



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:26 PM GMT

PDB ID : 4RV1
Title : Crystal Structure of Engineered Protein. Northeast Structural Genomics Consortium (NESG) Target OR497.
Authors : Vorobiev, S.; Parmeggiani, F.; Seetharaman, J.; Xiao, R.; Everett, J.K.; Acton, T.B.; Baker, D.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2014-11-24
Resolution : 2.57 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

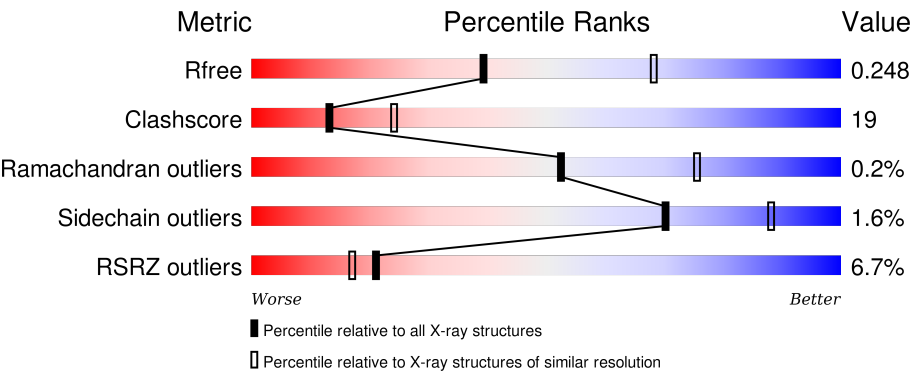
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	2636 (2.60-2.56)
Clashscore	102246	3003 (2.60-2.56)
Ramachandran outliers	100387	2956 (2.60-2.56)
Sidechain outliers	100360	2956 (2.60-2.56)
RSRZ outliers	91569	2642 (2.60-2.56)

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 <=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	420	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>73%25%.</div></div>
1	B	420	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>71%26%..</div></div>
1	C	420	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>77%21%.</div></div>
1	D	420	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>5%73%25%..</div></div>
1	E	420	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>15%53%43%..</div></div>

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Mol	Chain	Length	Quality of chain
1	F	420	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	C	501	-	-	-	X

2 Entry composition [i](#)

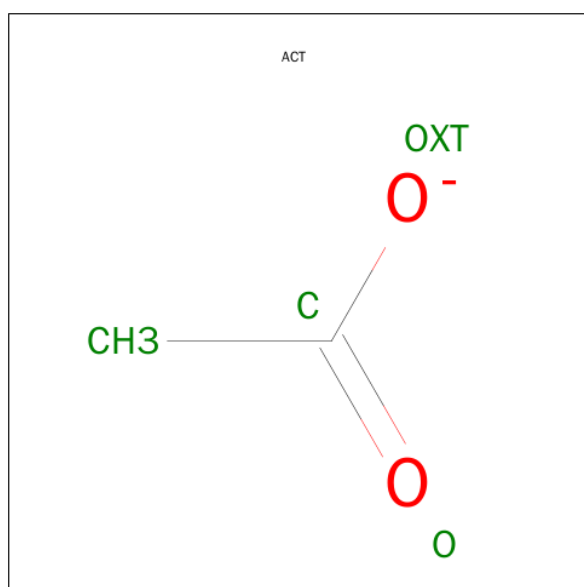
There are 3 unique types of molecules in this entry. The entry contains 18115 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Engineered Protein OR497.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	0	0	0
			2931	1815	496	619	1			
1	B	414	Total	C	N	O		0	0	0
			2950	1826	500	624				
1	C	412	Total	C	N	O		0	0	0
			2925	1811	496	618				
1	D	415	Total	C	N	O	S	0	0	0
			2954	1828	500	625	1			
1	E	412	Total	C	N	O	S	0	0	0
			2931	1814	496	620	1			
1	F	411	Total	C	N	O	S	0	0	0
			2917	1803	494	619	1			

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		

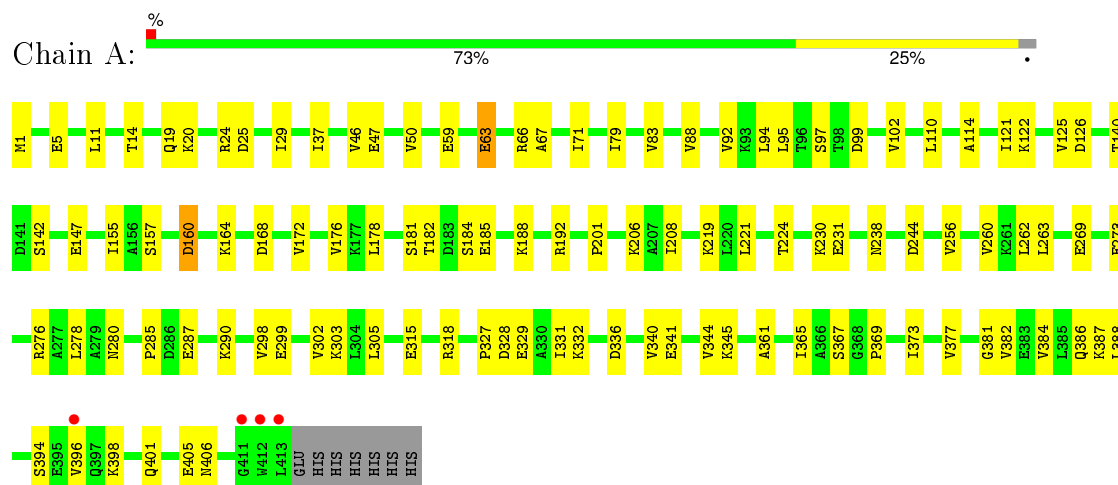
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	104	Total	O	0	0
			104	104		
3	B	104	Total	O	0	0
			104	104		
3	C	110	Total	O	0	0
			110	110		
3	D	93	Total	O	0	0
			93	93		
3	E	35	Total	O	0	0
			35	35		
3	F	53	Total	O	0	0
			53	53		

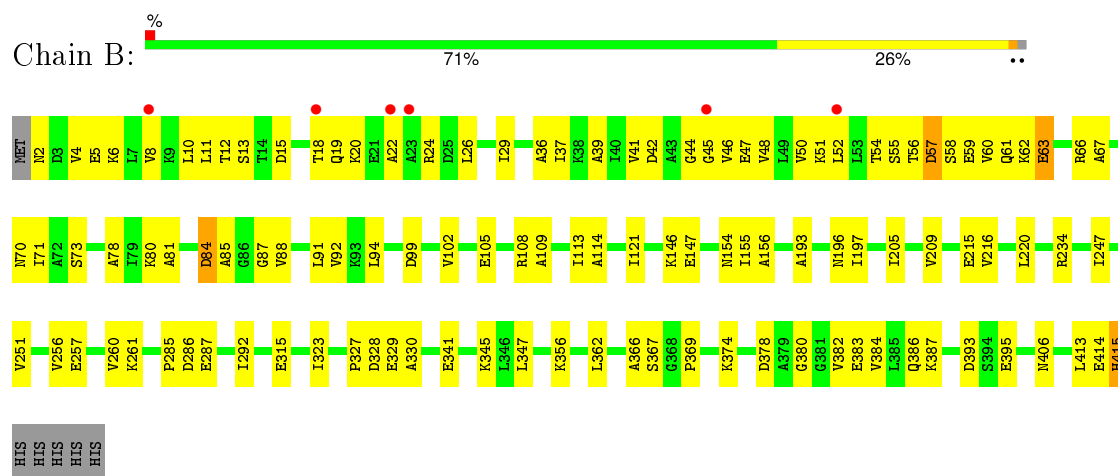
3 Residue-property plots

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.

