



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:23 PM GMT

PDB ID : 4I6J
Title : A ubiquitin ligase-substrate complex
Authors : Xing, W.; Busino, L.; Hinds, T.R.; Marionni, S.T.; Saifee, N.H.; Bush, M.F.; Pagano, M.; Zheng, N.
Deposited on : 2012-11-29
Resolution : 2.70 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

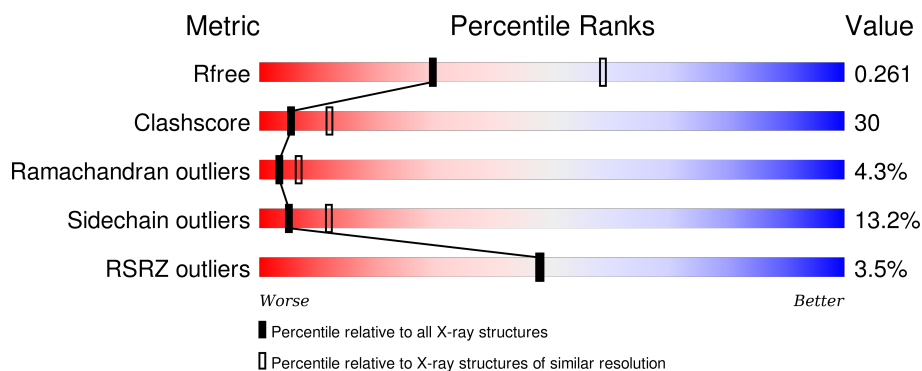
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	544	<div> <div>19%</div> <div>53%</div> <div>32%</div> <div>6%</div> <div>8%</div> </div>
2	B	428	<div> <div>54%</div> <div>30%</div> <div>7%</div> <div>8%</div> </div>
3	C	163	<div> <div>18%</div> <div>45%</div> <div>15%</div> <div>20%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8435 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 Cryptochrome-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	0	0
			4079	2616	723	718	22			

- Molecule 2 is a protein called F-box/LRR-repeat protein 3.

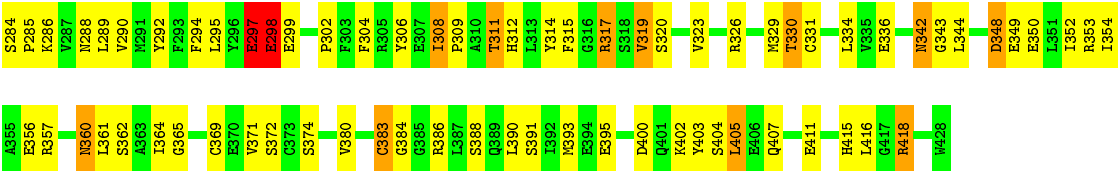
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	394	Total	C	N	O	S	0	0	0
			3156	2022	538	574	22			

- Molecule 3 is a protein called S-phase kinase-associated protein 1.

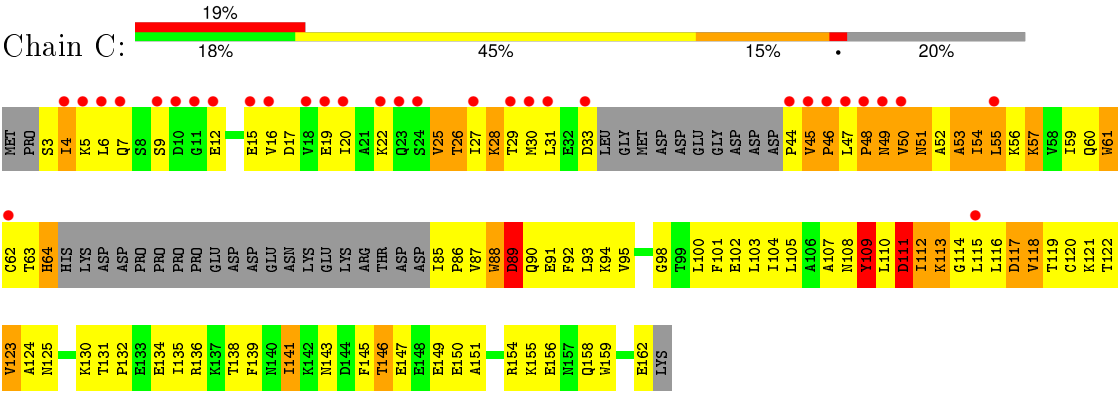
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	130	Total	C	N	O	S	0	0	0
			1044	667	168	204	5			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	93	Total	O	0	0
			93	93		
4	B	58	Total	O	0	0
			58	58		
4	C	5	Total	O	0	0
			5	5		



• Molecule 3: S-phase kinase-associated protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.39Å 125.39Å 145.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.52 – 2.70 48.57 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.52-2.70) 93.6 (48.57-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.27 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.203 , 0.265 0.200 , 0.261	Depositor DCC
R_{free} test set	1771 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.283	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 43.8	EDS
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 46412 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8435	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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	0.48	1/4195 (0.0%)	0.64	1/5691 (0.0%)
2	B	0.46	0/3233	0.63	0/4384
3	C	0.38	0/1059	0.58	0/1430
All	All	0.46	1/8487 (0.0%)	0.63	1/11505 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	342	PRO	N-CD	5.23	1.55	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	341	ASN	C-N-CD	5.60	140.16	128.40

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	4079	0	4012	201	0
2	B	3156	0	3153	169	0
3	C	1044	0	1054	143	0
4	A	93	0	0	10	0
4	B	58	0	0	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	5	0	0	0	0
All	All	8435	0	8219	495	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 30.

