:939:ARG:HD3	2.14	0.47
1:C:537:SER:HB3	1:C:583:GLY:O	2.15	0.47
1:A:155:PRO:HG2	1:A:159:MET:CE	2.30	0.47
1:C:982:LEU:C	1:C:983:ILE:HD12	2.35	0.47
1:E:293:ILE:CG2	1:E:306:ILE:HD12	2.45	0.47
1:B:53:ILE:HD11	1:B:295:ILE:HD11	1.95	0.47
1:E:228:MET:HE1	1:E:244:PHE:CE1	2.49	0.47
1:A:309:GLY:O	1:A:311:LEU:HD13	2.14	0.47
1:F:442:GLU:OE2	1:F:481:HIS:HD2	1.98	0.47
1:C:218:ASN:HB3	1:C:221:ALA:HB3	1.97	0.47
1:B:736:VAL:HA	1:B:739:GLN:HE21	1.79	0.47
1:A:327:GLU:O	1:A:328:ASP:C	2.53	0.47
1:E:110:PHE:CD2	1:E:121:ILE:HG13	2.50	0.47
1:F:791:GLU:CD	1:F:861:ARG:HE	2.18	0.47
1:A:401:GLU:N	1:A:401:GLU:OE2	2.43	0.47
1:C:286:LEU:HD11	1:C:293:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:557:ARG:NH2	1:D:393:ARG:HH12	2.12	0.47
1:E:319:ILE:HG23	1:E:677:PRO:HB3	1.96	0.47
1:F:537:SER:HB3	1:F:583:GLY:O	2.15	0.47
1:E:425:ARG:O	1:E:426:PHE:HB2	2.15	0.47
1:D:293:ILE:HG22	1:D:306:ILE:HD12	1.97	0.47
1:B:61:LEU:HB3	1:B:75:VAL:CG1	2.45	0.47
1:A:43:LEU:CD1	1:A:308:ILE:HD12	2.45	0.47
1:D:651:ARG:NH2	1:D:655:GLY:O	2.41	0.47
1:B:367:VAL:CG1	1:B:375:VAL:HG21	2.44	0.47
1:A:156:PHE:HD1	1:A:159:MET:CE	2.27	0.47
1:C:578:ILE:CG1	1:C:580:VAL:HG23	2.43	0.47
1:D:74:ILE:HG13	1:D:75:VAL:HG12	1.96	0.47
1:E:562:GLU:O	1:E:563:ALA:HB3	2.15	0.47
1:C:939:ARG:HD3	1:D:701:TYR:O	2.14	0.47
1:A:623:ASP:O	1:A:627:ARG:N	2.47	0.46
1:A:205:TYR:CZ	1:A:207:GLY:HA3	2.50	0.46
1:A:190:ARG:HH21	1:A:190:ARG:CG	2.28	0.46
1:C:676:ARG:NH1	1:F:811:ASP:OD1	2.48	0.46
1:C:758:ASP:HB3	2:C:4314:HOH:O	2.15	0.46
1:C:328:ASP:O	1:C:339:PHE:HA	2.14	0.46
1:C:1016:ARG:O	1:C:1017:ASP:HB2	2.15	0.46
1:C:493:ALA:HA	1:C:571:MET:HG3	1.96	0.46
1:E:203:LYS:HG2	1:E:274:TYR:CZ	2.50	0.46
1:E:501:TYR:CD2	1:E:501:TYR:N	2.82	0.46
1:E:373:THR:HG21	1:E:393:ARG:HD2	1.96	0.46
1:E:591:LEU:CD1	1:E:662:LEU:HD21	2.43	0.46
1:C:46:PRO:CG	1:C:286:LEU:HG	2.45	0.46
1:A:337:ILE:HG22	1:A:338:ALA:N	2.31	0.46
1:F:820:ASN:O	1:F:824:VAL:HG23	2.14	0.46
1:C:430:THR:HG23	1:C:441:ILE:HD11	1.97	0.46
1:A:949:ASN:ND2	1:B:475:TYR:OH	2.47	0.46
1:E:268:THR:CG2	1:E:303:ILE:HD11	2.41	0.46
1:A:393:ARG:NH1	1:C:557:ARG:NH2	2.62	0.46
1:D:222:PHE:H	1:D:1038:HIS:CD2	2.34	0.46
1:F:642:SER:HB3	1:F:647:THR:H	1.80	0.46
1:F:781:ALA:HB2	1:F:802:PRO:HG2	1.97	0.46
1:E:195:ASN:O	1:E:231:HIS:HE1	1.98	0.46
1:C:860:TYR:OH	1:C:885:PRO:HD3	2.14	0.46
1:D:222:PHE:H	1:D:1038:HIS:HD2	1.64	0.46
1:B:220:GLY:O	1:B:1038:HIS:HB3	2.15	0.46
1:C:92:LYS:HD3	1:C:110:PHE:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:731:LEU:HD22	1:D:735:ILE:HG13	1.97	0.46
1:E:550:ASN:HB3	1:E:553:LYS:HG3	1.96	0.46
1:D:986:ARG:HD3	1:D:1028:ASP:OD2	2.16	0.46
1:B:393:ARG:HH12	1:F:557:ARG:NE	2.14	0.46
1:A:872:HIS:CE1	1:A:902:GLU:OE1	2.67	0.46
1:F:589:ILE:HB	1:F:596:LEU:HB2	1.96	0.46
1:F:463:TYR:CE1	1:F:481:HIS:HB2	2.51	0.46
1:E:423:ASN:HD22	1:E:423:ASN:C	2.18	0.46
1:A:511:ASN:ND2	1:A:543:PRO:HA	2.30	0.46
1:C:580:VAL:HG22	1:C:622:TYR:CD2	2.51	0.46
1:A:167:ASN:O	1:A:170:ILE:HG12	2.15	0.46
1:D:1014:TRP:HB2	1:D:1020:PHE:CE2	2.50	0.46
1:A:110:PHE:HE2	1:A:146:LEU:HD22	1.81	0.46
1:D:300:THR:O	1:D:301:GLU:HB3	2.16	0.46
1:F:511:ASN:HD22	1:F:543:PRO:HA	1.81	0.46
1:E:53:ILE:HD12	1:E:306:ILE:HD13	1.97	0.46
1:B:228:MET:HE1	1:B:244:PHE:CE1	2.51	0.46
1:C:641:LEU:HD23	1:C:642:SER:H	1.81	0.46
1:A:992:VAL:CG1	1:A:1009:PRO:HB2	2.46	0.46
1:A:228:MET:HE1	1:A:244:PHE:CE1	2.51	0.46
1:A:618:VAL:CG2	1:A:631:GLU:HG3	2.46	0.46
1:B:700:ASN:HD22	1:B:1008:GLN:NE2	2.12	0.46
1:C:596:LEU:N	1:C:596:LEU:CD2	2.78	0.46
1:E:929:MET:CE	1:E:929:MET:HA	2.46	0.46
1:B:591:LEU:CD1	1:B:662:LEU:HD21	2.46	0.46
1:B:641:LEU:HD23	1:B:642:SER:H	1.80	0.46
1:A:355:VAL:HG12	1:A:676:ARG:HH21	1.81	0.46
1:A:425:ARG:O	1:A:426:PHE:HB2	2.16	0.46
1:E:735:ILE:O	1:E:739:GLN:HG3	2.16	0.46
1:C:855:ASP:HA	2:C:4221:HOH:O	2.16	0.46
1:B:565:GLU:HG2	1:B:566:TYR:N	2.30	0.46
1:A:639:LEU:HD23	1:A:639:LEU:C	2.36	0.46
1:C:892:LEU:HD13	1:C:920:VAL:HG21	1.96	0.46
1:F:423:ASN:ND2	1:F:425:ARG:HB2	2.32	0.46
1:F:190:ARG:NH2	1:F:222:PHE:CZ	2.84	0.46
1:E:123:TYR:OH	1:E:823:ARG:HD3	2.15	0.46
1:F:511:ASN:ND2	1:F:543:PRO:HA	2.30	0.46
1:E:992:VAL:HG11	1:E:1009:PRO:HB2	1.98	0.46
1:E:997:LYS:NZ	2:E:7168:HOH:O	2.47	0.46
1:B:156:PHE:CD1	1:B:159:MET:HE1	2.52	0.45
1:A:403:ASN:C	1:A:403:ASN:HD22	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:ARG:CB	1:D:190:ARG:HH21	2.28	0.45
1:E:218:ASN:O	1:E:220:GLY:N	2.49	0.45
1:E:368:ARG:O	1:E:375:VAL:HG23	2.16	0.45
1:F:369:ARG:HH21	1:F:369:ARG:HG3	1.79	0.45
1:E:562:GLU:HB3	1:E:563:ALA:H	1.60	0.45
1:D:387:LEU:HD13	1:D:388:GLY:N	2.31	0.45
1:A:807:ILE:HG12	1:A:837:LEU:CD2	2.46	0.45
1:B:442:GLU:OE2	1:B:481:HIS:HD2	1.97	0.45
1:E:706:VAL:HG12	1:E:710:ILE:CD1	2.46	0.45
1:A:1032:GLU:OE1	1:A:1034:GLU:OE2	2.34	0.45
1:F:959:THR:O	1:F:984:GLY:HA3	2.15	0.45
1:E:897:ARG:HG2	1:E:898:LEU:HD12	1.98	0.45
1:E:61:LEU:HD13	1:E:74:ILE:HD11	1.97	0.45
1:E:228:MET:HE1	1:E:232:VAL:HG22	1.98	0.45
1:A:418:PHE:HA	1:A:433:LEU:HG	1.98	0.45
1:B:369:ARG:HD2	1:B:371:GLY:H	1.80	0.45
1:B:579:ASN:ND2	1:B:627:ARG:NH1	2.64	0.45
1:E:418:PHE:HA	1:E:433:LEU:HG	1.98	0.45
1:B:195:ASN:O	1:B:231:HIS:HE1	1.99	0.45
1:D:528:VAL:HG12	1:D:529:LEU:N	2.31	0.45
1:B:578:ILE:CD1	1:B:595:ILE:HD12	2.46	0.45
1:C:681:SER:HB3	1:C:684:GLU:CG	2.45	0.45
1:E:589:ILE:HB	1:E:596:LEU:HB2	1.97	0.45
1:A:1055:LEU:O	1:A:1059:LEU:HD13	2.16	0.45
1:D:906:GLN:O	1:D:953:GLY:HA3	2.16	0.45
1:A:156:PHE:HD1	1:A:159:MET:HE1	1.81	0.45
1:F:580:VAL:HG22	1:F:622:TYR:CD2	2.52	0.45
1:D:373:THR:HG21	1:D:393:ARG:HD2	1.98	0.45
1:A:347:ILE:N	1:A:347:ILE:HD12	2.32	0.45
1:E:596:LEU:N	1:E:596:LEU:HD22	2.31	0.45
1:A:249:ASP:HB2	2:A:2014:HOH:O	2.16	0.45
1:D:402:GLU:HG3	1:D:438:PRO:HD3	1.98	0.45
1:A:369:ARG:HD2	1:A:371:GLY:H	1.81	0.45
1:A:57:CYS:HB3	1:A:62:TRP:CD1	2.51	0.45
1:E:790:GLY:HA2	2:E:6244:HOH:O	2.17	0.45
1:E:528:VAL:HG12	1:E:529:LEU:N	2.31	0.45
1:F:136:ASP:OD2	1:F:137:VAL:N	2.42	0.45
1:B:393:ARG:NH1	1:F:557:ARG:HD2	2.32	0.45
1:C:589:ILE:HD13	1:C:641:LEU:HD12	1.99	0.45
1:E:641:LEU:HD22	1:E:645:ARG:HA	1.98	0.45
1:D:232:VAL:HG13	1:D:244:PHE:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:886:ASP:O	1:C:891:GLY:HA3	2.17	0.45
1:D:44:LEU:HD22	1:D:733:ASN:ND2	2.32	0.45
1:D:690:TYR:CE2	1:D:719:ARG:HB2	2.52	0.45
1:F:1016:ARG:O	1:F:1017:ASP:HB2	2.16	0.45
1:B:53:ILE:HD13	1:B:306:ILE:HD13	1.98	0.45
1:C:781:ALA:HB2	1:C:802:PRO:HG2	1.98	0.45
1:E:619:LEU:HD13	1:E:639:LEU:CD1	2.47	0.45
1:E:1033:ILE:HD11	1:E:1050:TYR:CD2	2.51	0.45
1:B:63:GLU:OE1	1:B:72:ARG:NH1	2.50	0.45
1:B:977:LEU:HB2	1:B:979:LEU:CD1	2.47	0.45
1:E:893:ASN:OD1	1:F:522:PRO:HD3	2.16	0.45
1:D:537:SER:HB3	1:D:583:GLY:O	2.17	0.45
1:C:642:SER:HB2	1:C:647:THR:HB	1.99	0.45
1:E:467:LEU:C	1:E:467:LEU:HD12	2.37	0.45
1:F:860:TYR:CZ	1:F:864:VAL:HG21	2.52	0.45
1:A:393:ARG:HH12	1:C:557:ARG:CZ	2.30	0.45
1:D:235:PRO:HA	1:D:243:TYR:O	2.17	0.45
1:A:591:LEU:CD1	1:A:596:LEU:HD23	2.47	0.45
1:C:463:TYR:CE1	1:C:481:HIS:HB2	2.52	0.45
1:E:360:GLU:HB2	1:E:364:ILE:HD11	1.99	0.45