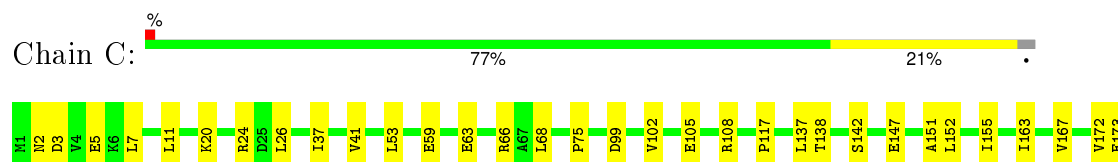
• Molecule 1: Engineered Protein OR497

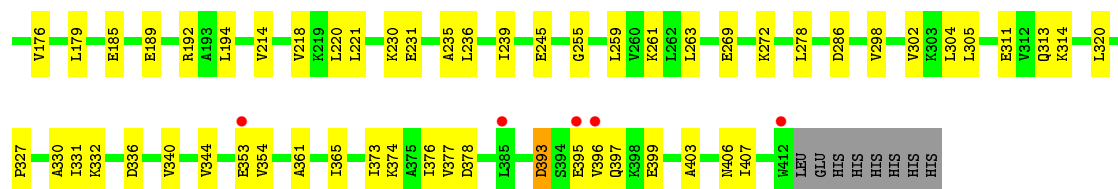


• Molecule 1: Engineered Protein OR497

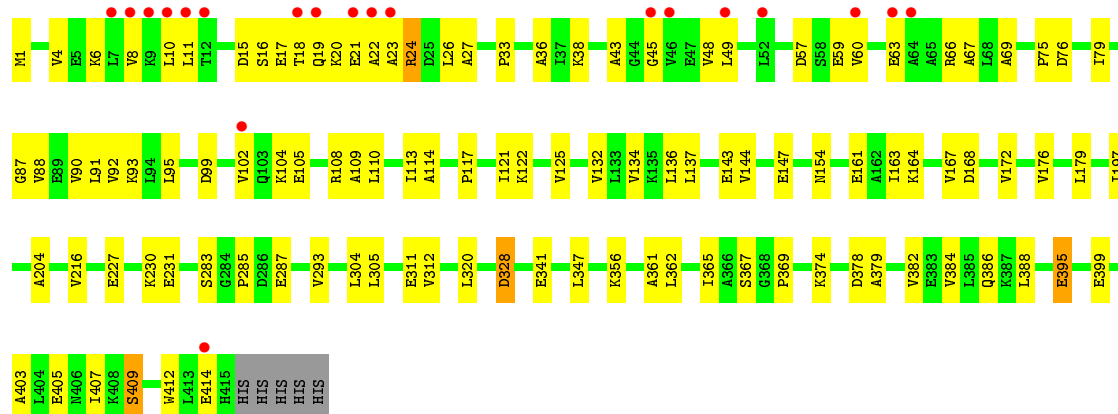


• Molecule 1: Engineered Protein OR497

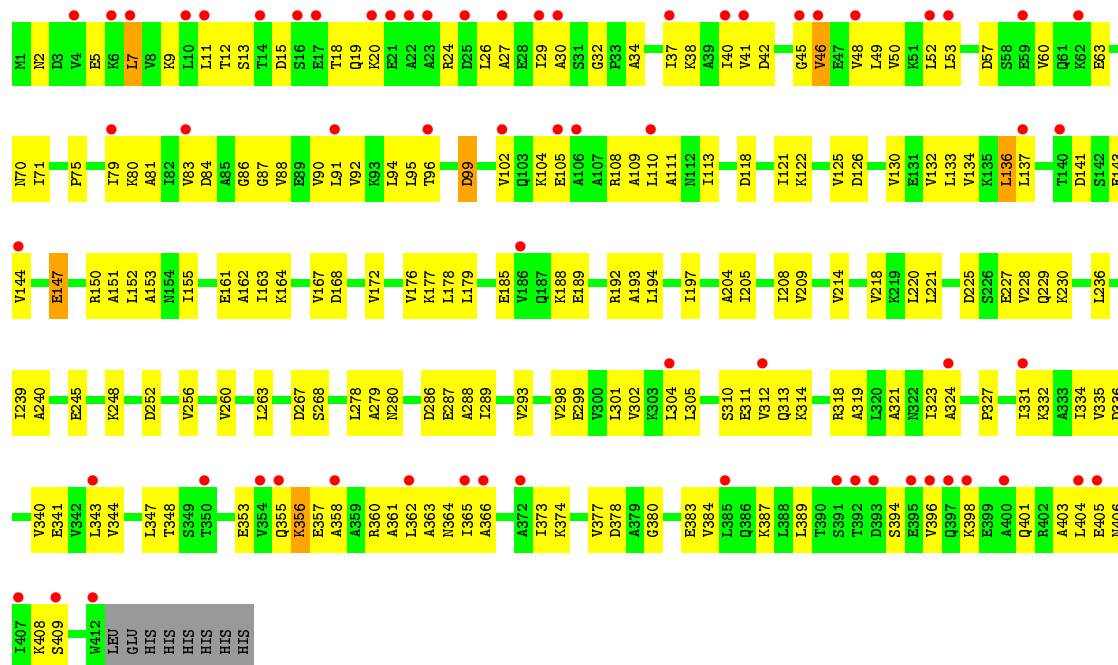




• Molecule 1: Engineered Protein OR497

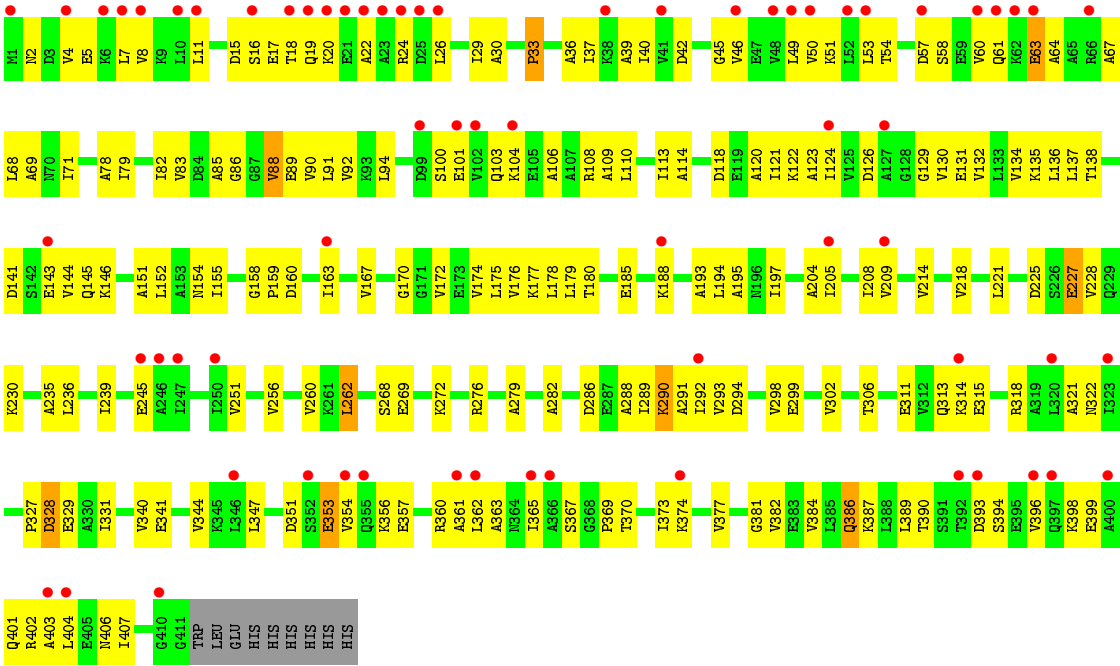


• Molecule 1: Engineered Protein OR497



• Molecule 1: Engineered Protein OR497





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.27 Å 99.27 Å 432.18 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.02 – 2.57 49.63 – 2.57	Depositor EDS
% Data completeness (in resolution range)	97.5 (48.02-2.57) 97.9 (49.63-2.57)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.58 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.201 , 0.237 0.217 , 0.248	Depositor DCC
R_{free} test set	3929 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.3	EDS
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 78237 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18115	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.68% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACT

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	0.35	0/2941	0.57	0/3993
1	B	0.36	0/2961	0.59	0/4019
1	C	0.38	0/2935	0.57	1/3984 (0.0%)
1	D	0.36	0/2965	0.56	0/4025
1	E	0.30	0/2941	0.54	0/3991
1	F	0.29	0/2925	0.53	0/3968
All	All	0.34	0/17668	0.56	1/23980 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	393	ASP	N-CA-C	-5.09	97.27	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2931	0	3050	78	0
1	B	2950	0	3066	96	0
1	C	2925	0	3045	64	0
1	D	2954	0	3067	93	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2931	0	3054	178	0
1	F	2917	0	3044	195	0
2	A	4	0	3	1	0
2	C	4	0	3	0	0
3	A	104	0	0	12	0
3	B	104	0	0	11	0
3	C	110	0	0	4	0
3	D	93	0	0	6	0
3	E	35	0	0	1	0
3	F	53	0	0	16	0
All	All	18115	0	18332	681	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 19.