All (495) 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)
3:C:112:ILE:HG22	3:C:115:LEU:N	1.57	1.20
2:B:311:THR:HG23	2:B:312:HIS:CD2	1.77	1.20
3:C:112:ILE:CG2	3:C:115:LEU:H	1.52	1.19
3:C:112:ILE:HG21	3:C:115:LEU:CB	1.74	1.17
2:B:216:ILE:HD11	2:B:235:LEU:HB3	1.11	1.06
3:C:112:ILE:CG2	3:C:115:LEU:HB2	1.85	1.05
1:A:155:ARG:HG3	1:A:155:ARG:HH11	1.26	0.99
2:B:263:ASN:HB2	2:B:264:PRO:HD3	1.44	0.99
2:B:278:ASP:HB3	4:B:557:HOH:O	1.59	0.99
1:A:21:ALA:O	1:A:47:ARG:HB3	1.64	0.98
2:B:311:THR:CG2	2:B:312:HIS:HD2	1.77	0.97
3:C:112:ILE:HG22	3:C:115:LEU:H	0.82	0.97
2:B:202:LEU:CD2	4:B:545:HOH:O	2.12	0.96
1:A:47:ARG:O	1:A:196:CYS:HB3	1.65	0.96
2:B:216:ILE:HD11	2:B:235:LEU:CB	1.96	0.95
3:C:51:ASN:ND2	3:C:54:ILE:HD11	1.80	0.95
2:B:278:ASP:CA	4:B:557:HOH:O	2.15	0.93
2:B:286:LYS:O	4:B:516:HOH:O	1.86	0.92
2:B:311:THR:HG23	2:B:312:HIS:HD2	1.16	0.92
2:B:350:GLU:HA	4:B:548:HOH:O	1.70	0.91
1:A:21:ALA:N	1:A:47:ARG:HB2	1.88	0.89
1:A:47:ARG:O	1:A:196:CYS:CB	2.20	0.89
2:B:182:THR:HG22	2:B:184:VAL:HG22	1.55	0.89
1:A:47:ARG:HG3	1:A:48:CYS:H	1.39	0.88
1:A:227:VAL:HG21	1:A:368:GLU:HG2	1.54	0.87
1:A:40:LEU:HD23	1:A:188:VAL:HG12	1.57	0.87
1:A:517:LEU:H	1:A:517:LEU:HD23	1.40	0.86
3:C:112:ILE:HG21	3:C:115:LEU:HB2	0.89	0.86
2:B:50:TYR:OH	3:C:117:ASP:OD2	1.92	0.85
2:B:360:ASN:O	4:B:508:HOH:O	1.94	0.84
2:B:263:ASN:HB2	2:B:264:PRO:CD	2.07	0.84
1:A:295:LYS:NZ	1:A:298:SER:OG	2.12	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:ASP:O	3:C:93:LEU:N	2.11	0.83
3:C:87:VAL:HG11	3:C:90:GLN:HG3	1.62	0.82
2:B:350:GLU:O	2:B:354:ILE:HG13	1.80	0.82
1:A:387:ASP:HA	1:A:494:THR:HG21	1.60	0.82
1:A:491:HIS:HD2	2:B:317:ARG:HE	1.28	0.82
3:C:61:TRP:HZ2	3:C:89:ASP:OD2	1.62	0.81
1:A:353:THR:HA	1:A:488:ILE:HD13	1.63	0.81
2:B:254:HIS:HA	4:B:531:HOH:O	1.81	0.81
3:C:87:VAL:HG12	3:C:89:ASP:HB2	1.62	0.81
1:A:354:GLY:HA3	1:A:487:PRO:HA	1.63	0.80
2:B:326:ARG:O	2:B:330:THR:HB	1.82	0.80
3:C:3:SER:HA	3:C:17:ASP:HA	1.62	0.80
1:A:55:LEU:O	1:A:57:PRO:HD3	1.82	0.79
3:C:7:GLN:HE21	3:C:12:GLU:HB3	1.49	0.77
2:B:256:ARG:NH1	2:B:258:ASP:OD1	2.17	0.77
1:A:88:ASN:HB2	1:A:197:ARG:NE	1.99	0.77
3:C:51:ASN:HD21	3:C:54:ILE:HD11	1.50	0.77
1:A:21:ALA:C	1:A:47:ARG:HG2	2.04	0.77
2:B:302:PRO:O	4:B:537:HOH:O	2.02	0.77
3:C:57:LYS:H	3:C:57:LYS:CD	1.95	0.77
2:B:278:ASP:CB	4:B:557:HOH:O	2.16	0.76
3:C:25:VAL:O	3:C:27:ILE:N	2.17	0.76
3:C:112:ILE:CG2	3:C:115:LEU:N	2.29	0.76
2:B:348:ASP:O	2:B:352:ILE:HG13	1.86	0.75
2:B:350:GLU:CA	4:B:548:HOH:O	2.30	0.75
3:C:4:ILE:HG22	3:C:5:LYS:H	1.52	0.75
1:A:486:ARG:N	4:A:630:HOH:O	2.19	0.74
1:A:120:SER:HB2	1:A:319:THR:HG23	1.70	0.74
3:C:87:VAL:HG11	3:C:90:GLN:CG	2.18	0.74