1:A:430:THR:HG23	1:A:441:ILE:HD11	1.99	0.45
1:F:141:ASP:HB2	1:F:142:PRO:HD2	1.98	0.45
1:E:885:PRO:O	1:E:915:ASN:HA	2.17	0.45
1:A:565:GLU:HG2	1:A:566:TYR:N	2.32	0.45
1:F:300:THR:HG22	1:F:300:THR:O	2.16	0.45
1:B:295:ILE:CG1	1:B:306:ILE:HD11	2.41	0.44
1:C:642:SER:HB3	1:C:647:THR:H	1.82	0.44
1:D:736:VAL:HA	1:D:739:GLN:HE21	1.82	0.44
1:B:309:GLY:O	1:B:311:LEU:HD13	2.18	0.44
1:A:195:ASN:O	1:A:231:HIS:HE1	2.00	0.44
1:F:912:VAL:O	1:F:915:ASN:HB2	2.17	0.44
1:A:929:MET:HA	1:A:929:MET:CE	2.47	0.44
1:A:403:ASN:HD22	1:A:404:LEU:N	2.16	0.44
1:F:731:LEU:HD22	1:F:735:ILE:CD1	2.47	0.44
1:B:441:ILE:HG23	1:B:483:TYR:CD1	2.52	0.44
1:C:279:ASN:HD22	1:C:279:ASN:HA	1.63	0.44
1:C:308:ILE:CG2	1:C:311:LEU:HD11	2.47	0.44
1:C:82:ASN:ND2	1:C:96:ARG:HH21	2.14	0.44
1:F:321:ILE:HB	1:F:324:LYS:HG3	1.99	0.44
1:F:47:ASP:OD1	1:F:85:ARG:HA	2.17	0.44
1:D:681:SER:HB3	1:D:684:GLU:CG	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:367:VAL:HG13	1:E:375:VAL:HG21	1.97	0.44
1:B:641:LEU:CD2	1:B:645:ARG:HA	2.48	0.44
1:A:228:MET:HE1	1:A:232:VAL:HG22	1.99	0.44
1:E:213:ILE:HB	1:E:226:VAL:HB	1.99	0.44
1:D:722:VAL:N	1:D:723:PRO:HD2	2.33	0.44
1:D:319:ILE:HA	1:D:678:LEU:O	2.18	0.44
1:B:988:TRP:CZ3	1:B:990:GLY:HA3	2.52	0.44
1:E:387:LEU:HD13	1:E:388:GLY:N	2.32	0.44
1:E:989:GLY:HA2	1:E:1026:GLY:HA2	2.00	0.44
1:B:1031:VAL:O	1:B:1033:ILE:HD12	2.17	0.44
1:A:404:LEU:HD22	1:A:429:MET:CE	2.42	0.44
1:F:738:MET:C	1:F:738:MET:SD	2.96	0.44
1:C:403:ASN:HD22	1:C:404:LEU:N	2.15	0.44
1:B:681:SER:HB3	1:B:684:GLU:CG	2.44	0.44
1:D:530:ASN:HD22	1:D:531:PHE:H	1.66	0.44
1:E:347:ILE:HD12	1:E:347:ILE:N	2.31	0.44
1:F:228:MET:HE1	1:F:244:PHE:CE1	2.53	0.44
1:C:203:LYS:O	1:C:743:ARG:HG2	2.17	0.44
1:C:130:GLY:HA3	2:C:4163:HOH:O	2.17	0.44
1:A:624:VAL:HG23	1:A:625:LYS:N	2.33	0.44
1:D:781:ALA:HB2	1:D:802:PRO:HG2	1.98	0.44
1:F:45:ASN:N	1:F:45:ASN:ND2	2.64	0.44
1:B:91:ARG:NH2	1:B:114:GLU:OE1	2.50	0.44
1:A:557:ARG:CZ	1:E:393:ARG:HH22	2.31	0.44
1:C:515:LEU:HD23	1:C:539:PRO:HA	1.99	0.44
1:F:350:VAL:CG2	1:F:669:ARG:NH1	2.80	0.44
1:E:253:GLN:NE2	1:E:268:THR:OG1	2.48	0.44
1:A:913:ARG:HH21	1:A:1047:GLN:NE2	2.16	0.44
1:E:452:PHE:HB3	1:E:463:TYR:HB3	2.00	0.44
1:B:327:GLU:O	1:B:328:ASP:O	2.35	0.44
1:C:289:LYS:HA	2:C:4095:HOH:O	2.17	0.44
1:B:890:MET:O	1:B:894:GLU:HG2	2.16	0.44
1:A:986:ARG:HD3	1:A:1028:ASP:OD2	2.16	0.44
1:B:501:TYR:CD2	1:B:501:TYR:N	2.85	0.44
1:C:651:ARG:NH2	1:C:655:GLY:O	2.46	0.44
1:F:578:ILE:CD1	1:F:595:ILE:HD12	2.47	0.44
1:F:253:GLN:HE21	1:F:253:GLN:HA	1.83	0.44
1:D:190:ARG:HH22	1:D:216:GLU:CD	2.21	0.44
1:D:218:ASN:O	1:D:220:GLY:N	2.50	0.44
1:A:82:ASN:HD21	1:A:96:ARG:HD3	1.82	0.44
1:E:694:TRP:HA	1:E:738:MET:HE1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:618:VAL:HG21	1:D:631:GLU:HG3	1.98	0.44
1:F:131:ARG:NH2	2:F:7157:HOH:O	2.50	0.44
1:E:45:ASN:N	1:E:45:ASN:ND2	2.65	0.44
1:F:480:ILE:N	1:F:494:THR:HG22	2.20	0.44
1:E:104:ASN:N	1:E:104:ASN:ND2	2.62	0.44
1:C:579:ASN:ND2	1:C:627:ARG:NH1	2.66	0.44
1:A:622:TYR:OH	1:A:627:ARG:HG2	2.18	0.44
1:D:642:SER:HB3	1:D:647:THR:H	1.83	0.44
1:F:308:ILE:HG22	1:F:311:LEU:CD1	2.48	0.44
1:F:913:ARG:HH21	1:F:1047:GLN:NE2	2.15	0.44
1:C:363:ARG:HH21	1:C:365:ARG:HH22	1.64	0.44
1:B:735:ILE:O	1:B:739:GLN:HG3	2.18	0.44
1:A:618:VAL:HG21	1:A:631:GLU:HG3	1.99	0.44
1:C:247:ASP:HA	1:C:251:PHE:O	2.18	0.44
1:A:834:ARG:HG3	1:A:846:ASP:OD2	2.18	0.44
1:C:179:PRO:HG2	2:C:4045:HOH:O	2.16	0.44
1:F:501:TYR:CD2	1:F:501:TYR:N	2.86	0.44
1:A:253:GLN:HE22	1:A:270:PHE:N	2.03	0.44
1:A:429:MET:HE3	1:A:438:PRO:CB	2.48	0.44
1:A:53:ILE:HD13	1:A:306:ILE:CD1	2.48	0.44
1:A:350:VAL:CG2	1:A:669:ARG:HH11	2.27	0.44
1:E:218:ASN:O	1:E:219:SER:C	2.56	0.44
1:B:393:ARG:NH1	1:F:557:ARG:CZ	2.80	0.44
1:B:499:HIS:HE1	2:B:3239:HOH:O	2.00	0.44
1:C:142:PRO:HD3	1:C:185:PHE:CD2	2.53	0.44
1:A:218:ASN:O	1:A:219:SER:C	2.55	0.44
1:B:623:ASP:O	1:B:627:ARG:N	2.50	0.44
1:C:57:CYS:HB3	1:C:62:TRP:NE1	2.33	0.44
1:C:284:ARG:HD3	2:C:4393:HOH:O	2.16	0.44
1:E:514:TYR:CZ	1:E:540:PHE:HB2	2.53	0.44
1:E:61:LEU:HB2	1:E:75:VAL:HG13	2.00	0.43
1:B:390:TYR:CD1	1:B:397:ALA:HB2	2.53	0.43
1:C:218:ASN:O	1:C:220:GLY:N	2.51	0.43
1:B:994:ILE:HG22	1:B:1008:GLN:O	2.18	0.43
1:F:776:TYR:CD1	1:F:816:GLY:HA2	2.53	0.43
1:A:1031:VAL:CG1	1:A:1033:ILE:HD11	2.48	0.43
1:C:729:TYR:O	1:C:732:SER:HB3	2.19	0.43
1:B:556:PRO:HD3	1:D:354:TYR:CD1	2.53	0.43
1:B:170:ILE:HD13	1:B:820:ASN:HB2	2.00	0.43
1:D:347:ILE:N	1:D:347:ILE:HD12	2.33	0.43
1:D:525:ASP:HB3	1:D:528:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:639:LEU:HD23	1:E:639:LEU:C	2.39	0.43
1:C:1014:TRP:CD1	1:C:1019:GLY:HA2	2.53	0.43
1:E:363:ARG:HG3	1:E:688:GLN:NE2	2.33	0.43
1:A:123:TYR:HB3	1:A:826:SER:OG	2.17	0.43
1:E:89:ASP:CG	1:E:91:ARG:HG3	2.38	0.43
1:F:53:ILE:HD13	1:F:306:ILE:CD1	2.49	0.43
1:B:82:ASN:HD21	1:B:96:ARG:HD3	1.84	0.43
1:D:218:ASN:O	1:D:219:SER:C	2.57	0.43
1:E:189:ARG:HD2	1:E:216:GLU:O	2.18	0.43
1:C:965:SER:C	1:C:967:GLY:N	2.71	0.43
1:F:220:GLY:O	1:F:1038:HIS:HB3	2.19	0.43
1:F:141:ASP:HB2	1:F:142:PRO:CD	2.48	0.43
1:F:882:ILE:HD11	1:F:899:PHE:HA	2.00	0.43
1:D:791:GLU:CD	1:D:861:ARG:HE	2.21	0.43
1:D:639:LEU:HD23	1:D:639:LEU:C	2.38	0.43
1:A:53:ILE:HD13	1:A:306:ILE:HD13	2.01	0.43
1:C:286:LEU:HD11	1:C:293:ILE:CG2	2.49	0.43
1:A:190:ARG:NH2	1:A:222:PHE:CZ	2.87	0.43
1:E:190:ARG:CG	1:E:190:ARG:HH21	2.30	0.43
1:C:308:ILE:HG22	1:C:311:LEU:CD1	2.48	0.43
1:C:373:THR:HG21	1:C:393:ARG:HD2	2.00	0.43
1:A:401:GLU:H	1:A:401:GLU:CD	2.20	0.43
1:D:466:PRO:HB3	2:D:5183:HOH:O	2.17	0.43
1:D:195:ASN:O	1:D:231:HIS:HE1	2.01	0.43
1:D:43:LEU:HD13	1:D:308:ILE:HD12	2.01	0.43
1:A:638:ASP:HB3	1:A:651:ARG:HB3	2.00	0.43
1:F:337:ILE:HG22	1:F:338:ALA:N	2.33	0.43
1:F:184:LEU:HB2	1:F:191:VAL:HB	2.00	0.43
1:B:314:PRO:HD2	1:B:726:LYS:CG	2.48	0.43
1:F:706:VAL:O	1:F:710:ILE:HG13	2.19	0.43
1:E:177:LEU:HD13	1:E:192:ILE:HD11	2.00	0.43
1:E:949:ASN:HB2	2:F:7075:HOH:O	2.18	0.43
1:A:142:PRO:HD3	1:A:185:PHE:CD2	2.53	0.43
1:A:557:ARG:CZ	1:E:393:ARG:HH12	2.29	0.43
1:D:530:ASN:ND2	1:D:531:PHE:N	2.64	0.43
1:A:628:LYS:HB3	1:A:628:LYS:HE2	1.88	0.43
1:E:489:LYS:HG3	1:E:491:PHE:HE1	1.78	0.43
1:C:872:HIS:CE1	1:C:902:GLU:OE1	2.67	0.43
1:F:218:ASN:HB3	1:F:221:ALA:HB3	1.99	0.43
1:F:442:GLU:OE2	1:F:490:ILE:HD13	2.18	0.43
1:F:802:PRO:O	1:F:805:TYR:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:GLY:O	1:B:438:PRO:HD3	2.18	0.43
1:C:528:VAL:HG21	1:C:896:TYR:CD2	2.53	0.43
1:D:905:TYR:HB2	2:D:5042:HOH:O	2.18	0.43
1:B:552:THR:HG21	1:B:578:ILE:HD12	2.00	0.43
1:F:319:ILE:HA	1:F:678:LEU:O	2.19	0.43
1:E:319:ILE:HA	1:E:678:LEU:O	2.19	0.43
1:E:616:LYS:HE2	1:E:653:ASP:CB	2.49	0.43
1:E:61:LEU:HB3	1:E:75:VAL:CG1	2.49	0.43
1:A:706:VAL:HG12	1:A:710:ILE:CD1	2.49	0.43
1:F:389:ILE:HD11	1:F:433:LEU:HB3	2.00	0.43
1:E:906:GLN:O	1:E:953:GLY:HA3	2.19	0.43
1:B:637:THR:OG1	1:B:651:ARG:HG3	2.19	0.43
1:D:501:TYR:CD2	1:D:501:TYR:N	2.86	0.43
1:D:982:LEU:C	1:D:983:ILE:HD12	2.39	0.43
1:C:53:ILE:HD13	1:C:306:ILE:CD1	2.48	0.43
1:A:333:ASP:CG	1:A:369:ARG:HE	2.22	0.43