All (681) 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:24:ARG:HG2	1:F:63:GLU:HG2	1.38	1.03
1:F:26:LEU:HD23	1:F:29:ILE:HD12	1.48	0.94
1:F:100:SER:HA	1:F:103:GLN:HE21	1.32	0.92
1:F:351:ASP:HB3	1:F:354:VAL:HG12	1.52	0.90
1:B:57:ASP:HB2	1:B:60:VAL:HG12	1.54	0.89
1:D:104:LYS:HD2	1:D:143:GLU:HG2	1.54	0.89
1:F:17:GLU:HA	1:F:20:LYS:HD2	1.55	0.87
1:B:382:VAL:O	1:B:386:GLN:HG2	1.75	0.85
1:E:214:VAL:O	1:E:218:VAL:HG23	1.77	0.85
1:E:408:LYS:HD3	1:E:409:SER:N	1.92	0.84
1:E:53:LEU:HB3	1:E:94:LEU:HD11	1.57	0.84
1:F:290:LYS:HG2	1:F:294:ASP:OD2	1.79	0.83
1:F:110:LEU:HA	1:F:113:ILE:HD12	1.61	0.82
1:F:367:SER:HB3	1:F:406:ASN:ND2	1.93	0.81
1:C:393:ASP:O	1:C:396:VAL:HG12	1.80	0.81
1:B:393:ASP:OD2	1:B:395:GLU:HG2	1.81	0.80
1:A:328:ASP:OD2	1:A:369:PRO:HD3	1.81	0.80
1:E:37:ILE:HD11	1:E:71:ILE:HA	1.63	0.80
1:F:68:LEU:HB2	3:F:547:HOH:O	1.81	0.79
1:C:340:VAL:O	1:C:344:VAL:HG23	1.81	0.79
1:B:15:ASP:HB2	1:B:18:THR:HG22	1.63	0.79
1:D:69:ALA:HB3	1:D:108:ARG:HH21	1.48	0.78
1:E:88:VAL:O	1:E:92:VAL:HG23	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:328:ASP:OD2	1:D:369:PRO:HD3	1.84	0.77
1:A:46:VAL:O	1:A:50:VAL:HG23	1.85	0.77
1:F:340:VAL:O	1:F:344:VAL:HG23	1.84	0.77
1:D:367:SER:HB2	1:D:414:GLU:HG3	1.68	0.76
1:F:88:VAL:O	1:F:92:VAL:HG23	1.85	0.76
1:F:290:LYS:HA	1:F:293:VAL:HG22	1.68	0.76
1:C:214:VAL:O	1:C:218:VAL:HG23	1.86	0.76
1:F:130:VAL:O	1:F:134:VAL:HG23	1.86	0.76
1:D:104:LYS:HB3	1:D:144:VAL:HG12	1.66	0.76
1:F:360:ARG:HA	1:F:399:GLU:OE1	1.87	0.75
1:A:276:ARG:HG3	1:A:315:GLU:OE2	1.86	0.75
1:B:2:ASN:HB3	1:B:5:GLU:CD	2.06	0.75
1:B:11:LEU:HB3	1:B:52:LEU:HD11	1.67	0.74
1:F:141:ASP:O	1:F:144:VAL:HG12	1.86	0.74
1:E:341:GLU:HG3	3:E:525:HOH:O	1.86	0.74
1:D:1:MET:HB3	1:D:6:LYS:HE3	1.69	0.74
1:A:244:ASP:OD2	1:A:285:PRO:HD3	1.88	0.74
1:D:20:LYS:HG2	1:D:60:VAL:HG22	1.69	0.74
1:F:272:LYS:HD2	1:F:311:GLU:HB3	1.68	0.73
1:F:141:ASP:HB2	1:F:144:VAL:CG1	2.18	0.73
1:F:109:ALA:O	1:F:113:ILE:HG13	1.89	0.72
1:E:87:GLY:O	1:E:91:LEU:HB2	1.90	0.72
1:E:355:GLN:HE21	1:E:396:VAL:HG11	1.53	0.72
1:F:58:SER:HA	1:F:61:GLN:OE1	1.89	0.72
1:E:34:ALA:HA	1:E:37:ILE:HG22	1.71	0.72
1:E:141:ASP:HB3	1:E:144:VAL:HG12	1.71	0.72
1:F:101:GLU:HA	1:F:104:LYS:NZ	2.05	0.71
1:B:374:LYS:HG2	1:B:378:ASP:OD2	1.89	0.71
1:D:172:VAL:O	1:D:176:VAL:HG23	1.90	0.71
1:D:17:GLU:OE2	1:D:21:GLU:HG3	1.91	0.70
1:F:152:LEU:HA	3:F:548:HOH:O	1.92	0.70
1:A:269:GLU:HG2	1:D:227:GLU:HG3	1.73	0.70
1:F:7:LEU:O	1:F:11:LEU:HD23	1.91	0.70
1:F:177:LYS:O	1:F:180:THR:HG22	1.92	0.69
1:E:225:ASP:OD2	1:E:228:VAL:HG23	1.91	0.69
1:D:21:GLU:HA	1:D:24:ARG:HD2	1.74	0.69
1:F:177:LYS:HB3	3:F:508:HOH:O	1.91	0.69
1:E:24:ARG:HH12	1:F:394:SER:HB2	1.56	0.69
1:D:356:LYS:HD3	1:D:395:GLU:HB3	1.74	0.69
1:D:109:ALA:O	1:D:113:ILE:HG13	1.93	0.69
1:E:19:GLN:HG2	1:E:52:LEU:HD21	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ILE:HG23	1:A:71:ILE:HG23	1.74	0.69
1:E:405:GLU:O	1:E:408:LYS:HB3	1.93	0.69
1:E:24:ARG:HH22	1:F:394:SER:HB2	1.58	0.69
1:E:57:ASP:HB3	1:E:60:VAL:HG23	1.74	0.69
1:E:130:VAL:O	1:E:134:VAL:HG23	1.92	0.69
1:B:387:LYS:HE2	3:D:580:HOH:O	1.93	0.69
1:E:355:GLN:NE2	1:E:396:VAL:HG11	2.08	0.68
1:C:298:VAL:O	1:C:302:VAL:HG23	1.93	0.68
1:F:205:ILE:O	1:F:209:VAL:HG23	1.94	0.68
1:F:121:ILE:HG23	1:F:155:ILE:HG23	1.76	0.68
1:D:104:LYS:HD2	1:D:143:GLU:CG	2.24	0.68
1:D:395:GLU:OE1	1:D:395:GLU:HA	1.92	0.68
1:F:318:ARG:HA	1:F:357:GLU:OE1	1.94	0.68
1:E:104:LYS:HE3	1:E:105:GLU:HG3	1.77	0.67
1:F:393:ASP:O	1:F:396:VAL:HG12	1.93	0.67
1:C:314:LYS:HG3	1:C:353:GLU:HB3	1.75	0.67
1:D:412:TRP:HA	1:E:245:GLU:OE1	1.93	0.67
1:F:79:ILE:HD13	1:F:113:ILE:HA	1.77	0.67
1:E:314:LYS:HD3	1:E:353:GLU:CB	2.24	0.67
1:E:361:ALA:O	1:E:365:ILE:HG13	1.93	0.67
3:B:570:HOH:O	1:C:75:PRO:HB2	1.94	0.66
1:F:155:ILE:HB	3:F:548:HOH:O	1.94	0.66
1:F:57:ASP:HB3	1:F:60:VAL:HG23	1.76	0.66
1:E:104:LYS:HD2	1:E:143:GLU:HG3	1.76	0.66
1:E:389:LEU:HD21	1:E:404:LEU:HD12	1.78	0.66
1:A:382:VAL:O	1:A:386:GLN:HG3	1.94	0.66
1:A:164:LYS:HG2	1:A:168:ASP:OD2	1.94	0.66
1:E:15:ASP:HB3	1:E:18:THR:HB	1.78	0.66
1:F:100:SER:HA	1:F:103:GLN:HG2	1.78	0.66
1:B:57:ASP:HB2	1:B:60:VAL:CG1	2.25	0.66
1:F:2:ASN:OD1	1:F:5:GLU:HG3	1.95	0.66
1:F:276:ARG:HA	1:F:315:GLU:HG2	1.78	0.65
1:F:135:LYS:O	1:F:138:THR:HG22	1.96	0.65
1:E:132:VAL:O	1:E:136:LEU:HD23	1.97	0.65
1:E:188:LYS:HZ2	1:F:268:SER:HB3	1.62	0.65
1:F:167:VAL:HG22	1:F:172:VAL:HG21	1.79	0.65
1:A:299:GLU:HG2	1:C:138:THR:O	1.97	0.65
1:D:163:ILE:HG23	1:D:197:ILE:HG23	1.78	0.65
1:B:51:LYS:O	1:B:54:THR:HG22	1.97	0.65
1:B:10:LEU:HD23	1:B:22:ALA:HB2	1.79	0.65
1:C:313:GLN:OE1	1:C:354:VAL:HG21	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:95:LEU:HD11	1:D:110:LEU:HD12	1.79	0.65
1:E:46:VAL:HG11	1:E:81:ALA:HB1	1.79	0.64
1:E:79:ILE:O	1:E:83:VAL:HG23	1.97	0.64
1:E:240:ALA:O	1:E:280:ASN:HB3	1.97	0.64
1:B:414:GLU:O	1:B:415:HIS:ND1	2.31	0.64
1:F:100:SER:HA	1:F:103:GLN:NE2	2.09	0.64
1:B:2:ASN:ND2	1:B:5:GLU:H	1.95	0.64
1:C:172:VAL:O	1:C:176:VAL:HG23	1.98	0.64
1:F:121:ILE:CG2	1:F:155:ILE:HG23	2.28	0.63
1:D:27:ALA:HB3	1:D:66:ARG:HH21	1.64	0.63
1:F:214:VAL:O	1:F:218:VAL:HG23	1.98	0.63
1:D:11:LEU:HD12	1:D:22:ALA:HB1	1.80	0.63
1:A:280:ASN:OD1	1:A:318:ARG:NH2	2.32	0.63
1:A:20:LYS:HD3	1:A:59:GLU:OE2	1.99	0.63
1:E:185:GLU:HG3	1:F:311:GLU:OE2	1.99	0.63
1:B:328:ASP:OD1	1:B:369:PRO:HD3	1.97	0.63
1:E:366:ALA:HB1	1:E:406:ASN:HB2	1.79	0.63
1:F:204:ALA:O	1:F:208:ILE:HG13	1.98	0.63
1:A:206:LYS:NZ	3:A:712:HOH:O	2.32	0.62
1:C:395:GLU:O	1:C:399:GLU:HB2	1.99	0.62
1:F:170:GLY:O	1:F:174:VAL:HG23	1.99	0.62
1:D:76:ASP:OD1	1:D:117:PRO:HD3	2.00	0.62
1:E:121:ILE:O	1:E:125:VAL:HG23	2.00	0.62
1:A:224:THR:HG22	3:A:717:HOH:O	1.99	0.62
1:E:19:GLN:CD	1:E:52:LEU:HD11	2.20	0.62
1:D:285:PRO:HG2	1:D:287:GLU:HG2	1.82	0.62
1:F:20:LYS:HB3	1:F:24:ARG:NH1	2.15	0.62
1:F:50:VAL:HG21	1:F:85:ALA:HB1	1.81	0.62
1:E:141:ASP:O	1:E:144:VAL:HG12	1.99	0.62
1:E:245:GLU:CD	1:E:245:GLU:H	2.02	0.61
1:E:185:GLU:OE1	1:F:311:GLU:HG3	2.00	0.61
1:D:104:LYS:CB	1:D:144:VAL:HG12	2.30	0.61
1:E:24:ARG:NH1	1:F:394:SER:HB2	2.14	0.61
1:B:57:ASP:C	1:B:59:GLU:H	2.02	0.61
1:D:38:LYS:HE3	1:D:75:PRO:HG3	1.83	0.61
1:F:167:VAL:HG22	1:F:172:VAL:CG2	2.31	0.61
1:F:384:VAL:HG23	1:F:387:LYS:HZ3	1.66	0.61
1:F:389:LEU:HD11	1:F:404:LEU:HD12	1.83	0.61
1:A:24:ARG:HG3	1:A:63:GLU:HG2	1.82	0.61
1:E:46:VAL:O	1:E:50:VAL:HG23	2.01	0.61
1:E:109:ALA:O	1:E:113:ILE:HG13	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:THR:HG23	3:A:787:HOH:O	1.99	0.60
1:E:80:LYS:HG2	1:E:84:ASP:OD2	2.00	0.60
1:A:47:GLU:CD	1:A:47:GLU:H	2.05	0.60
1:C:2:ASN:ND2	1:C:5:GLU:HG3	2.15	0.60
1:E:314:LYS:HD3	1:E:353:GLU:HB3	1.84	0.60
1:A:401:GLN:O	1:A:405:GLU:HG3	2.00	0.60
1:E:133:LEU:HA	1:E:136:LEU:HD21	1.82	0.60
1:D:23:ALA:HA	1:D:26:LEU:HD12	1.82	0.60
1:D:17:GLU:OE1	1:D:20:LYS:HD2	2.01	0.60
1:F:393:ASP:HB3	1:F:396:VAL:HG12	1.84	0.60
1:B:15:ASP:HB2	1:B:18:THR:CG2	2.32	0.60
1:E:227:GLU:HG2	1:F:269:GLU:HG2	1.84	0.60
1:F:172:VAL:O	1:F:176:VAL:HG23	2.01	0.60
1:A:373:ILE:O	1:A:377:VAL:HG23	2.02	0.60
1:B:99:ASP:OD2	1:B:102:VAL:HG23	2.02	0.60
1:B:2:ASN:HD21	1:B:4:VAL:HB	1.67	0.59
1:E:24:ARG:NH2	1:F:394:SER:HB2	2.16	0.59
1:E:188:LYS:HE3	1:F:268:SER:OG	2.02	0.59
1:F:298:VAL:O	1:F:302:VAL:HG23	2.02	0.59
1:B:108:ARG:HG3	1:B:147:GLU:OE2	2.01	0.59
1:D:79:ILE:HG23	1:D:113:ILE:HG23	1.84	0.59
1:F:374:LYS:HE3	3:F:509:HOH:O	2.02	0.59
1:F:282:ALA:O	1:F:322:ASN:HB3	2.02	0.59
1:B:413:LEU:N	1:B:413:LEU:HD12	2.17	0.59
1:B:60:VAL:HG13	1:B:61:GLN:N	2.18	0.59