2:B:179:ILE:O	2:B:182:THR:HB	1.88	0.74
1:A:56:ASP:OD2	1:A:59:PHE:HB2	1.88	0.73
1:A:439:ARG:NH2	2:B:343:GLY:O	2.22	0.73
1:A:470:GLU:O	1:A:474:LYS:HG3	1.88	0.73
3:C:61:TRP:HD1	3:C:64:HIS:CE1	2.07	0.73
1:A:221:GLU:HA	1:A:221:GLU:OE1	1.89	0.72
3:C:56:LYS:N	3:C:57:LYS:HE2	2.05	0.71
1:A:486:ARG:O	4:A:630:HOH:O	2.07	0.71
2:B:251:ARG:HD2	2:B:285:PRO:HD3	1.72	0.71
2:B:304:PHE:CD1	2:B:308:ILE:HD11	2.26	0.71
1:A:449:ARG:HD3	1:A:449:ARG:O	1.91	0.71
2:B:88:THR:HG23	2:B:118:ASP:OD2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:57:LYS:HB3	3:C:92:PHE:CZ	2.26	0.70
3:C:5:LYS:HB2	3:C:15:GLU:HG2	1.73	0.70
2:B:88:THR:HG21	2:B:120:SER:OG	1.90	0.70
1:A:189:SER:OG	4:A:669:HOH:O	2.07	0.70
3:C:114:GLY:O	3:C:118:VAL:HB	1.92	0.70
1:A:97:GLN:O	1:A:101:VAL:HB	1.91	0.70
1:A:387:ASP:HA	1:A:494:THR:CG2	2.22	0.70
2:B:40:LEU:HD22	2:B:42:ASP:H	1.56	0.69
1:A:491:HIS:CD2	2:B:317:ARG:HE	2.11	0.69
3:C:52:ALA:O	3:C:55:LEU:HD23	1.91	0.69
1:A:127:ARG:NE	1:A:128:ASP:OD1	2.23	0.69
1:A:262:LEU:O	4:A:611:HOH:O	2.09	0.69
2:B:357:ARG:O	4:B:549:HOH:O	2.11	0.69
3:C:50:VAL:HG12	3:C:51:ASN:H	1.57	0.69
2:B:278:ASP:O	4:B:557:HOH:O	2.10	0.69
2:B:202:LEU:HD21	4:B:545:HOH:O	1.82	0.69
2:B:297:GLU:O	2:B:299:GLU:N	2.25	0.69
2:B:288:ASN:N	4:B:531:HOH:O	2.08	0.69
3:C:110:LEU:O	3:C:112:ILE:HG13	1.93	0.69
2:B:330:THR:HG22	2:B:331:CYS:SG	2.33	0.69
1:A:134:MET:HG2	1:A:134:MET:O	1.92	0.69
3:C:131:THR:O	3:C:135:ILE:HG13	1.92	0.68
3:C:7:GLN:CG	3:C:12:GLU:HA	2.23	0.68
2:B:402:LYS:HG2	2:B:403:TYR:CD2	2.29	0.67
1:A:436:PHE:O	1:A:440:THR:HG22	1.95	0.67
2:B:40:LEU:O	2:B:41:GLN:HB2	1.95	0.66
2:B:216:ILE:CD1	2:B:235:LEU:HB3	2.07	0.66
2:B:304:PHE:H	2:B:326:ARG:HH21	1.41	0.66
1:A:200:ILE:HD13	1:A:200:ILE:H	1.61	0.66
2:B:173:SER:C	2:B:199:THR:HG21	2.15	0.66
2:B:239:GLU:OE1	4:B:532:HOH:O	2.12	0.66
3:C:108:ASN:O	3:C:109:TYR:C	2.34	0.65
1:A:22:SER:N	1:A:47:ARG:HG2	2.10	0.65
1:A:465:PRO:HB2	1:A:480:ILE:HD11	1.78	0.65
1:A:21:ALA:N	1:A:47:ARG:CB	2.58	0.65
1:A:54:ILE:HD13	1:A:54:ILE:N	2.12	0.65
3:C:53:ALA:C	3:C:57:LYS:HE3	2.17	0.65
3:C:93:LEU:O	3:C:95:VAL:N	2.29	0.65
2:B:228:GLU:HB3	2:B:254:HIS:HB3	1.79	0.65
1:A:491:HIS:HD2	2:B:317:ARG:NE	1.95	0.65
3:C:27:ILE:O	3:C:29:THR:N	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:44:ILE:HB	2:B:69:VAL:HG21	1.79	0.64
1:A:65:VAL:HG12	1:A:69:ARG:HD3	1.78	0.64
2:B:278:ASP:HA	4:B:557:HOH:O	1.90	0.64
1:A:361:ILE:HD12	1:A:375:ALA:HB1	1.79	0.64
1:A:47:ARG:HG3	1:A:48:CYS:N	2.12	0.64
3:C:108:ASN:O	3:C:110:LEU:N	2.30	0.64
3:C:89:ASP:HA	3:C:92:PHE:HB3	1.80	0.64
3:C:54:ILE:C	3:C:57:LYS:HG2	2.18	0.64
2:B:227:ARG:NH1	4:B:545:HOH:O	1.86	0.64
1:A:47:ARG:CG	1:A:48:CYS:H	2.08	0.63