1:B:400:PHE:CD2	1:B:436:GLY:HA3	2.54	0.43
1:E:774:ASP:HA	1:E:817:ALA:HB2	2.00	0.43
1:F:546:PRO:HG2	1:F:567:ASP:HB3	1.99	0.43
1:D:157:SER:HB3	1:D:856:ARG:NH1	2.34	0.43
1:C:312:GLU:HG2	1:C:314:PRO:HD3	2.00	0.43
1:F:780:LYS:HD3	1:F:782:TYR:CZ	2.54	0.43
1:D:771:LEU:C	1:D:771:LEU:HD13	2.39	0.43
1:C:622:TYR:OH	1:C:627:ARG:HG2	2.19	0.43
1:A:190:ARG:NH2	1:A:190:ARG:HG3	2.34	0.43
1:A:61:LEU:CB	1:A:75:VAL:CG1	2.96	0.43
1:A:61:LEU:HB3	1:A:75:VAL:CG1	2.49	0.43
1:D:965:SER:N	1:D:968:ASP:OD2	2.50	0.43
1:C:119:LYS:NZ	1:C:823:ARG:NH2	2.67	0.43
1:B:327:GLU:O	1:B:328:ASP:C	2.57	0.43
1:C:498:SER:HB2	2:C:5192:HOH:O	2.18	0.43
1:E:651:ARG:NH2	1:E:655:GLY:O	2.46	0.43
1:F:194:ARG:O	1:F:211:GLY:HA2	2.18	0.43
1:D:337:ILE:HG22	1:D:338:ALA:N	2.34	0.43
1:D:400:PHE:CD2	1:D:436:GLY:HA3	2.53	0.43
1:B:155:PRO:CD	1:B:159:MET:HE3	2.48	0.43
1:D:694:TRP:HA	1:D:738:MET:HE2	2.01	0.43
1:F:633:LYS:HE2	1:F:633:LYS:HB2	1.87	0.43
1:B:218:ASN:O	1:B:219:SER:C	2.57	0.43
1:A:43:LEU:C	1:A:44:LEU:HG	2.38	0.43
1:D:428:ILE:HG23	1:D:441:ILE:HB	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:605:GLU:CG	1:D:524:PRO:HD3	2.49	0.43
1:E:860:TYR:OH	1:E:885:PRO:HD3	2.19	0.43
1:B:637:THR:OG1	1:B:651:ARG:CG	2.67	0.43
1:A:373:THR:HA	1:A:392:TYR:CZ	2.54	0.43
1:F:53:ILE:CG2	1:F:286:LEU:HD21	2.46	0.42
1:D:480:ILE:N	1:D:494:THR:HG22	2.30	0.42
1:D:241:ARG:HH12	1:D:263:ASP:HB3	1.84	0.42
1:C:1055:LEU:O	1:C:1059:LEU:HD13	2.19	0.42
1:B:626:THR:O	1:B:627:ARG:HB2	2.18	0.42
1:B:235:PRO:HA	1:B:243:TYR:O	2.19	0.42
1:C:1031:VAL:O	1:C:1033:ILE:HD12	2.19	0.42
1:F:731:LEU:HD22	1:F:735:ILE:HG13	2.01	0.42
1:B:404:LEU:HD22	1:B:429:MET:HE1	2.01	0.42
1:D:929:MET:HA	1:D:929:MET:HE3	2.01	0.42
1:E:731:LEU:CD2	1:E:735:ILE:HG13	2.49	0.42
1:E:241:ARG:NH1	1:E:263:ASP:HB3	2.34	0.42
1:F:241:ARG:HH12	1:F:263:ASP:CG	2.22	0.42
1:B:739:GLN:NE2	2:B:3141:HOH:O	2.52	0.42
1:C:936:ASP:HB2	1:C:944:SER:HB2	2.01	0.42
1:A:994:ILE:HG22	1:A:1008:GLN:O	2.18	0.42
1:B:184:LEU:HB2	1:B:191:VAL:HB	1.99	0.42
1:D:992:VAL:HG11	1:D:1009:PRO:HB2	2.00	0.42
1:C:156:PHE:HD1	1:C:159:MET:HE1	1.84	0.42
1:F:1031:VAL:HG12	1:F:1033:ILE:HD11	2.01	0.42
1:C:922:GLN:HE22	1:D:948:THR:N	1.98	0.42
1:B:319:ILE:HA	1:B:678:LEU:O	2.19	0.42
1:B:676:ARG:HA	1:B:677:PRO:HD3	1.91	0.42
1:F:425:ARG:O	1:F:426:PHE:HB2	2.19	0.42
1:C:562:GLU:HB3	1:C:563:ALA:H	1.65	0.42
1:D:177:LEU:HD13	1:D:192:ILE:HD11	2.01	0.42
1:D:390:TYR:HD1	1:D:397:ALA:HB2	1.84	0.42
2:C:4075:HOH:O	1:D:949:ASN:HB2	2.18	0.42
1:F:146:LEU:HD23	1:F:165:VAL:HG21	2.01	0.42
1:F:110:PHE:CD2	1:F:121:ILE:HG13	2.54	0.42
1:D:45:ASN:N	1:D:45:ASN:ND2	2.64	0.42
1:F:1031:VAL:O	1:F:1033:ILE:HD12	2.19	0.42
1:A:46:PRO:CG	1:A:286:LEU:HG	2.49	0.42
1:A:578:ILE:CD1	1:A:595:ILE:HD12	2.49	0.42
1:B:562:GLU:HB3	1:B:563:ALA:H	1.59	0.42
1:C:764:ARG:HB3	1:C:855:ASP:OD1	2.19	0.42
1:B:321:ILE:HB	1:B:324:LYS:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:809:ASP:HB3	1:C:814:THR:HA	2.01	0.42
1:E:216:GLU:OE1	1:E:220:GLY:N	2.52	0.42
1:C:61:LEU:HB3	1:C:75:VAL:CG1	2.48	0.42
1:E:913:ARG:NH2	1:E:1047:GLN:HE21	2.15	0.42
1:B:228:MET:CE	1:B:232:VAL:HG22	2.49	0.42
1:D:368:ARG:O	1:D:375:VAL:CG2	2.67	0.42
1:B:367:VAL:HG12	1:B:375:VAL:HG21	2.01	0.42
1:E:389:ILE:HD11	1:E:433:LEU:HB3	2.01	0.42
1:E:279:ASN:ND2	2:E:6071:HOH:O	2.52	0.42
1:A:892:LEU:HD13	1:A:920:VAL:HG21	2.01	0.42
1:C:894:GLU:OE2	1:C:897:ARG:HD2	2.19	0.42
1:A:390:TYR:HD1	1:A:397:ALA:HB2	1.85	0.42
1:A:579:ASN:ND2	1:A:627:ARG:NH1	2.68	0.42
1:B:167:ASN:O	1:B:170:ILE:HG12	2.20	0.42
1:A:312:GLU:HG2	1:A:314:PRO:HD3	2.01	0.42
1:E:897:ARG:HB2	1:F:520:LEU:HD12	2.01	0.42
1:B:1045:ASP:HB3	1:B:1048:ILE:HG22	2.01	0.42
1:A:890:MET:O	1:A:894:GLU:HG2	2.19	0.42
1:A:157:SER:HB2	2:A:2397:HOH:O	2.19	0.42
1:F:936:ASP:HB2	1:F:944:SER:HB2	2.02	0.42
1:A:53:ILE:HG23	1:A:286:LEU:CD2	2.48	0.42
1:A:676:ARG:HA	1:A:677:PRO:HD3	1.89	0.42
1:C:596:LEU:N	1:C:596:LEU:HD22	2.35	0.42
1:E:926:GLU:CG	1:F:926:GLU:HG2	2.50	0.42
1:A:811:ASP:HB2	1:A:828:LYS:HE2	2.01	0.42
1:C:258:ASP:C	1:C:260:ASP:H	2.21	0.42
1:A:469:HIS:CG	1:A:470:GLY:N	2.86	0.42
1:C:926:GLU:CG	1:D:926:GLU:HG2	2.50	0.42
1:A:315:GLU:OE2	1:D:119:LYS:HD2	2.20	0.42
1:C:295:ILE:HG13	1:C:306:ILE:HD11	2.02	0.42
1:B:53:ILE:HG12	1:B:286:LEU:HD22	2.01	0.42
1:C:530:ASN:ND2	1:C:531:PHE:N	2.66	0.42
1:D:357:LYS:HB2	1:D:676:ARG:HH12	1.84	0.42
1:F:462:ALA:HA	1:F:481:HIS:O	2.20	0.42
1:C:887:MET:HB3	1:C:966:ASP:OD2	2.20	0.42
1:F:110:PHE:CE2	1:F:121:ILE:HG13	2.55	0.42
1:E:926:GLU:HG2	1:F:926:GLU:CG	2.49	0.42
1:F:230:THR:HG21	1:F:248:ILE:HA	2.02	0.42
1:C:1052:ILE:O	1:C:1056:ILE:HG13	2.19	0.42
1:D:153:MET:HG3	1:D:859:ARG:NH1	2.35	0.42
1:E:362:LEU:HA	1:E:362:LEU:HD23	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:362:LEU:HA	1:F:362:LEU:HD23	1.91	0.42
1:D:286:LEU:HD13	1:D:295:ILE:HG12	2.00	0.42
1:F:494:THR:HG21	1:F:500:ASP:OD1	2.20	0.42
1:D:494:THR:CG2	1:D:500:ASP:OD1	2.65	0.42
1:B:373:THR:HA	1:B:392:TYR:CZ	2.54	0.42
1:B:153:MET:HG3	1:B:859:ARG:NH1	2.34	0.42
1:B:217:VAL:HG23	1:B:218:ASN:N	2.35	0.42
1:C:153:MET:HG3	1:C:859:ARG:CZ	2.50	0.42
1:C:499:HIS:HD2	2:C:4176:HOH:O	2.02	0.42
1:A:635:ASN:HB3	1:A:653:ASP:OD1	2.19	0.42
1:C:367:VAL:CG1	1:C:375:VAL:HG21	2.50	0.42
1:A:501:TYR:CD2	1:A:501:TYR:N	2.87	0.42
1:F:929:MET:HA	1:F:929:MET:CE	2.49	0.42
1:C:362:LEU:HA	1:C:362:LEU:HD23	1.85	0.42
1:F:469:HIS:HD1	1:F:473:ASP:CG	2.23	0.42
1:C:350:VAL:HG11	1:C:669:ARG:NH1	2.35	0.42
1:E:206:ARG:N	1:E:1024:ASN:HD21	2.16	0.42
1:A:189:ARG:HB2	1:A:216:GLU:HB3	2.01	0.42
1:F:436:GLY:O	1:F:438:PRO:HD3	2.20	0.42
1:F:345:ALA:HB2	1:F:364:ILE:HG21	2.01	0.42
1:B:807:ILE:HG12	1:B:837:LEU:CD2	2.50	0.42
1:B:1031:VAL:HG12	1:B:1033:ILE:HD11	2.01	0.41
1:F:322:PRO:HG2	1:F:674:ASP:OD1	2.19	0.41
1:D:216:GLU:OE1	1:D:219:SER:HA	2.20	0.41
1:C:423:ASN:ND2	1:C:427:GLU:H	2.18	0.41
1:B:641:LEU:HD22	1:B:645:ARG:HA	2.02	0.41
1:C:977:LEU:HB2	1:C:979:LEU:CD1	2.49	0.41
1:E:423:ASN:ND2	1:E:425:ARG:HB2	2.35	0.41
1:D:390:TYR:CD1	1:D:397:ALA:HB2	2.55	0.41
1:D:589:ILE:HB	1:D:596:LEU:HB2	2.02	0.41
1:B:989:GLY:HA2	1:B:1026:GLY:HA2	2.03	0.41
1:C:117:GLU:HA	1:F:313:SER:HB3	2.01	0.41
1:A:279:ASN:HD22	1:A:279:ASN:HA	1.78	0.41
1:C:446:GLU:OE1	1:C:468:LYS:HE2	2.19	0.41
1:C:616:LYS:HE2	1:C:653:ASP:CB	2.49	0.41
1:B:119:LYS:HZ1	1:B:823:ARG:HH22	1.66	0.41
1:F:811:ASP:HB2	1:F:828:LYS:HE2	2.02	0.41
1:A:428:ILE:HG23	1:A:441:ILE:HB	2.02	0.41
1:F:203:LYS:HD3	1:F:740:GLY:C	2.41	0.41
1:C:402:GLU:HG3	1:C:438:PRO:HD3	2.02	0.41
1:B:278:LEU:HD23	1:B:287:PHE:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:469:HIS:CG	1:B:470:GLY:N	2.88	0.41
1:F:253:GLN:NE2	1:F:253:GLN:HA	2.35	0.41
1:C:241:ARG:HH12	1:C:263:ASP:HB3	1.84	0.41
1:B:425:ARG:HB3	1:B:427:GLU:HG3	2.02	0.41
1:B:731:LEU:HD22	1:B:735:ILE:HG13	2.02	0.41
1:A:228:MET:HE3	1:A:232:VAL:HG21	2.02	0.41
1:B:871:VAL:HG22	1:B:1052:ILE:HD11	2.01	0.41
1:C:875:SER:HB2	1:C:879:ILE:HG13	2.02	0.41
1:B:156:PHE:H	1:B:159:MET:CE	2.34	0.41
1:D:155:PRO:HB3	1:D:860:TYR:HA	2.02	0.41