1:B:2:ASN:HD22	1:B:5:GLU:HG2	1.68	0.59
1:E:172:VAL:O	1:E:176:VAL:HG23	2.03	0.59
1:F:120:ALA:O	1:F:124:ILE:HG13	2.02	0.59
1:F:141:ASP:HB2	1:F:144:VAL:HG12	1.84	0.58
1:F:221:LEU:HD11	1:F:236:LEU:CD1	2.32	0.58
1:F:68:LEU:HA	1:F:71:ILE:HD12	1.85	0.58
1:B:8:VAL:HG13	1:B:45:GLY:HA2	1.84	0.58
1:F:321:ALA:HB3	1:F:360:ARG:NH2	2.18	0.58
1:E:188:LYS:NZ	1:F:268:SER:HB3	2.18	0.58
1:B:247:ILE:O	1:B:251:VAL:HG23	2.03	0.58
1:D:10:LEU:HB3	1:D:22:ALA:HB2	1.85	0.58
1:D:95:LEU:HD11	1:D:110:LEU:CD1	2.33	0.58
1:F:327:PRO:HB2	1:F:329:GLU:OE2	2.04	0.58
1:C:340:VAL:HG11	1:C:376:ILE:HA	1.86	0.58
1:D:230:LYS:HG2	3:D:546:HOH:O	2.03	0.58
1:F:362:LEU:HD23	1:F:365:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:GLY:O	1:C:259:LEU:HG	2.04	0.58
1:F:114:ALA:O	1:F:154:ASN:HB3	2.03	0.58
1:C:361:ALA:O	1:C:365:ILE:HG13	2.03	0.58
1:D:6:LYS:O	1:D:10:LEU:HD13	2.03	0.58
1:D:114:ALA:O	1:D:154:ASN:HB3	2.03	0.58
1:F:78:ALA:O	1:F:82:ILE:HG13	2.04	0.58
1:B:29:ILE:HG22	1:B:36:ALA:HB1	1.86	0.58
1:B:37:ILE:O	1:B:41:VAL:HG23	2.04	0.57
1:A:184:SER:O	1:A:188:LYS:HG3	2.04	0.57
1:E:408:LYS:HD3	1:E:409:SER:H	1.66	0.57
1:F:306:THR:HA	1:F:313:GLN:HE21	1.70	0.57
1:E:86:GLY:O	1:E:90:VAL:HG12	2.05	0.57
1:E:401:GLN:O	1:E:405:GLU:HG2	2.04	0.57
1:D:21:GLU:HA	1:D:24:ARG:HB2	1.85	0.57
1:C:108:ARG:HD3	1:C:147:GLU:OE2	2.04	0.57
1:E:335:VAL:HG22	1:E:340:VAL:HG21	1.86	0.57
1:F:19:GLN:HG2	3:F:546:HOH:O	2.05	0.57
1:B:341:GLU:OE2	1:B:345:LYS:HE3	2.04	0.57
1:B:356:LYS:CE	1:B:395:GLU:HB2	2.34	0.57
1:F:386:GLN:HA	1:F:389:LEU:HD13	1.87	0.57
1:F:377:VAL:HG12	1:F:382:VAL:CG2	2.35	0.57
1:A:99:ASP:HB3	1:A:102:VAL:HG23	1.85	0.57
1:A:88:VAL:O	1:A:92:VAL:HG23	2.05	0.57
1:E:335:VAL:HA	1:E:340:VAL:HG23	1.87	0.57
1:C:137:LEU:HD11	1:C:152:LEU:HD12	1.85	0.57
1:F:369:PRO:O	1:F:373:ILE:HG13	2.04	0.56
1:A:238:ASN:OD1	1:A:276:ARG:NH2	2.35	0.56
1:C:37:ILE:O	1:C:41:VAL:HG23	2.06	0.56
1:B:383:GLU:O	1:B:386:GLN:HB2	2.05	0.56
1:F:67:ALA:O	1:F:71:ILE:HG13	2.06	0.56
1:E:104:LYS:CD	1:E:143:GLU:HG3	2.36	0.56
1:C:263:LEU:HD11	1:C:278:LEU:HD12	1.86	0.56
1:B:413:LEU:HD21	3:B:586:HOH:O	2.05	0.56
1:E:24:ARG:HH22	1:F:394:SER:CB	2.19	0.56
1:E:197:ILE:HG22	1:E:204:ALA:HB1	1.88	0.56
1:B:52:LEU:HB3	3:B:593:HOH:O	2.06	0.56
1:F:104:LYS:HD2	1:F:143:GLU:CG	2.35	0.56
1:F:57:ASP:HB3	1:F:60:VAL:CG2	2.35	0.56
1:A:344:VAL:HG13	1:A:384:VAL:HG11	1.87	0.56
1:B:2:ASN:ND2	1:B:5:GLU:HG2	2.21	0.55
1:D:403:ALA:O	1:D:407:ILE:HG13	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:227:GLU:OE1	1:F:227:GLU:N	2.39	0.55
1:F:227:GLU:HB3	3:F:542:HOH:O	2.05	0.55
1:D:20:LYS:CG	1:D:60:VAL:HG22	2.37	0.55
1:F:5:GLU:O	1:F:8:VAL:HB	2.06	0.55
1:F:384:VAL:HG23	1:F:387:LYS:NZ	2.21	0.55
1:E:221:LEU:HD11	1:E:236:LEU:CD1	2.37	0.55
1:C:397:GLN:NE2	3:C:759:HOH:O	2.39	0.55
1:E:152:LEU:HD23	1:E:155:ILE:HD12	1.89	0.55
1:A:332:LYS:HE3	1:C:173:GLU:OE2	2.07	0.55
1:E:57:ASP:HB3	1:E:60:VAL:CG2	2.37	0.55
1:E:318:ARG:HB2	1:E:357:GLU:OE2	2.06	0.55
1:F:177:LYS:N	3:F:508:HOH:O	2.41	0.54
1:A:405:GLU:HG2	3:A:800:HOH:O	2.07	0.54
1:E:256:VAL:O	1:E:260:VAL:HG23	2.07	0.54
1:C:137:LEU:HD11	1:C:152:LEU:CD1	2.36	0.54
1:E:108:ARG:HB2	1:E:147:GLU:HG2	1.89	0.54
1:E:286:ASP:OD1	1:E:327:PRO:HD3	2.07	0.54
1:E:406:ASN:HD22	1:E:406:ASN:N	2.05	0.54
1:B:41:VAL:HG12	1:B:41:VAL:O	2.07	0.54
1:E:304:LEU:HD22	1:E:312:VAL:CG1	2.37	0.54
1:A:298:VAL:O	1:A:302:VAL:HG23	2.08	0.54
1:C:2:ASN:CG	1:C:5:GLU:HG3	2.27	0.54
1:E:301:LEU:O	1:E:305:LEU:HG	2.07	0.54
1:F:377:VAL:HG12	1:F:382:VAL:HG23	1.88	0.54
1:F:15:ASP:OD1	1:F:18:THR:N	2.40	0.54
1:F:104:LYS:HB3	1:F:104:LYS:NZ	2.23	0.54
1:E:298:VAL:O	1:E:302:VAL:HG23	2.08	0.54
3:B:563:HOH:O	1:C:142:SER:HB2	2.08	0.54
1:D:69:ALA:HB1	1:D:108:ARG:HE	1.73	0.54
1:A:384:VAL:HA	1:A:387:LYS:HE3	1.90	0.54
1:D:405:GLU:O	1:D:409:SER:HB3	2.07	0.54
1:E:319:ALA:O	1:E:323:ILE:HG13	2.08	0.54
1:F:20:LYS:HB3	1:F:24:ARG:HH12	1.73	0.54
1:D:104:LYS:HG3	1:D:105:GLU:N	2.23	0.54
1:E:12:THR:HG22	1:E:48:VAL:HG21	1.89	0.54
1:F:100:SER:CA	1:F:103:GLN:HE21	2.15	0.53
1:A:67:ALA:O	1:A:71:ILE:HG13	2.07	0.53
1:B:94:LEU:HD22	1:B:102:VAL:HG11	1.90	0.53
1:E:374:LYS:HA	1:E:377:VAL:HG22	1.89	0.53
1:B:196:ASN:OD1	1:B:234:ARG:NH2	2.37	0.53
1:E:151:ALA:O	1:E:155:ILE:HG13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:370:THR:HA	1:F:373:ILE:HD12	1.90	0.53
1:F:83:VAL:HG13	1:F:88:VAL:HG11	1.90	0.53
1:B:20:LYS:NZ	1:B:59:GLU:HB2	2.22	0.53
1:E:79:ILE:CG2	1:E:113:ILE:HG23	2.39	0.53
1:F:8:VAL:O	1:F:11:LEU:HB2	2.09	0.53
1:F:374:LYS:CE	3:F:509:HOH:O	2.56	0.53
1:E:37:ILE:HD11	1:E:71:ILE:CA	2.37	0.53
1:B:356:LYS:HE3	1:B:395:GLU:HB2	1.90	0.53
1:C:272:LYS:CD	1:C:311:GLU:HB3	2.38	0.53
1:C:263:LEU:HB3	1:C:304:LEU:HD11	1.91	0.53
1:D:11:LEU:O	1:D:19:GLN:HG2	2.09	0.53
1:E:91:LEU:HD21	1:E:109:ALA:CB	2.38	0.53
1:B:146:LYS:HG2	3:B:587:HOH:O	2.08	0.53
1:E:164:LYS:O	1:E:167:VAL:HG12	2.09	0.53
1:F:179:LEU:HD11	1:F:194:LEU:CD1	2.40	0.52
1:D:90:VAL:O	1:D:93:LYS:HB3	2.09	0.52
1:E:7:LEU:HD22	1:E:26:LEU:HG	1.91	0.52
1:D:24:ARG:HH11	1:D:24:ARG:HG3	1.75	0.52
1:F:328:ASP:OD2	1:F:369:PRO:HD3	2.09	0.52
1:F:299:GLU:HB2	3:F:520:HOH:O	2.09	0.52
1:D:341:GLU:OE1	1:D:379:ALA:HB2	2.10	0.52
1:C:3:ASP:O	1:C:7:LEU:HG	2.08	0.52
1:A:384:VAL:O	1:A:387:LYS:HG2	2.09	0.52
1:C:192:ARG:HA	1:C:231:GLU:OE1	2.09	0.52
1:E:380:GLY:O	1:E:384:VAL:HG23	2.10	0.52
1:B:256:VAL:O	1:B:260:VAL:HG23	2.09	0.52
1:C:163:ILE:O	1:C:167:VAL:HG23	2.10	0.52
1:F:118:ASP:HB3	1:F:159:PRO:HD3	1.91	0.52
1:D:49:LEU:HD21	1:D:67:ALA:CB	2.40	0.52
1:E:38:LYS:HG3	1:E:42:ASP:OD2	2.10	0.52
1:F:37:ILE:CG2	1:F:71:ILE:HG23	2.40	0.52
1:D:163:ILE:CG2	1:D:197:ILE:HG23	2.38	0.52
1:F:49:LEU:HD11	1:F:67:ALA:HB1	1.91	0.52
1:E:355:GLN:HE21	1:E:396:VAL:HG21	1.74	0.52
1:C:53:LEU:HD11	1:C:68:LEU:CD1	2.40	0.52
1:D:8:VAL:HG21	1:D:43:ALA:HB1	1.92	0.52
1:A:122:LYS:HG2	1:A:126:ASP:OD2	2.10	0.52
1:C:221:LEU:HD11	1:C:236:LEU:HD12	1.92	0.52
1:C:374:LYS:HG2	1:C:378:ASP:OD2	2.10	0.51
1:B:329:GLU:CD	1:B:329:GLU:H	2.14	0.51
1:D:11:LEU:HD12	1:D:22:ALA:CB	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:LYS:HD3	3:F:535:HOH:O	2.09	0.51
1:A:25:ASP:O	1:A:29:ILE:HG13	2.10	0.51
1:E:136:LEU:HD23	1:E:136:LEU:H	1.75	0.51
1:C:314:LYS:HD3	1:C:353:GLU:CD	2.31	0.51
1:E:340:VAL:O	1:E:344:VAL:HG13	2.10	0.51
1:E:24:ARG:HG3	1:E:63:GLU:HG2	1.93	0.51
1:E:314:LYS:HD3	1:E:353:GLU:HB2	1.93	0.51
1:F:363:ALA:HB3	1:F:402:ARG:NH2	2.25	0.51
1:E:37:ILE:O	1:E:41:VAL:HG23	2.10	0.51
1:F:45:GLY:O	1:F:49:LEU:HB2	2.11	0.51
1:E:121:ILE:HG23	1:E:155:ILE:HG23	1.92	0.51
1:B:66:ARG:HG3	1:B:105:GLU:OE2	2.11	0.51
1:B:205:ILE:O	1:B:209:VAL:HG23	2.11	0.51
1:B:59:GLU:HA	1:B:62:LYS:HE3	1.92	0.51
1:F:152:LEU:HD23	3:F:548:HOH:O	2.11	0.51
1:D:231:GLU:HA	1:D:231:GLU:OE1	2.11	0.51
1:E:185:GLU:OE2	1:E:185:GLU:N	2.42	0.50
1:F:4:VAL:HG11	1:F:40:ILE:HD13	1.93	0.50
1:E:121:ILE:CG2	1:E:155:ILE:HG23	2.41	0.50
1:E:11:LEU:O	1:E:19:GLN:HG3	2.10	0.50
1:F:386:GLN:O	1:F:389:LEU:HD13	2.11	0.50
1:A:340:VAL:O	1:A:344:VAL:HG23	2.11	0.50
1:F:306:THR:HA	1:F:313:GLN:NE2	2.26	0.50
1:B:60:VAL:CG1	1:B:61:GLN:N	2.75	0.50
1:F:4:VAL:CG1	1:F:40:ILE:HD13	2.41	0.50
1:E:20:LYS:O	1:E:24:ARG:HG3	2.11	0.50
1:D:374:LYS:HG2	1:D:378:ASP:OD2	2.11	0.50
1:E:194:LEU:HA	1:E:197:ILE:HD12	1.94	0.50
1:F:131:GLU:H	1:F:131:GLU:CD	2.15	0.50
1:A:381:GLY:HA2	1:A:384:VAL:HG12	1.92	0.50
1:C:272:LYS:HD2	1:C:311:GLU:HB3	1.94	0.50
1:B:286:ASP:OD2	1:B:327:PRO:HD3	2.11	0.50
1:A:221:LEU:HB3	1:A:262:LEU:HD11	1.94	0.50
1:D:88:VAL:O	1:D:92:VAL:HG23	2.12	0.50