2:B:350:GLU:O	4:B:548:HOH:O	2.15	0.63
1:A:354:GLY:HA3	1:A:487:PRO:CA	2.28	0.63
1:A:517:LEU:CD2	1:A:517:LEU:H	2.10	0.63
2:B:45:LEU:HD22	2:B:72:MET:HE2	1.80	0.63
2:B:278:ASP:C	4:B:557:HOH:O	2.36	0.63
1:A:465:PRO:HB2	1:A:480:ILE:CD1	2.28	0.63
2:B:320:SER:HB3	2:B:323:VAL:HG23	1.81	0.63
1:A:356:PRO:HB2	1:A:447:ILE:HD13	1.81	0.63
3:C:112:ILE:CG2	3:C:115:LEU:CA	2.77	0.63
1:A:106:PHE:HA	1:A:111:VAL:HG23	1.81	0.62
3:C:111:ASP:C	3:C:111:ASP:OD1	2.36	0.62
3:C:56:LYS:H	3:C:57:LYS:HE2	1.64	0.62
1:A:23:SER:OG	1:A:42:ALA:O	2.11	0.62
3:C:104:ILE:HG12	3:C:119:THR:OG1	1.99	0.62
1:A:496:ARG:HA	2:B:294:PHE:CZ	2.35	0.62
1:A:194:GLU:N	1:A:194:GLU:OE1	2.31	0.61
2:B:35:ASP:N	2:B:35:ASP:OD1	2.33	0.61
3:C:26:THR:HB	3:C:110:LEU:HA	1.82	0.61
3:C:61:TRP:CE3	3:C:115:LEU:HD21	2.35	0.61
1:A:315:TYR:OH	1:A:407:ASP:OD2	2.16	0.61
3:C:53:ALA:C	3:C:54:ILE:HD13	2.21	0.61
1:A:426:GLN:NE2	1:A:518:LEU:HA	2.16	0.61
1:A:336:ILE:HG12	1:A:505:ILE:HD13	1.82	0.61
2:B:44:ILE:HD12	2:B:66:TRP:CD1	2.35	0.61
3:C:87:VAL:CG1	3:C:90:GLN:H	2.14	0.61
1:A:288:TRP:CZ3	1:A:292:LYS:HG2	2.36	0.61
3:C:25:VAL:C	3:C:27:ILE:H	2.05	0.60
1:A:145:GLU:OE1	4:A:651:HOH:O	2.17	0.60
1:A:194:GLU:HA	1:A:197:ARG:HD2	1.82	0.60
1:A:46:ALA:O	1:A:47:ARG:HB3	2.01	0.60
1:A:296:ARG:O	1:A:298:SER:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:ARG:HG3	1:A:449:ARG:HH11	1.66	0.60
2:B:212:SER:O	2:B:215:GLY:N	2.33	0.60
1:A:452:PRO:C	1:A:454:LEU:H	2.04	0.60
3:C:111:ASP:O	3:C:112:ILE:HG13	2.01	0.60
2:B:88:THR:CG2	2:B:118:ASP:OD2	2.50	0.60
3:C:112:ILE:HG21	3:C:115:LEU:CA	2.32	0.60
3:C:112:ILE:CG2	3:C:115:LEU:CB	2.61	0.59
3:C:7:GLN:HG3	3:C:12:GLU:HA	1.84	0.59
2:B:118:ASP:C	2:B:118:ASP:OD1	2.40	0.59
2:B:286:LYS:C	4:B:516:HOH:O	2.35	0.59
3:C:87:VAL:HG12	3:C:90:GLN:H	1.68	0.59
1:A:40:LEU:CD2	1:A:188:VAL:HG12	2.28	0.59
3:C:52:ALA:C	3:C:54:ILE:H	2.05	0.59
3:C:61:TRP:HD1	3:C:64:HIS:HE1	1.46	0.59
3:C:61:TRP:CZ2	3:C:89:ASP:OD2	2.52	0.59
2:B:251:ARG:HD3	2:B:283:HIS:O	2.01	0.59
2:B:227:ARG:HB2	2:B:227:ARG:HH11	1.68	0.59
2:B:38:ASN:O	2:B:39:LEU:C	2.41	0.59
3:C:57:LYS:CD	3:C:57:LYS:N	2.66	0.58
1:A:155:ARG:NH1	1:A:155:ARG:HG3	2.02	0.58
2:B:329:MET:HG2	2:B:353:ARG:HH11	1.67	0.58
1:A:436:PHE:O	1:A:440:THR:CG2	2.52	0.58
2:B:304:PHE:HD1	2:B:308:ILE:HD11	1.68	0.58
1:A:105:LEU:HD22	1:A:109:TRP:CH2	2.38	0.58
1:A:105:LEU:HD22	1:A:109:TRP:CZ3	2.38	0.58
1:A:295:LYS:HG3	1:A:295:LYS:O	2.04	0.58
1:A:21:ALA:O	1:A:47:ARG:CB	2.47	0.58
2:B:202:LEU:HD13	2:B:228:GLU:HG3	1.85	0.57
1:A:106:PHE:HA	1:A:111:VAL:CG2	2.34	0.57
2:B:263:ASN:CB	2:B:264:PRO:HD3	2.27	0.57
3:C:3:SER:O	3:C:4:ILE:HD13	2.04	0.57
3:C:47:LEU:HD23	3:C:48:PRO:N	2.20	0.57