1:E:253:GLN:HB2	1:E:255:TYR:CE1	2.55	0.41
1:D:218:ASN:O	1:D:221:ALA:N	2.53	0.41
1:D:241:ARG:NH1	1:D:263:ASP:HB3	2.35	0.41
1:C:82:ASN:HD21	1:C:96:ARG:HH21	1.67	0.41
1:D:676:ARG:NH2	2:D:5370:HOH:O	2.53	0.41
1:D:368:ARG:O	1:D:375:VAL:HG23	2.21	0.41
1:A:110:PHE:CD2	1:A:121:ILE:HG13	2.54	0.41
1:F:905:TYR:HB2	2:F:7042:HOH:O	2.18	0.41
1:F:807:ILE:HG12	1:F:837:LEU:CD2	2.50	0.41
1:E:247:ASP:HA	1:E:251:PHE:O	2.20	0.41
1:B:401:GLU:N	1:B:401:GLU:OE2	2.47	0.41
1:D:881:TYR:O	1:D:902:GLU:HG3	2.20	0.41
1:E:642:SER:HB3	1:E:647:THR:H	1.84	0.41
1:C:184:LEU:HB2	1:C:191:VAL:HB	2.01	0.41
1:D:735:ILE:O	1:D:739:GLN:HG3	2.20	0.41
1:B:78:LEU:HD11	1:B:118:ILE:HD11	2.02	0.41
1:F:992:VAL:HG11	1:F:1009:PRO:HB2	2.02	0.41
1:D:947:PRO:HD2	1:D:950:SER:HB3	2.02	0.41
1:F:89:ASP:OD1	1:F:91:ARG:HG3	2.21	0.41
1:B:46:PRO:CG	1:B:286:LEU:HG	2.50	0.41
1:C:319:ILE:HA	1:C:678:LEU:O	2.20	0.41
1:B:618:VAL:CG2	1:B:631:GLU:HG3	2.51	0.41
1:C:43:LEU:HD13	1:C:308:ILE:HD12	2.03	0.41
1:A:524:PRO:HD3	1:B:605:GLU:HG3	2.01	0.41
1:D:228:MET:HE1	1:D:244:PHE:CE1	2.55	0.41
1:F:767:CYS:HA	1:F:780:LYS:O	2.20	0.41
1:A:194:ARG:O	1:A:211:GLY:HA2	2.21	0.41
1:F:155:PRO:HB3	1:F:860:TYR:HA	2.03	0.41
1:A:1031:VAL:O	1:A:1033:ILE:HD12	2.21	0.41
1:A:295:ILE:HG13	1:A:306:ILE:HD11	2.02	0.41
1:D:703:ASN:C	1:D:703:ASN:ND2	2.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:HG13	1:B:75:VAL:HG12	2.02	0.41
1:E:74:ILE:HG13	1:E:75:VAL:HG12	2.03	0.41
1:E:228:MET:HE2	1:E:244:PHE:CZ	2.56	0.41
1:B:228:MET:CE	1:B:244:PHE:CE1	3.04	0.41
1:B:423:ASN:ND2	1:B:425:ARG:HB2	2.36	0.41
1:B:333:ASP:CG	1:B:369:ARG:HE	2.24	0.41
1:F:912:VAL:HG22	1:F:958:ILE:O	2.21	0.41
1:B:1055:LEU:O	1:B:1059:LEU:HD13	2.21	0.41
1:D:423:ASN:HD22	1:D:423:ASN:C	2.24	0.41
1:C:350:VAL:CG2	1:C:669:ARG:NH1	2.83	0.41
1:F:170:ILE:HD13	1:F:820:ASN:HB2	2.02	0.41
1:C:118:ILE:HG22	1:F:314:PRO:HA	2.02	0.41
1:F:119:LYS:NZ	1:F:823:ARG:HH22	2.19	0.41
1:E:722:VAL:N	1:E:723:PRO:HD2	2.36	0.41
1:E:791:GLU:CD	1:E:861:ARG:HE	2.24	0.41
1:D:155:PRO:HD2	1:D:159:MET:HE3	2.02	0.41
1:A:156:PHE:CD1	1:A:159:MET:CE	3.04	0.41
1:C:253:GLN:HB2	1:C:255:TYR:HE1	1.86	0.41
1:E:580:VAL:HG22	1:E:622:TYR:CD2	2.56	0.41
1:C:480:ILE:N	1:C:494:THR:HG22	2.28	0.41
1:D:268:THR:HG22	1:D:303:ILE:CD1	2.45	0.41
1:F:46:PRO:HB2	1:F:286:LEU:HD23	2.02	0.41
1:D:190:ARG:NH2	1:D:190:ARG:CG	2.83	0.41
1:F:628:LYS:HE2	1:F:628:LYS:HB3	1.88	0.41
1:B:624:VAL:HG23	1:B:625:LYS:N	2.36	0.41
1:F:160:THR:O	1:F:179:PRO:HA	2.21	0.41
1:B:591:LEU:HD11	1:B:662:LEU:HD21	2.02	0.41
1:F:242:ILE:O	1:F:256:SER:HA	2.21	0.41
1:B:119:LYS:NZ	1:B:823:ARG:NH2	2.69	0.41
1:E:1016:ARG:O	1:E:1017:ASP:CB	2.69	0.41
1:C:96:ARG:NH2	1:C:133:MET:HB3	2.35	0.41
1:A:802:PRO:O	1:A:805:TYR:HB2	2.21	0.41
1:B:965:SER:N	1:B:968:ASP:OD2	2.51	0.41
1:D:599:SER:HB3	1:D:618:VAL:HG13	2.03	0.41
1:A:591:LEU:HD12	1:A:596:LEU:HD23	2.02	0.41
1:F:706:VAL:HG12	1:F:710:ILE:HD11	2.02	0.41
1:E:565:GLU:CG	1:E:566:TYR:N	2.83	0.41
1:F:546:PRO:CG	1:F:567:ASP:HB3	2.51	0.41
1:A:886:ASP:O	1:A:891:GLY:HA3	2.21	0.41
1:F:708:LYS:O	1:F:712:GLU:HG3	2.21	0.41
1:C:714:ILE:HG21	1:C:741:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:ASP:OD2	1:E:137:VAL:N	2.44	0.41
1:D:895:PHE:CE2	1:D:924:ILE:HG23	2.56	0.41
1:B:694:TRP:HA	1:B:738:MET:CE	2.51	0.41
1:E:236:VAL:HG23	1:E:243:TYR:HB2	2.03	0.41
1:F:383:GLU:HA	1:F:383:GLU:OE2	2.20	0.41
1:A:85:ARG:HD3	2:A:2104:HOH:O	2.21	0.41
1:C:253:GLN:NE2	1:C:268:THR:OG1	2.49	0.41
1:F:739:GLN:NE2	2:F:7141:HOH:O	2.53	0.41
1:F:591:LEU:HD11	1:F:662:LEU:HD21	2.03	0.41
1:B:123:TYR:OH	1:B:823:ARG:HD3	2.21	0.41
1:B:628:LYS:HB3	1:B:628:LYS:HE2	1.94	0.41
1:B:892:LEU:HA	1:B:892:LEU:HD12	1.96	0.41
1:C:393:ARG:HH12	1:E:557:ARG:HD2	1.86	0.41
1:C:216:GLU:OE1	1:C:219:SER:HA	2.21	0.41
1:A:72:ARG:HG3	1:D:72:ARG:HG3	2.03	0.41
1:C:887:MET:O	1:C:920:VAL:HG22	2.21	0.41
1:A:130:GLY:HA3	2:A:2163:HOH:O	2.20	0.41
1:B:346:PHE:C	1:B:347:ILE:HD12	2.42	0.41
1:A:286:LEU:HD11	1:A:293:ILE:HG22	2.03	0.40
1:C:735:ILE:O	1:C:738:MET:HG3	2.21	0.40
1:D:403:ASN:HD22	1:D:404:LEU:N	2.19	0.40
1:C:947:PRO:HG3	2:C:4038:HOH:O	2.20	0.40
1:B:498:SER:OG	1:B:499:HIS:N	2.54	0.40
1:E:731:LEU:HD22	1:E:735:ILE:CD1	2.52	0.40
1:B:337:ILE:CG2	1:B:338:ALA:N	2.84	0.40
1:F:373:THR:HG21	1:F:393:ARG:HD2	2.03	0.40
1:F:956:ILE:HG22	1:F:1055:LEU:HD11	2.01	0.40
1:A:308:ILE:HG22	1:A:311:LEU:HD11	2.02	0.40
1:A:110:PHE:CE2	1:A:146:LEU:HD22	2.55	0.40
1:A:618:VAL:HG23	1:A:633:LYS:O	2.20	0.40
1:C:499:HIS:HE1	2:C:4239:HOH:O	2.04	0.40
1:C:194:ARG:O	1:C:211:GLY:HA2	2.22	0.40
1:D:499:HIS:HD2	2:D:5176:HOH:O	2.04	0.40
1:D:134:PHE:O	1:D:135:THR:HB	2.21	0.40
1:A:466:PRO:HB3	2:A:2183:HOH:O	2.20	0.40
1:B:297:ASN:O	1:B:301:GLU:N	2.46	0.40
1:C:210:ARG:HH21	1:C:210:ARG:HG2	1.87	0.40
1:C:183:ILE:HG23	1:C:183:ILE:O	2.21	0.40
1:F:155:PRO:HD2	1:F:159:MET:HE3	2.04	0.40
1:B:156:PHE:HD1	1:B:159:MET:HE1	1.84	0.40
1:E:872:HIS:CE1	1:E:902:GLU:OE1	2.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:LEU:HD11	1:B:338:ALA:HB2	2.03	0.40
1:E:338:ALA:HA	1:E:346:PHE:O	2.21	0.40
1:C:300:THR:O	1:C:301:GLU:HB3	2.21	0.40
1:F:929:MET:HE3	1:F:929:MET:HA	2.02	0.40
1:D:88:PRO:HG3	1:D:144:GLY:HA2	2.01	0.40
1:B:690:TYR:OH	1:B:718:TYR:HB2	2.21	0.40
1:C:175:LEU:O	1:C:176:ASN:HB2	2.21	0.40
1:A:350:VAL:CG2	1:A:669:ARG:NH1	2.83	0.40
1:C:423:ASN:ND2	1:C:425:ARG:HB2	2.36	0.40
1:B:811:ASP:HB2	1:B:828:LYS:HE2	2.03	0.40
1:C:141:ASP:HB2	1:C:142:PRO:CD	2.51	0.40
1:A:589:ILE:HB	1:A:596:LEU:HB2	2.04	0.40
1:B:860:TYR:OH	1:B:885:PRO:HD3	2.21	0.40
1:F:279:ASN:ND2	2:F:7071:HOH:O	2.54	0.40
1:B:559:MET:HG2	1:D:356:LEU:HD11	2.02	0.40
1:E:892:LEU:HD13	1:E:920:VAL:HG21	2.03	0.40
1:C:633:LYS:HE2	1:C:633:LYS:HB2	1.88	0.40
1:E:446:GLU:CD	1:E:468:LYS:HG3	2.42	0.40
1:A:387:LEU:HD12	1:A:400:PHE:CE1	2.56	0.40
1:B:123:TYR:HB3	1:B:826:SER:OG	2.22	0.40
1:F:884:ILE:HA	1:F:885:PRO:HD2	1.83	0.40
1:A:319:ILE:HG23	1:A:677:PRO:CB	2.51	0.40
1:A:235:PRO:HA	1:A:243:TYR:O	2.20	0.40
1:E:628:LYS:HE3	2:E:6366:HOH:O	2.22	0.40
1:E:183:ILE:HA	1:E:191:VAL:O	2.21	0.40
1:A:731:LEU:HD22	1:A:735:ILE:HG13	2.04	0.40
1:F:640:ARG:HG2	1:F:640:ARG:HH21	1.86	0.40
1:C:156:PHE:H	1:C:159:MET:CE	2.35	0.40
1:A:270:PHE:CE2	1:A:289:LYS:HE2	2.56	0.40
1:C:578:ILE:O	1:C:580:VAL:N	2.50	0.40
1:A:489:LYS:HE2	1:A:491:PHE:CZ	2.53	0.40
1:B:342:ARG:NE	1:B:685:GLU:OE1	2.51	0.40
1:B:530:ASN:ND2	1:B:531:PHE:H	2.20	0.40
1:C:589:ILE:HG21	1:C:641:LEU:CD1	2.52	0.40
1:E:619:LEU:HD13	1:E:639:LEU:HD13	2.04	0.40
1:E:141:ASP:HB2	1:E:142:PRO:HD2	2.04	0.40
1:F:703:ASN:C	1:F:703:ASN:HD22	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1021/1045 (98%)	979 (96%)	38 (4%)	4 (0%)	39	33
1	B	1021/1045 (98%)	977 (96%)	41 (4%)	3 (0%)	46	41
1	C	1021/1045 (98%)	961 (94%)	53 (5%)	7 (1%)	26	19
1	D	1021/1045 (98%)	979 (96%)	38 (4%)	4 (0%)	39	33
1	E	1021/1045 (98%)	975 (96%)	43 (4%)	3 (0%)	46	41
1	F	1021/1045 (98%)	971 (95%)	44 (4%)	6 (1%)	30	22
All	All	6126/6270 (98%)	5842 (95%)	257 (4%)	27 (0%)	39	33