1:B:57:ASP:O	1:B:61:GLN:HG2	2.12	0.50
1:A:24:ARG:HG3	1:A:63:GLU:CG	2.42	0.50
1:E:383:GLU:CD	1:E:383:GLU:H	2.14	0.50
1:C:20:LYS:HE2	1:C:59:GLU:HB3	1.94	0.50
1:D:108:ARG:HG3	1:D:147:GLU:OE2	2.12	0.50
1:F:218:VAL:HA	1:F:221:LEU:HD12	1.94	0.50
1:F:145:GLN:HG3	1:F:146:LYS:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:PRO:HB2	1:B:287:GLU:OE1	2.11	0.49
1:B:67:ALA:O	1:B:71:ILE:HG13	2.11	0.49
1:B:380:GLY:O	1:B:384:VAL:HG23	2.12	0.49
1:F:188:LYS:CG	1:F:228:VAL:HG22	2.42	0.49
1:B:80:LYS:HG2	1:B:84:ASP:OD1	2.12	0.49
1:E:24:ARG:CG	1:E:63:GLU:HG2	2.42	0.49
1:B:11:LEU:HD11	1:B:26:LEU:HD12	1.94	0.49
1:E:104:LYS:CE	1:E:105:GLU:HG3	2.42	0.49
1:A:47:GLU:CD	1:A:47:GLU:N	2.65	0.49
1:A:160:ASP:OD2	1:A:201:PRO:HD3	2.12	0.49
1:C:185:GLU:O	1:C:189:GLU:HG2	2.12	0.49
1:B:10:LEU:HD23	1:B:22:ALA:CB	2.42	0.49
1:E:155:ILE:HG22	1:E:162:ALA:HB1	1.93	0.49
1:A:302:VAL:O	1:A:305:LEU:HB2	2.12	0.49
1:E:363:ALA:HB2	1:E:403:ALA:HB2	1.95	0.49
1:E:152:LEU:HA	1:E:155:ILE:HD12	1.95	0.49
1:C:373:ILE:O	1:C:377:VAL:HG22	2.12	0.49
1:E:287:GLU:HG3	1:E:288:ALA:N	2.27	0.49
1:A:11:LEU:O	1:A:19:GLN:HG3	2.12	0.49
1:A:172:VAL:HG11	1:A:208:ILE:HA	1.94	0.49
1:F:69:ALA:HB1	1:F:108:ARG:CZ	2.42	0.49
1:B:11:LEU:HD23	1:B:22:ALA:HB3	1.94	0.49
1:F:30:ALA:O	1:F:37:ILE:HD11	2.13	0.49
1:E:179:LEU:HB3	1:E:220:LEU:HD11	1.95	0.49
1:E:179:LEU:HD22	1:E:220:LEU:CD1	2.42	0.49
1:F:79:ILE:CG2	1:F:113:ILE:HG23	2.43	0.49
1:D:15:ASP:HB3	1:D:18:THR:OG1	2.13	0.49
1:F:83:VAL:HG13	1:F:88:VAL:CG1	2.43	0.49
1:B:2:ASN:HD22	1:B:5:GLU:CG	2.26	0.48
1:E:263:LEU:HD21	1:E:278:LEU:HD12	1.95	0.48
1:B:292:ILE:HG21	1:B:323:ILE:HD11	1.94	0.48
1:A:147:GLU:HA	1:A:147:GLU:OE1	2.12	0.48
1:D:382:VAL:O	1:D:386:GLN:HG3	2.13	0.48
1:A:244:ASP:CG	1:A:285:PRO:HD3	2.34	0.48
1:F:290:LYS:CA	1:F:293:VAL:HG22	2.41	0.48
1:E:374:LYS:O	1:E:378:ASP:HB2	2.13	0.48
1:E:5:GLU:O	1:E:9:LYS:HG2	2.13	0.48
1:A:121:ILE:O	1:A:125:VAL:HG23	2.13	0.48
1:A:185:GLU:HG3	1:D:311:GLU:HG2	1.94	0.48
1:F:290:LYS:HA	1:F:293:VAL:CG2	2.42	0.48
1:F:122:LYS:HG3	1:F:126:ASP:OD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:ARG:HA	1:A:231:GLU:OE1	2.14	0.48
1:D:10:LEU:HB3	1:D:22:ALA:CB	2.43	0.48
1:F:188:LYS:HG2	1:F:228:VAL:HG22	1.96	0.48
1:E:343:LEU:HD22	1:E:358:ALA:HA	1.96	0.48
1:E:29:ILE:HB	1:E:40:ILE:HD11	1.94	0.48
1:E:321:ALA:HB3	1:E:360:ARG:NH2	2.28	0.48
1:A:256:VAL:O	1:A:260:VAL:HG23	2.14	0.48
1:F:155:ILE:HD12	3:F:548:HOH:O	2.14	0.48
1:E:99:ASP:HB2	1:E:102:VAL:HB	1.96	0.48
1:D:399:GLU:OE1	1:D:399:GLU:HA	2.13	0.47
1:A:367:SER:HB3	1:A:406:ASN:ND2	2.29	0.47
1:F:272:LYS:CD	1:F:311:GLU:HB3	2.40	0.47
1:E:389:LEU:HD21	1:E:404:LEU:CD1	2.44	0.47
1:A:394:SER:O	1:A:398:LYS:HG3	2.14	0.47
1:D:59:GLU:HA	1:D:59:GLU:OE1	2.14	0.47
1:A:315:GLU:HA	1:A:315:GLU:OE1	2.15	0.47
1:E:90:VAL:HG13	1:E:91:LEU:N	2.30	0.47
1:F:225:ASP:OD2	1:F:227:GLU:HG2	2.14	0.47
1:A:263:LEU:HD11	1:A:278:LEU:CD1	2.44	0.47
1:D:384:VAL:O	1:D:388:LEU:HD13	2.14	0.47
1:E:122:LYS:HE2	1:E:126:ASP:OD2	2.14	0.47
1:B:109:ALA:O	1:B:113:ILE:HG13	2.14	0.47
1:F:104:LYS:HB3	1:F:104:LYS:HZ3	1.79	0.47
1:F:341:GLU:N	3:F:523:HOH:O	2.47	0.47
1:A:331:ILE:HG23	1:A:365:ILE:HG23	1.95	0.47
1:B:13:SER:OG	1:B:18:THR:HG21	2.14	0.47
1:D:21:GLU:CA	1:D:24:ARG:HB2	2.45	0.47
1:F:151:ALA:O	1:F:155:ILE:HG13	2.14	0.47
1:C:176:VAL:O	1:C:179:LEU:HB2	2.15	0.47
1:A:332:LYS:HZ3	1:A:336:ASP:CG	2.18	0.47
1:E:299:GLU:O	1:E:302:VAL:HB	2.15	0.47
1:B:24:ARG:HG3	1:B:63:GLU:CG	2.45	0.47
1:D:33:PRO:HG2	1:D:36:ALA:HB2	1.97	0.47
1:D:87:GLY:O	1:D:91:LEU:HG	2.15	0.47
1:E:30:ALA:C	1:E:32:GLY:H	2.17	0.47
1:E:188:LYS:NZ	1:E:225:ASP:OD2	2.43	0.47
1:E:2:ASN:OD1	1:E:5:GLU:HG3	2.15	0.47
1:F:39:ALA:O	1:F:42:ASP:HB3	2.15	0.47
1:B:261:LYS:NZ	3:B:537:HOH:O	2.47	0.47
1:F:356:LYS:O	1:F:356:LYS:HD2	2.14	0.47
1:F:174:VAL:C	3:F:508:HOH:O	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:ALA:O	1:E:37:ILE:HG22	2.15	0.47
1:E:24:ARG:CZ	1:F:394:SER:HB2	2.45	0.46
1:C:105:GLU:OE1	1:C:108:ARG:NH2	2.46	0.46
1:A:332:LYS:HD3	3:A:785:HOH:O	2.15	0.46
1:B:78:ALA:O	1:B:81:ALA:HB3	2.15	0.46
1:B:216:VAL:O	1:B:220:LEU:HD13	2.15	0.46
1:B:2:ASN:HB3	1:B:5:GLU:OE1	2.15	0.46
1:F:403:ALA:O	1:F:407:ILE:HG13	2.14	0.46
1:A:94:LEU:HA	3:A:792:HOH:O	2.16	0.46
1:F:61:GLN:HG2	3:F:530:HOH:O	2.13	0.46
1:E:360:ARG:HH11	1:E:360:ARG:HG2	1.81	0.46
1:F:88:VAL:HG11	1:F:123:ALA:HB1	1.96	0.46
1:A:361:ALA:O	1:A:365:ILE:HG13	2.15	0.46
1:F:33:PRO:O	1:F:36:ALA:HB3	2.16	0.46
1:C:332:LYS:HE2	1:C:336:ASP:OD1	2.16	0.46
1:E:304:LEU:HD22	1:E:312:VAL:HG12	1.97	0.46
1:F:175:LEU:O	1:F:179:LEU:HG	2.16	0.46
1:D:45:GLY:O	1:D:49:LEU:HB2	2.15	0.46
1:F:121:ILE:HA	1:F:124:ILE:HD12	1.97	0.46
1:B:366:ALA:O	1:B:406:ASN:HB3	2.16	0.46
1:E:289:ILE:O	1:E:293:VAL:HG23	2.15	0.46
1:C:314:LYS:CG	1:C:353:GLU:HB3	2.45	0.46
1:D:49:LEU:HD21	1:D:67:ALA:HB1	1.96	0.46
1:A:327:PRO:HB2	1:A:329:GLU:OE1	2.16	0.46
1:A:230:LYS:HD2	1:D:227:GLU:OE2	2.15	0.46
1:F:276:ARG:HA	1:F:315:GLU:CG	2.46	0.46
1:D:4:VAL:O	1:D:8:VAL:HG23	2.16	0.46
1:B:42:ASP:C	1:B:44:GLY:H	2.19	0.46
1:E:408:LYS:HD3	1:E:409:SER:OG	2.16	0.46
1:C:374:LYS:O	1:C:377:VAL:HG23	2.15	0.46
1:B:24:ARG:HG3	1:B:63:GLU:HG2	1.98	0.46
1:D:304:LEU:HD22	1:D:312:VAL:HG11	1.97	0.46
1:E:70:ASN:HD22	1:E:70:ASN:N	2.13	0.46
1:D:227:GLU:HA	1:D:230:LYS:HE2	1.98	0.45
1:F:230:LYS:HD3	1:F:269:GLU:HB3	1.98	0.45
1:F:179:LEU:HD11	1:F:194:LEU:HD12	1.98	0.45
1:E:153:ALA:HB2	1:E:193:ALA:HB2	1.98	0.45
1:E:394:SER:O	1:E:398:LYS:HG3	2.16	0.45
1:F:60:VAL:O	1:F:60:VAL:HG12	2.16	0.45
1:A:95:LEU:HD11	1:A:110:LEU:CD1	2.46	0.45
1:C:332:LYS:HE2	1:C:336:ASP:OD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:288:ALA:O	1:F:291:ALA:HB3	2.17	0.45
1:B:57:ASP:C	1:B:59:GLU:N	2.69	0.45
1:F:118:ASP:OD1	1:F:158:GLY:HA2	2.16	0.45
1:B:2:ASN:O	1:B:6:LYS:HG2	2.16	0.45
1:C:396:VAL:CG1	1:C:397:GLN:N	2.79	0.45
1:F:197:ILE:HG22	1:F:208:ILE:HD11	1.98	0.45
1:C:66:ARG:NH2	3:C:745:HOH:O	2.48	0.45
1:B:55:SER:OG	1:B:60:VAL:HG11	2.17	0.45
1:E:408:LYS:CD	1:E:409:SER:N	2.74	0.45
1:D:21:GLU:C	1:D:24:ARG:HB2	2.37	0.45
1:B:327:PRO:O	1:B:330:ALA:HB3	2.16	0.45
1:D:305:LEU:HD11	1:D:320:LEU:HD12	1.99	0.45
1:A:287:GLU:O	1:A:290:LYS:HB3	2.17	0.45
1:B:55:SER:OG	1:B:56:THR:N	2.47	0.45
1:E:332:LYS:HG2	1:E:336:ASP:OD2	2.17	0.45
1:E:34:ALA:HA	1:E:37:ILE:CG2	2.42	0.45
1:E:91:LEU:HD21	1:E:109:ALA:HB3	1.97	0.45
1:F:221:LEU:O	1:F:262:LEU:HD11	2.16	0.45
1:E:45:GLY:O	1:E:49:LEU:HD13	2.17	0.45
1:F:351:ASP:HB3	1:F:354:VAL:CG1	2.36	0.45
1:A:114:ALA:HB1	1:A:155:ILE:HG13	1.98	0.45
1:B:114:ALA:O	1:B:154:ASN:HB3	2.16	0.45
1:A:341:GLU:O	1:A:345:LYS:HG2	2.16	0.45
1:C:327:PRO:O	1:C:330:ALA:HB3	2.17	0.45
1:A:388:LEU:HD22	1:A:396:VAL:HG11	1.99	0.45
1:E:137:LEU:HD22	1:E:178:LEU:CD2	2.47	0.45
1:F:256:VAL:O	1:F:260:VAL:HG23	2.16	0.45
1:B:15:ASP:CB	1:B:18:THR:HG22	2.42	0.44
1:E:108:ARG:CB	1:E:147:GLU:HG2	2.47	0.44
1:E:289:ILE:HG23	1:E:323:ILE:HG23	1.99	0.44
1:C:406:ASN:HD22	1:C:406:ASN:N	2.15	0.44
1:E:347:LEU:HD21	1:E:362:LEU:HD12	1.99	0.44
1:F:135:LYS:C	1:F:137:LEU:H	2.21	0.44
1:C:403:ALA:O	1:C:407:ILE:HG13	2.17	0.44
1:C:11:LEU:HD11	1:C:26:LEU:CD1	2.48	0.44
1:F:57:ASP:CB	1:F:60:VAL:HG23	2.46	0.44
1:D:163:ILE:O	1:D:167:VAL:HG23	2.17	0.44
1:F:361:ALA:O	1:F:365:ILE:HG13	2.18	0.44
1:C:99:ASP:HB3	1:C:102:VAL:HG23	1.98	0.44
1:D:122:LYS:HG3	1:D:161:GLU:OE1	2.17	0.44
1:E:408:LYS:NZ	1:E:409:SER:OG	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:178:LEU:C	1:F:180:THR:H	2.20	0.44
1:E:19:GLN:OE1	1:E:60:VAL:HG11	2.17	0.44