1:A:443:SER:O	1:A:448:ARG:NH2	2.38	0.57
1:A:88:ASN:HB2	1:A:197:ARG:CZ	2.34	0.56
2:B:251:ARG:HG3	2:B:284:SER:OG	2.05	0.56
3:C:9:SER:HB2	3:C:48:PRO:C	2.25	0.56
1:A:460:ARG:HD3	1:A:461:TYR:CE2	2.40	0.56
3:C:25:VAL:H	3:C:110:LEU:HD21	1.71	0.56
1:A:469:PRO:HG2	1:A:472:VAL:HG23	1.88	0.56
2:B:179:ILE:O	2:B:179:ILE:HG23	2.06	0.56
3:C:7:GLN:HG2	3:C:12:GLU:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:383:CYS:HA	2:B:386:ARG:NH2	2.21	0.56
3:C:61:TRP:CD1	3:C:64:HIS:HE1	2.24	0.56
2:B:263:ASN:CB	2:B:264:PRO:CD	2.83	0.56
3:C:57:LYS:HD3	3:C:57:LYS:N	2.21	0.55
3:C:27:ILE:HD12	3:C:110:LEU:HD12	1.87	0.55
1:A:45:GLY:O	1:A:46:ALA:HB3	2.06	0.55
2:B:342:ASN:HB3	2:B:369:CYS:HB3	1.88	0.55
2:B:266:GLN:HE22	2:B:297:GLU:HG2	1.70	0.55
1:A:292:LYS:O	1:A:296:ARG:HA	2.07	0.55
3:C:105:LEU:O	3:C:108:ASN:OD1	2.25	0.55
3:C:51:ASN:CG	3:C:52:ALA:H	2.10	0.55
2:B:45:LEU:HD22	2:B:72:MET:CE	2.37	0.55
2:B:292:TYR:CD1	2:B:314:TYR:HB3	2.42	0.55
2:B:304:PHE:CE1	2:B:308:ILE:HD11	2.42	0.55
1:A:128:ASP:O	1:A:132:MET:HG2	2.07	0.55
1:A:321:ASN:O	1:A:324:PHE:HB2	2.07	0.55
1:A:359:ASP:HB2	1:A:451:LEU:HD11	1.88	0.55
1:A:356:PRO:CB	1:A:447:ILE:HD13	2.37	0.54
2:B:228:GLU:CB	2:B:254:HIS:HB3	2.37	0.54
3:C:110:LEU:O	3:C:111:ASP:C	2.45	0.54
3:C:89:ASP:OD1	3:C:89:ASP:N	2.39	0.54
3:C:57:LYS:HD3	3:C:57:LYS:H	1.72	0.54
1:A:194:GLU:HA	1:A:197:ARG:CD	2.37	0.54
2:B:297:GLU:HG3	2:B:298:GLU:N	2.22	0.54
1:A:86:LYS:HD3	1:A:86:LYS:O	2.08	0.54
1:A:95:ARG:HH11	1:A:95:ARG:HG3	1.71	0.54
2:B:253:GLU:C	4:B:531:HOH:O	2.46	0.53
2:B:179:ILE:CG2	2:B:179:ILE:O	2.56	0.53
1:A:43:VAL:HG13	1:A:192:GLN:HG2	1.90	0.53
2:B:92:LYS:HB3	3:C:162:GLU:HB2	1.90	0.53
1:A:21:ALA:C	1:A:47:ARG:CG	2.76	0.53
2:B:281:ILE:HD13	2:B:309:PRO:HB3	1.91	0.53
2:B:342:ASN:OD1	2:B:342:ASN:C	2.46	0.53
2:B:250:VAL:HG22	4:B:522:HOH:O	2.08	0.53
2:B:308:ILE:HG22	2:B:309:PRO:HD2	1.89	0.53
1:A:212:SER:OG	1:A:215:GLU:HG3	2.09	0.53
1:A:125:LYS:CE	1:A:319:THR:HG22	2.39	0.53
2:B:294:PHE:C	2:B:295:LEU:HD23	2.29	0.53
3:C:4:ILE:HG22	3:C:5:LYS:N	2.22	0.53
3:C:57:LYS:HD2	3:C:92:PHE:CE1	2.44	0.53
3:C:131:THR:HG23	3:C:134:GLU:OE2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:60:GLN:HG3	3:C:88:TRP:CE2	2.44	0.52
1:A:190:SER:O	1:A:193:MET:N	2.24	0.52
1:A:56:ASP:CG	1:A:59:PHE:HB2	2.29	0.52
1:A:158:GLU:HG3	1:A:162:GLN:NE2	2.25	0.52
3:C:132:PRO:O	3:C:136:ARG:HG3	2.10	0.52
1:A:270:SER:OG	1:A:271:PRO:HD3	2.09	0.52
1:A:94:VAL:HG21	1:A:105:LEU:HD11	1.92	0.52
2:B:264:PRO:HD2	2:B:267:THR:HG22	1.92	0.52
3:C:51:ASN:CG	3:C:52:ALA:N	2.64	0.52
2:B:251:ARG:CD	2:B:283:HIS:O	2.57	0.52
1:A:150:LEU:N	1:A:312:GLU:OE2	2.29	0.51
2:B:342:ASN:OD1	2:B:343:GLY:N	2.44	0.51