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	328	ASP
1	B	328	ASP
1	C	219	SER
1	C	579	ASN
1	D	219	SER
1	E	219	SER
1	F	219	SER
1	F	579	ASN
1	A	562	GLU
1	B	562	GLU
1	B	579	ASN
1	C	562	GLU
1	E	562	GLU
1	E	579	ASN
1	F	562	GLU
1	F	563	ALA
1	D	562	GLU
1	A	219	SER
1	C	328	ASP
1	D	563	ALA

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Mol	Chain	Res	Type
1	D	579	ASN
1	F	259	LEU
1	A	579	ASN
1	C	563	ALA
1	C	665	PRO
1	C	45	ASN
1	F	682	ILE

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	883/904 (98%)	857 (97%)	26 (3%)	50	49
1	B	883/904 (98%)	853 (97%)	30 (3%)	44	41
1	C	883/904 (98%)	860 (97%)	23 (3%)	54	54
1	D	883/904 (98%)	856 (97%)	27 (3%)	47	46
1	E	883/904 (98%)	857 (97%)	26 (3%)	50	49
1	F	883/904 (98%)	857 (97%)	26 (3%)	50	49
All	All	5298/5424 (98%)	5140 (97%)	158 (3%)	48	47

All (158) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LEU
1	A	46	PRO
1	A	61	LEU
1	A	104	ASN
1	A	190	ARG
1	A	279	ASN
1	A	311	LEU
1	A	313	SER
1	A	363	ARG
1	A	375	VAL
1	A	403	ASN