1:E:406:ASN:N	1:E:406:ASN:ND2	2.65	0.44
1:C:272:LYS:HD3	1:C:311:GLU:HB3	2.00	0.44
1:D:164:LYS:HG2	1:D:168:ASP:OD2	2.18	0.44
1:B:121:ILE:HG23	1:B:155:ILE:HG23	1.99	0.44
1:B:20:LYS:HZ1	1:B:59:GLU:HB2	1.82	0.44
1:F:110:LEU:HD23	1:F:113:ILE:HD12	1.99	0.44
1:E:141:ASP:HB3	1:E:144:VAL:CG1	2.45	0.44
1:F:389:LEU:HD11	1:F:404:LEU:CD1	2.48	0.44
1:E:27:ALA:O	1:E:30:ALA:HB3	2.18	0.44
1:F:129:GLY:O	1:F:132:VAL:HG13	2.18	0.44
1:D:361:ALA:O	1:D:365:ILE:HG13	2.17	0.44
1:C:230:LYS:HD2	1:C:269:GLU:HB3	2.00	0.44
1:F:393:ASP:HB3	1:F:396:VAL:CG1	2.46	0.44
1:C:305:LEU:HD11	1:C:320:LEU:CD1	2.47	0.44
1:F:235:ALA:O	1:F:239:ILE:HG13	2.18	0.44
1:E:311:GLU:OE1	1:F:185:GLU:HG3	2.18	0.44
1:B:46:VAL:O	1:B:48:VAL:N	2.51	0.44
1:D:11:LEU:HD23	1:D:48:VAL:HG12	2.00	0.44
1:E:122:LYS:HB2	1:E:122:LYS:HE3	1.78	0.44
1:B:88:VAL:O	1:B:92:VAL:HG23	2.17	0.44
1:D:132:VAL:O	1:D:136:LEU:HD13	2.18	0.44
1:B:347:LEU:HD11	1:B:362:LEU:CD1	2.48	0.44
1:E:177:LYS:HD2	1:E:177:LYS:O	2.18	0.44
1:F:16:SER:O	1:F:20:LYS:HG3	2.19	0.43
1:E:225:ASP:O	1:E:229:GLN:HG3	2.18	0.43
1:F:60:VAL:O	1:F:64:ALA:HB2	2.18	0.43
1:E:356:LYS:HG3	1:E:357:GLU:N	2.33	0.43
1:A:221:LEU:HD22	1:A:262:LEU:CD1	2.49	0.43
1:D:33:PRO:O	1:D:36:ALA:HB3	2.18	0.43
1:E:205:ILE:HG23	1:E:239:ILE:HG23	2.00	0.43
1:E:24:ARG:HH12	1:F:394:SER:CB	2.29	0.43
1:E:334:ILE:HG21	1:E:365:ILE:HD11	2.00	0.43
1:E:327:PRO:O	1:E:331:ILE:HG13	2.18	0.43
1:B:257:GLU:HB2	3:B:576:HOH:O	2.18	0.43
1:D:283:SER:HB3	3:D:538:HOH:O	2.18	0.43
1:B:87:GLY:O	1:B:91:LEU:HD12	2.17	0.43
1:F:322:ASN:OD1	1:F:360:ARG:NH2	2.50	0.43
1:E:324:ALA:O	1:E:364:ASN:HB3	2.18	0.43
1:D:293:VAL:HA	3:D:508:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:21:GLU:HA	1:D:24:ARG:CD	2.46	0.43
1:E:227:GLU:OE2	1:E:230:LYS:HE2	2.18	0.43
1:C:286:ASP:CG	1:C:327:PRO:HD3	2.38	0.43
1:F:251:VAL:HG22	1:F:256:VAL:HG21	1.99	0.43
1:F:290:LYS:O	1:F:293:VAL:HG22	2.19	0.43
1:E:164:LYS:HG2	1:E:168:ASP:OD2	2.18	0.43
1:F:86:GLY:O	1:F:90:VAL:HG23	2.19	0.43
1:B:367:SER:HB2	1:B:413:LEU:HD11	2.00	0.43
1:F:327:PRO:O	1:F:331:ILE:HG13	2.18	0.43
1:E:189:GLU:OE1	1:E:192:ARG:NH1	2.51	0.43
1:B:50:VAL:HG11	1:B:85:ALA:O	2.18	0.43
1:D:21:GLU:O	1:D:24:ARG:HB2	2.18	0.43
1:F:286:ASP:OD2	1:F:327:PRO:HD3	2.18	0.43
1:D:179:LEU:HB2	1:D:216:VAL:HG11	2.01	0.43
1:F:143:GLU:HG3	1:F:143:GLU:O	2.18	0.43
1:E:45:GLY:O	1:E:48:VAL:HG12	2.18	0.43
1:F:363:ALA:HB1	1:F:402:ARG:CZ	2.49	0.43
1:B:11:LEU:CD2	1:B:22:ALA:HB3	2.49	0.43
1:D:18:THR:O	1:D:22:ALA:HB2	2.19	0.43
1:D:134:VAL:O	1:D:137:LEU:HB2	2.19	0.43
1:B:315:GLU:HA	1:B:315:GLU:OE1	2.19	0.43
1:D:347:LEU:HD11	1:D:362:LEU:CD1	2.49	0.43
1:F:68:LEU:HD23	1:F:71:ILE:HD12	2.00	0.43
1:F:101:GLU:HA	1:F:104:LYS:HZ3	1.84	0.43
1:E:133:LEU:HA	1:E:136:LEU:CD2	2.47	0.42
1:B:36:ALA:O	1:B:39:ALA:HB3	2.19	0.42
1:E:163:ILE:HG23	1:E:197:ILE:HG23	2.00	0.42
1:E:373:ILE:O	1:E:377:VAL:HG13	2.19	0.42
1:E:150:ARG:HG3	1:E:189:GLU:OE1	2.19	0.42
1:A:66:ARG:HD3	3:A:768:HOH:O	2.19	0.42
1:B:70:ASN:O	1:B:73:SER:HB3	2.19	0.42
1:A:401:GLN:OE1	1:A:401:GLN:HA	2.20	0.42
1:B:413:LEU:N	1:B:413:LEU:CD1	2.82	0.42
1:B:46:VAL:O	1:B:47:GLU:C	2.58	0.42
1:A:303:LYS:NZ	3:A:714:HOH:O	2.52	0.42
1:D:99:ASP:OD1	1:D:102:VAL:HB	2.19	0.42
1:E:136:LEU:HD12	1:E:144:VAL:HG22	2.02	0.42
1:A:206:LYS:HE3	3:A:728:HOH:O	2.20	0.42
1:C:117:PRO:HG2	3:C:785:HOH:O	2.19	0.42
1:F:53:LEU:HD11	1:F:68:LEU:CD1	2.50	0.42
1:B:15:ASP:O	1:B:19:GLN:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:ASP:CG	1:D:60:VAL:HG23	2.40	0.42
1:F:4:VAL:O	1:F:8:VAL:HG23	2.20	0.42
1:E:179:LEU:HD11	1:E:194:LEU:HD12	2.01	0.42
1:F:195:ALA:HA	1:F:235:ALA:HA	2.02	0.42
1:B:193:ALA:O	1:B:197:ILE:HG13	2.20	0.42
1:C:396:VAL:HG13	1:C:397:GLN:N	2.35	0.42
1:F:46:VAL:O	1:F:50:VAL:HG13	2.20	0.42
1:F:314:LYS:HD3	1:F:353:GLU:HB3	2.01	0.42
1:A:140:THR:HG23	3:A:774:HOH:O	2.19	0.42
1:F:11:LEU:HD22	1:F:22:ALA:CB	2.50	0.42
1:D:79:ILE:CG2	1:D:113:ILE:HG23	2.49	0.42
1:D:197:ILE:HG22	1:D:204:ALA:HB1	2.01	0.42
1:E:366:ALA:HB1	1:E:406:ASN:CB	2.47	0.42
1:F:227:GLU:CD	1:F:227:GLU:H	2.22	0.42
1:E:95:LEU:HD21	1:E:110:LEU:HD12	2.01	0.42
1:A:157:SER:O	2:A:601:ACT:C	2.68	0.42
1:A:273:GLU:OE1	1:A:276:ARG:NH1	2.53	0.42
1:B:413:LEU:CD2	3:B:586:HOH:O	2.65	0.42
1:E:289:ILE:CG2	1:E:323:ILE:HG23	2.50	0.42
1:F:91:LEU:O	1:F:94:LEU:HB2	2.20	0.42
1:C:245:GLU:CD	1:C:245:GLU:H	2.22	0.42
1:E:305:LEU:O	1:E:313:GLN:NE2	2.52	0.42
1:C:235:ALA:O	1:C:239:ILE:HG13	2.19	0.42
1:E:348:THR:O	1:E:348:THR:HG22	2.20	0.42
1:B:215:GLU:HG3	3:B:599:HOH:O	2.20	0.42
1:E:205:ILE:O	1:E:209:VAL:HG23	2.20	0.41
1:E:13:SER:C	1:E:15:ASP:N	2.74	0.41
1:F:225:ASP:OD2	1:F:228:VAL:HG23	2.21	0.41
1:F:289:ILE:O	1:F:292:ILE:N	2.52	0.41
1:B:12:THR:O	1:B:12:THR:HG22	2.20	0.41
1:F:390:THR:HG23	1:F:390:THR:O	2.20	0.41
1:D:104:LYS:HB2	1:D:104:LYS:HE3	1.79	0.41
1:D:110:LEU:HA	1:D:110:LEU:HD23	1.89	0.41
1:B:60:VAL:HG22	3:B:593:HOH:O	2.20	0.41
1:A:92:VAL:O	1:A:95:LEU:HB2	2.20	0.41
1:F:50:VAL:HG23	1:F:51:LYS:N	2.36	0.41
1:F:279:ALA:HB3	1:F:318:ARG:HH21	1.85	0.41
1:A:1:MET:HG2	1:A:5:GLU:OE1	2.21	0.41
1:D:16:SER:HB2	3:D:574:HOH:O	2.19	0.41
1:F:88:VAL:HG23	1:F:89:GLU:H	1.85	0.41
1:E:310:SER:CB	1:F:146:LYS:HZ2	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:LYS:HG2	1:E:252:ASP:OD2	2.20	0.41
1:E:268:SER:HB3	1:F:227:GLU:HG3	2.03	0.41
1:E:260:VAL:O	1:E:263:LEU:HB2	2.20	0.41
1:E:301:LEU:HD23	1:E:304:LEU:HD12	2.03	0.41
1:E:279:ALA:HB2	1:E:319:ALA:HB2	2.03	0.41
1:F:193:ALA:O	1:F:197:ILE:HG13	2.20	0.41
1:D:386:GLN:NE2	3:D:509:HOH:O	2.53	0.41
1:C:331:ILE:HD11	3:C:715:HOH:O	2.20	0.41
1:F:398:LYS:O	1:F:401:GLN:HG2	2.21	0.41
1:C:24:ARG:HD3	1:C:63:GLU:OE2	2.21	0.41
1:B:382:VAL:HG12	3:B:584:HOH:O	2.21	0.41
1:F:106:ALA:O	1:F:109:ALA:HB3	2.20	0.41
1:C:314:LYS:CD	1:C:353:GLU:HB3	2.51	0.41
1:E:362:LEU:HD23	1:E:365:ILE:HD12	2.03	0.41
1:E:18:THR:O	1:E:18:THR:HG22	2.21	0.41
1:C:179:LEU:HD22	1:C:220:LEU:CD1	2.50	0.41
1:F:381:GLY:O	1:F:384:VAL:HG12	2.21	0.41
1:E:172:VAL:HG11	1:E:208:ILE:HA	2.02	0.41
1:A:219:LYS:NZ	1:B:345:LYS:NZ	2.69	0.41
1:A:97:SER:N	3:A:792:HOH:O	2.54	0.41
1:A:181:SER:OG	1:A:182:THR:N	2.54	0.41
1:A:206:LYS:CE	3:A:712:HOH:O	2.68	0.41
1:E:179:LEU:HD22	1:E:220:LEU:HD11	2.02	0.41
1:E:357:GLU:OE1	1:E:357:GLU:HA	2.21	0.41
1:C:151:ALA:O	1:C:155:ILE:HG13	2.21	0.41
1:F:46:VAL:HG11	1:F:82:ILE:HG12	2.03	0.40
1:E:111:ALA:HB2	1:E:151:ALA:HB2	2.03	0.40
1:B:156:ALA:O	1:B:196:ASN:HB3	2.20	0.40
1:C:179:LEU:HD11	1:C:194:LEU:CD1	2.51	0.40
1:E:194:LEU:HD23	1:E:197:ILE:HD12	2.03	0.40
1:E:153:ALA:HB3	1:E:192:ARG:NH1	2.36	0.40
1:D:121:ILE:O	1:D:125:VAL:HG23	2.21	0.40
1:F:160:ASP:HA	1:F:163:ILE:HG13	2.04	0.40
1:D:24:ARG:NH1	1:D:63:GLU:HG3	2.37	0.40
1:F:20:LYS:O	1:F:24:ARG:HG3	2.20	0.40
1:F:46:VAL:HG13	1:F:68:LEU:CD2	2.51	0.40
1:F:344:VAL:O	1:F:347:LEU:HB2	2.21	0.40
1:E:118:ASP:HA	1:E:121:ILE:HD12	2.03	0.40
1:A:172:VAL:O	1:A:176:VAL:HG23	2.22	0.40
1:C:63:GLU:OE1	1:C:63:GLU:HA	2.20	0.40
1:A:79:ILE:O	1:A:83:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:251:VAL:HA	1:F:256:VAL:HG23	2.03	0.40
1:F:245:GLU:CD	1:F:245:GLU:H	2.24	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	411/420 (98%)	399 (97%)	12 (3%)	0	100	100
1	B	412/420 (98%)	390 (95%)	21 (5%)	1 (0%)	52	75
1	C	410/420 (98%)	405 (99%)	5 (1%)	0	100	100
1	D	413/420 (98%)	395 (96%)	18 (4%)	0	100	100
1	E	410/420 (98%)	384 (94%)	24 (6%)	2 (0%)	34	58
1	F	409/420 (97%)	363 (89%)	43 (10%)	3 (1%)	26	49
All	All	2465/2520 (98%)	2336 (95%)	123 (5%)	6 (0%)	52	75