2:B:254:HIS:CA	4:B:531:HOH:O	2.50	0.51
3:C:87:VAL:HG21	3:C:90:GLN:OE1	2.11	0.51
3:C:16:VAL:HG22	3:C:17:ASP:O	2.10	0.51
2:B:159:HIS:NE2	4:B:538:HOH:O	2.16	0.51
1:A:479:ILE:HG22	1:A:479:ILE:O	2.09	0.51
3:C:56:LYS:HB3	3:C:57:LYS:NZ	2.26	0.51
1:A:516:CYS:HB3	2:B:336:GLU:OE2	2.10	0.51
1:A:512:TYR:CZ	1:A:514:GLY:HA3	2.45	0.51
1:A:479:ILE:HG22	1:A:482:VAL:HB	1.93	0.51
1:A:384:THR:HG21	1:A:419:SER:HB3	1.91	0.51
1:A:65:VAL:CG1	1:A:69:ARG:HH11	2.24	0.50
3:C:56:LYS:HA	3:C:59:ILE:HB	1.94	0.50
2:B:92:LYS:HB3	3:C:162:GLU:CB	2.42	0.50
3:C:87:VAL:HB	3:C:88:TRP:O	2.12	0.50
1:A:517:LEU:CD2	1:A:517:LEU:N	2.74	0.50
2:B:357:ARG:HB3	2:B:357:ARG:HH11	1.76	0.50
2:B:76:TRP:CZ3	2:B:102:ILE:HD12	2.47	0.50
3:C:110:LEU:O	3:C:111:ASP:O	2.30	0.50
3:C:52:ALA:HA	3:C:55:LEU:HD23	1.94	0.50
1:A:109:TRP:HB2	1:A:111:VAL:HG22	1.94	0.50
1:A:355:PHE:CD2	1:A:433:PRO:HB2	2.47	0.50
2:B:229:LEU:HD21	2:B:231:LEU:HD21	1.94	0.50
3:C:61:TRP:CD1	3:C:64:HIS:CE1	2.94	0.50
1:A:46:ALA:O	1:A:47:ARG:CB	2.57	0.50
3:C:49:ASN:O	3:C:50:VAL:HG22	2.12	0.49
1:A:194:GLU:H	1:A:194:GLU:CD	2.16	0.49
1:A:452:PRO:C	1:A:454:LEU:N	2.66	0.49
1:A:288:TRP:CZ3	1:A:300:PRO:HD3	2.47	0.49
2:B:229:LEU:HD11	2:B:231:LEU:HD23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:SER:HA	1:A:231:GLY:HA2	1.94	0.49
3:C:85:ILE:HG12	3:C:121:LYS:CE	2.42	0.49
1:A:21:ALA:C	1:A:47:ARG:CB	2.81	0.49
2:B:173:SER:O	2:B:199:THR:HG21	2.12	0.49
3:C:112:ILE:HG22	3:C:112:ILE:O	2.12	0.49
3:C:51:ASN:OD1	3:C:52:ALA:N	2.45	0.49
2:B:311:THR:CG2	2:B:312:HIS:CD2	2.59	0.49
2:B:295:LEU:HD23	2:B:295:LEU:N	2.28	0.49
3:C:112:ILE:C	3:C:114:GLY:H	2.15	0.49
2:B:44:ILE:HG22	2:B:48:PHE:CE1	2.48	0.49
1:A:182:LYS:O	1:A:281:ARG:HD3	2.13	0.49
3:C:57:LYS:HD2	3:C:92:PHE:HE1	1.77	0.48
2:B:98:LEU:O	2:B:102:ILE:HG12	2.13	0.48
3:C:143:ASN:C	3:C:143:ASN:OD1	2.50	0.48
3:C:87:VAL:HA	3:C:88:TRP:C	2.33	0.48
3:C:145:PHE:HB3	3:C:150:GLU:HB2	1.94	0.48
2:B:83:LEU:HB2	2:B:117:VAL:HG22	1.95	0.48
1:A:353:THR:O	1:A:359:ASP:OD2	2.31	0.48
3:C:60:GLN:HG3	3:C:88:TRP:CZ2	2.48	0.48
2:B:228:GLU:HA	2:B:254:HIS:O	2.13	0.48
1:A:21:ALA:C	1:A:47:ARG:HB3	2.30	0.48
1:A:95:ARG:NH2	1:A:209:GLY:O	2.47	0.48
1:A:250:ALA:O	1:A:251:ASN:HB2	2.14	0.48
2:B:254:HIS:N	4:B:531:HOH:O	2.47	0.48
2:B:289:LEU:H	2:B:311:THR:CG2	2.26	0.48
1:A:221:GLU:OE1	1:A:221:GLU:CA	2.60	0.48
1:A:357:TRP:O	1:A:361:ILE:HG12	2.14	0.48
3:C:116:LEU:C	3:C:116:LEU:HD13	2.34	0.48
1:A:256:ARG:NH1	1:A:256:ARG:N	2.62	0.48
1:A:478:CYS:HA	1:A:483:ASP:OD2	2.13	0.48
2:B:125:GLU:HG3	2:B:155:LEU:CD2	2.44	0.48
1:A:274:ARG:HD2	1:A:404:LEU:O	2.14	0.48
1:A:194:GLU:HA	1:A:197:ARG:CG	2.44	0.47
1:A:63:SER:C	1:A:65:VAL:H	2.17	0.47