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Mol	Chain	Res	Type
1	A	423	ASN
1	A	469	HIS
1	A	562	GLU
1	A	578	ILE
1	A	641	LEU
1	A	678	LEU
1	A	687	LEU
1	A	703	ASN
1	A	719	ARG
1	A	731	LEU
1	A	738	MET
1	A	929	MET
1	A	965	SER
1	A	1024	ASN
1	A	1035	TYR
1	B	44	LEU
1	B	61	LEU
1	B	75	VAL
1	B	104	ASN
1	B	114	GLU
1	B	153	MET
1	B	190	ARG
1	B	279	ASN
1	B	311	LEU
1	B	313	SER
1	B	330	SER
1	B	363	ARG
1	B	403	ASN
1	B	423	ASN
1	B	469	HIS
1	B	481	HIS
1	B	557	ARG
1	B	562	GLU
1	B	578	ILE
1	B	641	LEU
1	B	678	LEU
1	B	687	LEU
1	B	703	ASN
1	B	717	LYS
1	B	719	ARG
1	B	731	LEU
1	B	738	MET

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Mol	Chain	Res	Type
1	B	892	LEU
1	B	1024	ASN
1	B	1035	TYR
1	C	61	LEU
1	C	75	VAL
1	C	82	ASN
1	C	104	ASN
1	C	279	ASN
1	C	353	THR
1	C	363	ARG
1	C	403	ASN
1	C	423	ASN
1	C	469	HIS
1	C	481	HIS
1	C	557	ARG
1	C	562	GLU
1	C	578	ILE
1	C	641	LEU
1	C	687	LEU
1	C	703	ASN
1	C	719	ARG
1	C	731	LEU
1	C	738	MET
1	C	892	LEU
1	C	1024	ASN
1	C	1035	TYR
1	D	61	LEU
1	D	75	VAL
1	D	82	ASN
1	D	104	ASN
1	D	114	GLU
1	D	190	ARG
1	D	218	ASN
1	D	279	ASN
1	D	311	LEU
1	D	363	ARG
1	D	403	ASN
1	D	423	ASN
1	D	469	HIS
1	D	532	SER
1	D	557	ARG
1	D	562	GLU

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Mol	Chain	Res	Type
1	D	578	ILE
1	D	641	LEU
1	D	687	LEU
1	D	703	ASN
1	D	719	ARG
1	D	731	LEU
1	D	738	MET
1	D	809	ASP
1	D	892	LEU
1	D	1024	ASN
1	D	1035	TYR
1	E	44	LEU
1	E	61	LEU
1	E	75	VAL
1	E	82	ASN
1	E	104	ASN
1	E	114	GLU
1	E	190	ARG
1	E	209	THR
1	E	218	ASN
1	E	311	LEU
1	E	363	ARG
1	E	403	ASN
1	E	423	ASN
1	E	469	HIS
1	E	557	ARG
1	E	562	GLU
1	E	578	ILE
1	E	641	LEU
1	E	703	ASN
1	E	719	ARG
1	E	731	LEU
1	E	738	MET
1	E	809	ASP
1	E	892	LEU
1	E	1024	ASN
1	E	1035	TYR
1	F	44	LEU
1	F	46	PRO
1	F	61	LEU
1	F	75	VAL
1	F	190	ARG