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	54	THR
1	F	136	LEU
1	B	58	SER
1	E	75	PRO
1	F	33	PRO
1	E	46	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	308/317 (97%)	304 (99%)	4 (1%)	76	91
1	B	311/317 (98%)	307 (99%)	4 (1%)	76	91
1	C	307/317 (97%)	306 (100%)	1 (0%)	94	99
1	D	311/317 (98%)	307 (99%)	4 (1%)	76	91
1	E	309/317 (98%)	300 (97%)	9 (3%)	50	76
1	F	308/317 (97%)	300 (97%)	8 (3%)	54	78
All	All	1854/1902 (98%)	1824 (98%)	30 (2%)	70	88

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	GLU
1	A	142	SER
1	A	160	ASP
1	A	178	LEU
1	B	57	ASP
1	B	63	GLU
1	B	84	ASP
1	B	415	HIS
1	C	261	LYS
1	D	24	ARG
1	D	328	ASP
1	D	395	GLU
1	D	409	SER
1	E	7	LEU
1	E	96	THR
1	E	99	ASP
1	E	136	LEU
1	E	147	GLU
1	E	161	GLU
1	E	267	ASP
1	E	356	LYS
1	E	387	LYS

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Mol	Chain	Res	Type
1	F	63	GLU
1	F	88	VAL
1	F	227	GLU
1	F	262	LEU
1	F	290	LYS
1	F	328	ASP
1	F	353	GLU
1	F	386	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2	ASN
1	C	406	ASN
1	E	70	ASN
1	E	280	ASN
1	E	355	GLN
1	E	406	ASN
1	F	103	GLN
1	F	196	ASN
1	F	313	GLN
1	F	386	GLN
1	F	401	GLN
1	F	406	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	A	601	-	1,3,3	1.74	0	0,3,3	0.00	-
2	ACT	C	501	-	1,3,3	0.29	0	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACT	A	601	-	-	0/0/0/0	0/0/0/0
2	ACT	C	501	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ACT	1	0