1:A:251:ASN:O	4:A:638:HOH:O	2.20	0.47
2:B:251:ARG:HB2	4:B:522:HOH:O	2.13	0.47
2:B:418:ARG:NH2	4:B:551:HOH:O	2.46	0.47
2:B:390:LEU:HD23	2:B:416:LEU:HD11	1.96	0.47
2:B:393:MET:HG3	2:B:395:GLU:OE1	2.13	0.47
3:C:88:TRP:O	3:C:91:GLU:N	2.26	0.47
3:C:44:PRO:HA	3:C:46:PRO:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:LYS:HG2	3:C:28:LYS:O	2.15	0.47
1:A:155:ARG:NH1	1:A:155:ARG:CG	2.73	0.47
1:A:291:TYR:CE1	1:A:300:PRO:HB3	2.49	0.47
1:A:244:GLU:OE1	1:A:246:LYS:HG2	2.14	0.47
2:B:380:VAL:HG12	2:B:415:HIS:HB2	1.95	0.47
1:A:291:TYR:CD1	1:A:300:PRO:HB3	2.50	0.47
1:A:120:SER:O	1:A:319:THR:CG2	2.63	0.47
1:A:510:SER:OG	1:A:522:PRO:HD3	2.15	0.47
1:A:47:ARG:CG	1:A:48:CYS:N	2.76	0.47
1:A:67:ILE:HD12	1:A:68:ASN:H	1.80	0.46
3:C:111:ASP:C	3:C:112:ILE:HG13	2.36	0.46
2:B:353:ARG:HE	2:B:353:ARG:HB2	1.47	0.46
1:A:287:LEU:HD13	1:A:304:LEU:HD22	1.98	0.46
1:A:32:ARG:HD2	1:A:34:HIS:CE1	2.50	0.46
1:A:428:PHE:C	1:A:428:PHE:CD1	2.89	0.46
1:A:102:PHE:N	1:A:103:PRO:CD	2.79	0.46
3:C:52:ALA:C	3:C:54:ILE:N	2.69	0.46
2:B:245:SER:OG	2:B:280:PHE:HA	2.16	0.46
1:A:123:PHE:C	1:A:123:PHE:CD1	2.89	0.46
1:A:469:PRO:HG2	1:A:472:VAL:CG2	2.46	0.46
3:C:44:PRO:HA	3:C:45:VAL:HA	1.73	0.46
1:A:296:ARG:HG3	1:A:297:ASN:H	1.81	0.46
2:B:308:ILE:HG13	2:B:330:THR:HG23	1.97	0.46
2:B:189:LEU:O	2:B:192:LEU:HB3	2.16	0.46
2:B:234:HIS:ND1	2:B:235:LEU:HD23	2.31	0.46
1:A:517:LEU:HD23	2:B:336:GLU:OE1	2.16	0.46
1:A:59:PHE:O	1:A:62:SER:HB3	2.16	0.46
1:A:454:LEU:O	1:A:455:LYS:C	2.55	0.46
1:A:497:LEU:HD22	1:A:501:ARG:NH1	2.31	0.46
2:B:95:HIS:ND1	2:B:96:PRO:HD2	2.31	0.46
3:C:112:ILE:C	3:C:114:GLY:N	2.69	0.45
3:C:57:LYS:H	3:C:57:LYS:CE	2.29	0.45
2:B:250:VAL:HG13	2:B:251:ARG:N	2.31	0.45
1:A:256:ARG:HH11	1:A:256:ARG:N	2.14	0.45
1:A:190:SER:O	1:A:194:GLU:OE1	2.34	0.45
1:A:338:TRP:CG	1:A:391:SER:HA	2.51	0.45
2:B:290:VAL:HG22	2:B:312:HIS:HB2	1.98	0.45
1:A:288:TRP:CH2	1:A:300:PRO:HD3	2.51	0.45
1:A:65:VAL:HB	1:A:70:TRP:NE1	2.31	0.45
1:A:67:ILE:HD12	1:A:67:ILE:N	2.31	0.45
3:C:102:GLU:O	3:C:102:GLU:OE2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:PRO:O	1:A:106:PHE:HB2	2.17	0.45
2:B:39:LEU:C	2:B:39:LEU:HD12	2.37	0.45
3:C:107:ALA:HB1	3:C:116:LEU:HB2	1.98	0.45
1:A:497:LEU:HD22	1:A:501:ARG:HH12	1.81	0.45
1:A:295:LYS:HZ3	1:A:298:SER:CB	2.23	0.45
2:B:251:ARG:N	4:B:522:HOH:O	2.07	0.45
1:A:449:ARG:HG3	1:A:449:ARG:NH1	2.32	0.45
1:A:101:VAL:N	1:A:103:PRO:HD2	2.31	0.45
2:B:274:LYS:HD2	2:B:306:TYR:HB2	1.99	0.45
3:C:122:THR:O	3:C:123:VAL:C	2.56	0.45
1:A:354:GLY:O	1:A:356:PRO:HD3	2.17	0.45
2:B:374:SER:OG	2:B:400:ASP:OD2	2.32	0.45
3:C:151:ALA:HA	3:C:154:ARG:HG2	1.99	0.45
1:A:264:ALA:HB2	4:A:610:HOH:O	2.16	0.45