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Mol	Chain	Res	Type
1	F	209	THR
1	F	279	ASN
1	F	363	ARG
1	F	403	ASN
1	F	423	ASN
1	F	469	HIS
1	F	481	HIS
1	F	557	ARG
1	F	562	GLU
1	F	578	ILE
1	F	641	LEU
1	F	687	LEU
1	F	703	ASN
1	F	719	ARG
1	F	731	LEU
1	F	738	MET
1	F	892	LEU
1	F	929	MET
1	F	1008	GLN
1	F	1024	ASN
1	F	1035	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (193) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	64	HIS
1	A	82	ASN
1	A	104	ASN
1	A	176	ASN
1	A	253	GLN
1	A	267	HIS
1	A	279	ASN
1	A	403	ASN
1	A	415	ASN
1	A	423	ASN
1	A	481	HIS
1	A	497	ASN
1	A	499	HIS
1	A	511	ASN
1	A	530	ASN
1	A	579	ASN

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Mol	Chain	Res	Type
1	A	611	GLN
1	A	635	ASN
1	A	703	ASN
1	A	733	ASN
1	A	739	GLN
1	A	867	ASN
1	A	872	HIS
1	A	922	GLN
1	A	930	ASN
1	A	949	ASN
1	A	1008	GLN
1	A	1024	ASN
1	A	1038	HIS
1	A	1047	GLN
1	B	45	ASN
1	B	64	HIS
1	B	82	ASN
1	B	104	ASN
1	B	253	GLN
1	B	267	HIS
1	B	279	ASN
1	B	403	ASN
1	B	415	ASN
1	B	423	ASN
1	B	481	HIS
1	B	497	ASN
1	B	499	HIS
1	B	511	ASN
1	B	530	ASN
1	B	579	ASN
1	B	611	GLN
1	B	635	ASN
1	B	703	ASN
1	B	733	ASN
1	B	739	GLN
1	B	867	ASN
1	B	872	HIS
1	B	922	GLN
1	B	930	ASN
1	B	949	ASN
1	B	1008	GLN
1	B	1024	ASN

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Mol	Chain	Res	Type
1	B	1038	HIS
1	B	1047	GLN
1	C	45	ASN
1	C	49	HIS
1	C	64	HIS
1	C	82	ASN
1	C	104	ASN
1	C	195	ASN
1	C	253	GLN
1	C	267	HIS
1	C	279	ASN
1	C	403	ASN
1	C	423	ASN
1	C	497	ASN
1	C	499	HIS
1	C	511	ASN
1	C	530	ASN
1	C	579	ASN
1	C	611	GLN
1	C	635	ASN
1	C	703	ASN
1	C	720	ASN
1	C	733	ASN
1	C	739	GLN
1	C	867	ASN
1	C	872	HIS
1	C	922	GLN
1	C	930	ASN
1	C	949	ASN
1	C	1008	GLN
1	C	1024	ASN
1	C	1038	HIS
1	C	1047	GLN
1	D	45	ASN
1	D	49	HIS
1	D	64	HIS
1	D	82	ASN
1	D	104	ASN
1	D	253	GLN
1	D	267	HIS
1	D	279	ASN
1	D	403	ASN

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Mol	Chain	Res	Type
1	D	415	ASN
1	D	423	ASN
1	D	481	HIS
1	D	497	ASN
1	D	499	HIS
1	D	511	ASN
1	D	530	ASN
1	D	569	ASN
1	D	611	GLN
1	D	635	ASN
1	D	703	ASN
1	D	720	ASN
1	D	733	ASN
1	D	739	GLN
1	D	867	ASN
1	D	872	HIS
1	D	922	GLN
1	D	930	ASN
1	D	937	ASN
1	D	949	ASN
1	D	1008	GLN
1	D	1024	ASN
1	D	1038	HIS
1	D	1047	GLN
1	E	45	ASN
1	E	49	HIS
1	E	64	HIS
1	E	82	ASN
1	E	104	ASN
1	E	253	GLN
1	E	267	HIS
1	E	279	ASN
1	E	403	ASN
1	E	415	ASN
1	E	423	ASN
1	E	481	HIS
1	E	497	ASN
1	E	499	HIS
1	E	511	ASN
1	E	530	ASN
1	E	569	ASN
1	E	611	GLN

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Mol	Chain	Res	Type
1	E	635	ASN
1	E	703	ASN
1	E	720	ASN
1	E	733	ASN
1	E	739	GLN
1	E	867	ASN
1	E	872	HIS
1	E	901	ASN
1	E	922	GLN
1	E	930	ASN
1	E	949	ASN
1	E	1008	GLN
1	E	1024	ASN
1	E	1038	HIS
1	E	1047	GLN
1	F	45	ASN
1	F	64	HIS
1	F	82	ASN
1	F	104	ASN
1	F	145	ASN
1	F	176	ASN
1	F	253	GLN
1	F	267	HIS
1	F	279	ASN
1	F	403	ASN
1	F	415	ASN
1	F	423	ASN
1	F	481	HIS
1	F	497	ASN
1	F	499	HIS
1	F	511	ASN
1	F	530	ASN
1	F	569	ASN
1	F	579	ASN
1	F	611	GLN
1	F	635	ASN
1	F	703	ASN
1	F	720	ASN
1	F	733	ASN
1	F	739	GLN
1	F	867	ASN
1	F	872	HIS

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Mol	Chain	Res	Type
1	F	901	ASN
1	F	922	GLN
1	F	930	ASN
1	F	949	ASN
1	F	1008	GLN
1	F	1024	ASN
1	F	1038	HIS
1	F	1047	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	1022/1045 (97%)	0.29	34 (3%)	50	51	14, 26, 43, 56	19 (1%)
1	B	1022/1045 (97%)	0.28	34 (3%)	50	51	16, 26, 43, 55	19 (1%)
1	C	1022/1045 (97%)	0.75	122 (11%)	6	6	20, 33, 46, 56	19 (1%)
1	D	1022/1045 (97%)	0.32	50 (4%)	33	35	18, 28, 45, 54	19 (1%)
1	E	1022/1045 (97%)	0.30	41 (4%)	42	44	17, 28, 45, 55	19 (1%)
1	F	1022/1045 (97%)	0.70	114 (11%)	7	7	21, 32, 46, 55	19 (1%)
All	All	6132/6270 (97%)	0.44	395 (6%)	23	24	14, 30, 45, 56	114 (1%)

All (395) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	219	SER	9.2
1	F	219	SER	9.2
1	A	841	GLY	9.0
1	F	220	GLY	8.5
1	D	219	SER	8.2
1	E	219	SER	8.0
1	C	841	GLY	7.7
1	E	220	GLY	7.6
1	F	563	ALA	7.4
1	C	220	GLY	7.0
1	C	218	ASN	6.6
1	C	188	GLY	6.5
1	E	218	ASN	6.5
1	D	220	GLY	6.4
1	C	238	VAL	6.2
1	C	842	GLY	5.8
1	C	563	ALA	5.8
1	F	839	GLY	5.7
1	F	840	LYS	5.5