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	413/420 (98%)	-0.00	4 (0%) 84 82	37, 56, 92, 118	0
1	B	414/420 (98%)	-0.02	6 (1%) 78 75	36, 54, 108, 169	0
1	C	412/420 (98%)	-0.02	5 (1%) 81 78	36, 54, 93, 124	0
1	D	415/420 (98%)	0.23	20 (4%) 34 29	35, 63, 127, 176	0
1	E	412/420 (98%)	0.79	65 (15%) 3 2	56, 103, 152, 196	0
1	F	411/420 (97%)	0.88	67 (16%) 2 1	61, 101, 155, 194	0
All	All	2477/2520 (98%)	0.31	167 (6%) 21 17	35, 71, 135, 196	0

All (167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	396	VAL	11.8
1	F	11	LEU	8.7
1	E	358	ALA	7.2
1	F	392	THR	6.1
1	E	393	ASP	5.9
1	E	397	GLN	5.8
1	F	354	VAL	5.7
1	F	23	ALA	5.7
1	F	25	ASP	5.6
1	E	6	LYS	5.6
1	E	10	LEU	5.5
1	D	22	ALA	5.5
1	F	400	ALA	5.3
1	E	102	VAL	5.1
1	E	30	ALA	5.0
1	F	21	GLU	5.0
1	F	410	GLY	4.9
1	E	391	SER	4.9
1	F	18	THR	4.9

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Mol	Chain	Res	Type	RSRZ
1	D	60	VAL	4.8
1	E	392	THR	4.8
1	E	96	THR	4.7
1	F	362	LEU	4.7
1	F	250	ILE	4.6
1	D	11	LEU	4.6
1	E	21	GLU	4.6
1	F	19	GLN	4.5
1	F	4	VAL	4.4
1	E	324	ALA	4.3
1	D	9	LYS	4.3
1	F	101	GLU	4.3
1	F	62	LYS	4.3
1	E	362	LEU	4.2
1	F	24	ARG	4.2
1	F	22	ALA	4.1
1	D	8	VAL	4.1
1	F	361	ALA	4.0
1	D	23	ALA	4.0
1	F	49	LEU	3.9
1	F	365	ILE	3.9
1	E	22	ALA	3.9
1	E	365	ILE	3.9
1	F	393	ASP	3.9
1	F	50	VAL	3.8
1	B	23	ALA	3.8
1	F	403	ALA	3.8
1	D	10	LEU	3.8
1	F	355	GLN	3.7
1	F	57	ASP	3.6
1	F	352	SER	3.6
1	F	61	GLN	3.6
1	F	366	ALA	3.5
1	E	17	GLU	3.5
1	E	400	ALA	3.5
1	D	46	VAL	3.5
1	E	16	SER	3.5
1	F	246	ALA	3.4
1	F	60	VAL	3.4
1	B	18	THR	3.4
1	F	8	VAL	3.4
1	E	37	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	405	GLU	3.3
1	E	46	VAL	3.3
1	E	40	ILE	3.3
1	F	63	GLU	3.3
1	A	411	GLY	3.3
1	F	26	LEU	3.2
1	E	11	LEU	3.2
1	E	14	THR	3.2
1	E	23	ALA	3.2
1	F	396	VAL	3.1
1	E	59	GLU	3.1
1	F	52	LEU	3.1
1	E	7	LEU	3.1
1	E	62	LYS	3.1
1	E	83	VAL	3.1
1	F	10	LEU	3.0
1	F	48	VAL	3.0
1	C	385	LEU	3.0
1	E	110	LEU	3.0
1	F	404	LEU	3.0
1	E	20	LYS	3.0
1	F	7	LEU	3.0
1	E	105	GLU	3.0
1	F	46	VAL	2.9
1	F	320	LEU	2.9
1	D	19	GLN	2.9
1	A	413	LEU	2.8
1	F	6	LYS	2.8
1	F	20	LYS	2.8
1	F	53	LEU	2.8
1	F	104	LYS	2.8
1	F	38	LYS	2.8
1	F	205	ILE	2.8
1	E	350	THR	2.8
1	C	353	GLU	2.8
1	C	396	VAL	2.7
1	E	354	VAL	2.7
1	F	163	ILE	2.7
1	E	186	VAL	2.7
1	F	102	VAL	2.7
1	D	63	GLU	2.6
1	F	323	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	91	LEU	2.6
1	D	45	GLY	2.6
1	D	7	LEU	2.6
1	E	53	LEU	2.6
1	F	16	SER	2.6
1	F	374	LYS	2.6
1	D	12	THR	2.6
1	F	209	VAL	2.6
1	F	143	GLU	2.6
1	D	64	ALA	2.5
1	F	314	LYS	2.5
1	E	41	VAL	2.5
1	E	79	ILE	2.5
1	E	304	LEU	2.5
1	E	343	LEU	2.5
1	E	366	ALA	2.5
1	E	106	ALA	2.4
1	E	407	ILE	2.4
1	F	245	GLU	2.4
1	E	355	GLN	2.4
1	D	52	LEU	2.4
1	E	412	TRP	2.4
1	E	312	VAL	2.4
1	B	8	VAL	2.4
1	E	29	ILE	2.3
1	D	102	VAL	2.3
1	D	18	THR	2.3
1	B	45	GLY	2.3
1	F	292	ILE	2.3
1	F	397	GLN	2.3
1	E	331	ILE	2.3
1	E	404	LEU	2.3
1	F	188	LYS	2.3
1	E	409	SER	2.2
1	F	346	LEU	2.2
1	F	66	ARG	2.2
1	E	398	LYS	2.2
1	B	52	LEU	2.2
1	E	137	LEU	2.2
1	E	25	ASP	2.2
1	F	1	MET	2.2
1	D	49	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	124	ILE	2.2
1	F	99	ASP	2.2
1	D	21	GLU	2.1
1	C	412	TRP	2.1
1	C	395	GLU	2.1
1	E	27	ALA	2.1
1	F	41	VAL	2.1
1	E	45	GLY	2.1
1	E	372	ALA	2.1
1	E	395	GLU	2.1
1	D	414	GLU	2.1
1	B	22	ALA	2.1
1	F	247	ILE	2.0
1	E	385	LEU	2.0
1	E	4	VAL	2.0
1	E	140	THR	2.0
1	F	127	ALA	2.0
1	A	396	VAL	2.0
1	E	48	VAL	2.0
1	E	144	VAL	2.0
1	E	52	LEU	2.0
1	A	412	TRP	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ACT	C	501	4/4	0.94	0.30	5.70	63,69,77,78	0
2	ACT	A	601	4/4	0.91	0.14	-	84,86,87,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.