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Mol	Chain	Res	Type	RSRZ
1	C	217	VAL	5.4
1	F	299	ASP	5.3
1	F	706	VAL	5.3
1	B	563	ALA	5.2
1	C	300	THR	5.2
1	F	69	GLY	5.2
1	C	116	GLY	5.1
1	C	706	VAL	5.0
1	D	842	GLY	5.0
1	D	841	GLY	5.0
1	F	188	GLY	5.0
1	C	299	ASP	4.9
1	F	67	LYS	4.9
1	C	774	ASP	4.9
1	B	218	ASN	4.9
1	C	840	LYS	4.8
1	D	563	ALA	4.8
1	F	843	ASP	4.7
1	D	435	THR	4.7
1	F	842	GLY	4.7
1	C	66	LEU	4.7
1	C	562	GLU	4.6
1	C	843	ASP	4.6
1	D	218	ASN	4.5
1	C	69	GLY	4.5
1	C	67	LYS	4.4
1	D	840	LYS	4.4
1	C	806	LEU	4.3
1	C	221	ALA	4.3
1	D	436	GLY	4.3
1	D	706	VAL	4.3
1	D	469	HIS	4.2
1	B	841	GLY	4.2
1	C	239	GLY	4.2
1	C	142	PRO	4.2
1	F	771	LEU	4.2
1	F	774	ASP	4.2
1	C	817	ALA	4.2
1	C	114	GLU	4.1
1	F	434	GLU	4.1
1	F	218	ASN	4.1
1	F	262	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	F	561	SER	4.1
1	C	752	GLY	4.1
1	F	217	VAL	4.0
1	F	238	VAL	4.0
1	C	839	GLY	4.0
1	C	318	ILE	4.0
1	F	305	LYS	4.0
1	F	806	LEU	3.9
1	F	393	ARG	3.9
1	C	707	ALA	3.9
1	F	401	GLU	3.9
1	A	563	ALA	3.9
1	C	68	SER	3.8
1	F	187	ASP	3.8
1	D	434	GLU	3.8
1	C	777	VAL	3.7
1	F	435	THR	3.7
1	C	1043	GLY	3.7
1	F	705	ALA	3.7
1	E	842	GLY	3.6
1	F	841	GLY	3.6
1	E	469	HIS	3.6
1	D	299	ASP	3.6
1	F	300	THR	3.6
1	B	434	GLU	3.6
1	C	237	ILE	3.6
1	C	654	ASP	3.6
1	D	1019	GLY	3.6
1	D	843	ASP	3.6
1	C	187	ASP	3.6
1	D	667	ASP	3.6
1	F	612	GLY	3.5
1	F	70	SER	3.5
1	F	488	ARG	3.5
1	B	39	MET	3.5
1	F	65	ASP	3.5
1	F	722	VAL	3.4
1	F	704	GLU	3.4
1	C	397	ALA	3.4
1	A	434	GLU	3.4
1	C	51	ASP	3.4
1	D	286	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	260	ASP	3.3
1	F	297	ASN	3.3
1	F	66	LEU	3.3
1	C	144	GLY	3.3
1	F	215	ILE	3.3
1	C	65	ASP	3.3
1	C	667	ASP	3.3
1	C	561	SER	3.3
1	A	839	GLY	3.3
1	E	841	GLY	3.3
1	C	271	THR	3.3
1	B	488	ARG	3.2
1	D	653	ASP	3.2
1	F	307	GLU	3.2
1	E	299	ASP	3.2
1	E	840	LYS	3.2
1	C	303	ILE	3.2
1	F	221	ALA	3.1
1	E	562	GLU	3.1
1	C	844	LYS	3.1
1	B	435	THR	3.1
1	F	114	GLU	3.1
1	F	258	ASP	3.1
1	E	91	ARG	3.1
1	B	612	GLY	3.1
1	C	401	GLU	3.1
1	E	563	ALA	3.1
1	F	362	LEU	3.1
1	F	716	GLU	3.1
1	B	628	LYS	3.1
1	C	168	ASP	3.1
1	C	91	ARG	3.1
1	F	91	ARG	3.1
1	A	437	LYS	3.1
1	F	272	ASP	3.1
1	D	613	ALA	3.0
1	B	923	LEU	3.0
1	F	51	ASP	3.0
1	F	1043	GLY	3.0
1	F	562	GLU	3.0
1	C	202	TRP	3.0
1	F	189	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	186	ALA	3.0
1	F	303	ILE	2.9
1	C	286	LEU	2.9
1	C	722	VAL	2.9
1	C	1038	HIS	2.9
1	E	435	THR	2.9
1	D	91	ARG	2.9
1	D	839	GLY	2.9
1	F	773	GLY	2.9
1	F	415	ASN	2.9
1	F	68	SER	2.9
1	C	297	ASN	2.9
1	B	469	HIS	2.9
1	D	716	GLU	2.9
1	D	1059	LEU	2.9
1	C	845	ARG	2.9
1	A	494	THR	2.9
1	C	439	THR	2.9
1	C	434	GLU	2.9
1	C	1042	SER	2.9
1	A	67	LYS	2.9
1	A	199	LEU	2.9
1	C	705	ALA	2.9
1	D	705	ALA	2.9
1	F	817	ALA	2.9
1	E	434	GLU	2.9
1	E	1017	ASP	2.9
1	C	488	ARG	2.8
1	B	928	LEU	2.8
1	C	469	HIS	2.8
1	F	436	GLY	2.8
1	F	667	ASP	2.8
1	A	840	LYS	2.8
1	A	469	HIS	2.8
1	C	487	GLY	2.8
1	C	653	ASP	2.8
1	C	50	GLY	2.8
1	A	218	ASN	2.8
1	F	50	GLY	2.8
1	F	775	HIS	2.7
1	D	114	GLU	2.7
1	E	436	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	239	GLY	2.7
1	B	924	ILE	2.7
1	E	706	VAL	2.7
1	A	562	GLU	2.7
1	D	239	GLY	2.7
1	D	437	LYS	2.7
1	C	262	LYS	2.7
1	C	435	THR	2.7
1	F	469	HIS	2.7
1	A	39	MET	2.7
1	A	488	ARG	2.7
1	C	185	PHE	2.7
1	F	185	PHE	2.7
1	C	393	ARG	2.7
1	C	613	ALA	2.7
1	E	592	GLU	2.7
1	F	1059	LEU	2.6
1	D	612	GLY	2.6
1	F	844	LYS	2.6
1	F	628	LYS	2.6
1	C	812	GLY	2.6
1	E	114	GLU	2.6
1	A	44	LEU	2.6
1	C	1041	LEU	2.6
1	C	803	THR	2.6
1	F	170	ILE	2.6
1	B	562	GLU	2.6
1	D	557	ARG	2.6
1	D	562	GLU	2.6
1	B	1017	ASP	2.6
1	D	1017	ASP	2.6
1	C	724	LEU	2.6
1	C	70	SER	2.6
1	F	142	PRO	2.6
1	C	612	GLY	2.6
1	F	308	ILE	2.6
1	C	663	GLU	2.6
1	C	243	TYR	2.6
1	E	653	ASP	2.6
1	A	928	LEU	2.6
1	D	560	THR	2.6
1	C	415	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1017	ASP	2.6
1	C	258	ASP	2.6
1	E	665	PRO	2.5
1	C	838	SER	2.5
1	C	100	GLY	2.5
1	C	665	PRO	2.5
1	F	270	PHE	2.5
1	C	716	GLU	2.5
1	A	842	GLY	2.5
1	C	436	GLY	2.5
1	C	494	THR	2.5
1	B	286	LEU	2.5
1	D	199	LEU	2.5
1	B	167	ASN	2.5
1	C	683	HIS	2.5
1	B	557	ARG	2.5
1	D	665	PRO	2.5
1	C	236	VAL	2.5
1	F	756	ASP	2.5
1	F	494	THR	2.5
1	D	905	TYR	2.5
1	F	613	ALA	2.4
1	A	612	GLY	2.4
1	F	144	GLY	2.4
1	F	282	GLY	2.4
1	F	237	ILE	2.4
1	F	293	ILE	2.4
1	B	842	GLY	2.4
1	E	397	ALA	2.4
1	C	64	HIS	2.4
1	C	305	LYS	2.4
1	B	705	ALA	2.4
1	C	145	ASN	2.4
1	A	286	LEU	2.4
1	F	609	TYR	2.4
1	E	612	GLY	2.4
1	F	326	ALA	2.4
1	B	437	LYS	2.4
1	B	494	THR	2.4
1	C	304	GLU	2.4
1	D	308	ILE	2.3
1	E	401	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	625	LYS	2.3
1	C	758	ASP	2.3
1	C	445	ARG	2.3
1	E	627	ARG	2.3
1	A	217	VAL	2.3
1	C	800	ILE	2.3
1	F	374	LYS	2.3
1	F	240	HIS	2.3
1	A	1059	LEU	2.3
1	C	771	LEU	2.3
1	E	634	ASN	2.3
1	C	326	ALA	2.3
1	A	627	ARG	2.3
1	F	758	ASP	2.3
1	C	165	VAL	2.3
1	C	753	THR	2.3
1	C	704	GLU	2.3
1	C	709	GLU	2.3
1	C	853	ASP	2.3
1	A	330	SER	2.3
1	C	39	MET	2.3
1	B	592	GLU	2.3
1	C	628	LYS	2.3
1	F	261	GLY	2.2
1	C	402	GLU	2.2
1	E	565	GLU	2.2
1	A	557	ARG	2.2
1	F	761	ARG	2.2
1	F	168	ASP	2.2
1	F	372	ASP	2.2
1	C	186	ALA	2.2
1	F	707	ALA	2.2
1	C	382	ARG	2.2
1	D	935	TYR	2.2
1	F	71	THR	2.2
1	A	641	LEU	2.2
1	C	115	ASN	2.2
1	D	614	PRO	2.2
1	E	400	PHE	2.2
1	B	663	GLU	2.2
1	C	808	GLU	2.2
1	E	97	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	716	GLU	2.2
1	C	321	ILE	2.2
1	A	705	ALA	2.2
1	F	557	ARG	2.2
1	C	263	ASP	2.2
1	D	471	GLU	2.2
1	B	561	SER	2.2
1	F	799	GLY	2.2
1	C	89	ASP	2.2
1	B	199	LEU	2.2
1	F	39	MET	2.2
1	F	400	PHE	2.2
1	C	1017	ASP	2.2
1	F	653	ASP	2.2
1	F	772	ASP	2.2
1	A	565	GLU	2.2
1	F	592	GLU	2.2
1	D	297	ASN	2.2
1	F	138	ALA	2.2
1	A	924	ILE	2.2
1	D	480	ILE	2.2
1	F	265	ARG	2.1
1	D	774	ASP	2.1
1	E	663	GLU	2.1
1	A	329	PHE	2.1
1	B	329	PHE	2.1
1	A	663	GLU	2.1
1	C	49	HIS	2.1
1	C	592	GLU	2.1
1	F	319	ILE	2.1
1	E	667	ASP	2.1
1	B	67	LYS	2.1
1	C	269	SER	2.1
1	F	1041	LEU	2.1
1	F	805	TYR	2.1
1	F	802	PRO	2.1
1	A	299	ASP	2.1
1	D	683	HIS	2.1
1	F	334	GLY	2.1
1	E	937	ASN	2.1
1	D	382	ARG	2.1
1	E	286	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	382	ARG	2.1
1	C	712	GLU	2.1
1	D	39	MET	2.1
1	D	569	ASN	2.1
1	E	337	ILE	2.1
1	A	653	ASP	2.1
1	F	49	HIS	2.1
1	F	395	GLY	2.1
1	B	219	SER	2.1
1	C	265	ARG	2.1
1	C	627	ARG	2.1
1	E	561	SER	2.1
1	B	541	VAL	2.1
1	C	988	TRP	2.1
1	E	437	LYS	2.1
1	C	308	ILE	2.1
1	B	503	PRO	2.1
1	E	402	GLU	2.1
1	F	304	GLU	2.1
1	F	402	GLU	2.1
1	B	91	ARG	2.1
1	F	171	ASN	2.1
1	F	1020	PHE	2.1
1	C	71	THR	2.0
1	E	260	ASP	2.1
1	F	1036	ALA	2.0
1	D	494	THR	2.0
1	E	560	THR	2.0
1	E	67	LYS	2.0
1	D	661	PRO	2.0
1	F	145	ASN	2.0
1	C	1014	TRP	2.0
1	D	108	LEU	2.0
1	D	592	GLU	2.0
1	E	372	ASP	2.0
1	F	709	GLU	2.0
1	A	167	ASN	2.0
1	B	234	SER	2.0
1	B	840	LYS	2.0
1	C	215	ILE	2.0

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

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.