1:A:348:TRP:CZ2	1:A:379:VAL:HG13	2.52	0.44
2:B:206:SER:O	2:B:207:SER:HB3	2.17	0.44
3:C:88:TRP:HB3	3:C:89:ASP:OD1	2.18	0.44
2:B:262:GLU:O	2:B:263:ASN:OD1	2.35	0.44
3:C:145:PHE:O	3:C:146:THR:C	2.54	0.44
1:A:274:ARG:HD3	1:A:275:PHE:CD1	2.52	0.44
3:C:87:VAL:HG21	3:C:90:GLN:CD	2.38	0.44
1:A:243:LEU:CD1	1:A:286:ARG:HB3	2.47	0.44
1:A:64:SER:C	1:A:65:VAL:HG22	2.37	0.44
2:B:202:LEU:HD22	4:B:545:HOH:O	1.99	0.44
3:C:113:LYS:O	3:C:113:LYS:HG2	2.18	0.44
2:B:37:GLY:N	3:C:141:ILE:HD13	2.33	0.44
3:C:156:GLU:HG2	3:C:159:TRP:CZ3	2.53	0.44
1:A:428:PHE:CZ	1:A:429:HIS:CE1	3.06	0.44
2:B:315:PHE:HB3	2:B:319:VAL:HG22	1.98	0.44
3:C:52:ALA:O	3:C:54:ILE:N	2.48	0.44
1:A:287:LEU:HA	1:A:287:LEU:HD23	1.70	0.44
2:B:233:TYR:CE1	2:B:236:LEU:HD23	2.53	0.44
1:A:191:GLN:OE1	4:A:687:HOH:O	2.21	0.43
1:A:71:ARG:HD2	1:A:75:GLN:NE2	2.33	0.43
3:C:112:ILE:O	3:C:114:GLY:N	2.51	0.43
1:A:439:ARG:HH21	2:B:343:GLY:CA	2.31	0.43
1:A:100:ASP:O	1:A:100:ASP:OD1	2.36	0.43
2:B:44:ILE:HG22	2:B:48:PHE:CD1	2.53	0.43
3:C:131:THR:OG1	3:C:134:GLU:HG3	2.18	0.43
1:A:384:THR:O	1:A:389:TRP:HA	2.18	0.43
2:B:37:GLY:HA2	3:C:141:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ARG:O	1:A:75:GLN:HG3	2.19	0.43
2:B:179:ILE:HA	2:B:179:ILE:HD12	1.84	0.43
2:B:41:GLN:HA	2:B:44:ILE:HG13	2.01	0.43
2:B:64:ARG:NH2	3:C:149:GLU:OE2	2.51	0.43
1:A:194:GLU:C	1:A:196:CYS:H	2.22	0.43
1:A:152:ASP:OD1	1:A:154:ASP:HB2	2.19	0.43
1:A:120:SER:O	1:A:319:THR:HG23	2.18	0.43
3:C:61:TRP:HB3	3:C:62:CYS:H	1.58	0.43
3:C:86:PRO:C	3:C:87:VAL:HG13	2.39	0.43
2:B:172:LYS:HA	2:B:172:LYS:HD2	1.84	0.43
2:B:238:ASP:OD1	2:B:272:ILE:HG23	2.19	0.43
2:B:160:PHE:HE2	2:B:184:VAL:HG13	1.84	0.43
3:C:57:LYS:O	3:C:61:TRP:HE3	2.02	0.42
2:B:264:PRO:HD2	2:B:267:THR:CG2	2.49	0.42
1:A:190:SER:O	1:A:191:GLN:C	2.57	0.42
1:A:49:VAL:HG13	1:A:49:VAL:O	2.19	0.42
2:B:404:SER:OG	2:B:407:GLN:HG3	2.19	0.42
2:B:251:ARG:CB	4:B:522:HOH:O	2.68	0.42
1:A:157:ILE:HG22	1:A:162:GLN:HA	2.01	0.42
1:A:438:ARG:HA	1:A:463:TYR:CE2	2.55	0.42
3:C:27:ILE:CG2	3:C:28:LYS:N	2.82	0.42
3:C:55:LEU:N	3:C:57:LYS:HE2	2.34	0.42
3:C:54:ILE:N	3:C:57:LYS:HE3	2.35	0.42
2:B:176:SER:CB	2:B:202:LEU:HB2	2.49	0.42
3:C:122:THR:O	3:C:125:ASN:N	2.52	0.42
2:B:37:GLY:CA	3:C:141:ILE:HD13	2.49	0.42
3:C:130:LYS:HE3	3:C:138:THR:OG1	2.19	0.42
2:B:330:THR:O	2:B:330:THR:HG23	2.19	0.42
2:B:202:LEU:HD13	2:B:228:GLU:CG	2.49	0.42
2:B:403:TYR:CE1	2:B:411:GLU:HG3	2.54	0.42
1:A:251:ASN:HB2	1:A:256:ARG:HH22	1.85	0.42
2:B:186:ASP:HB2	2:B:187:PRO:HD3	2.02	0.42
1:A:302:LEU:HD22	1:A:309:LEU:HD11	2.01	0.42
3:C:87:VAL:HG11	3:C:90:GLN:CD	2.40	0.42
3:C:88:TRP:O	3:C:90:GLN:N	2.53	0.42
3:C:93:LEU:O	3:C:95:VAL:HG22	2.20	0.42
1:A:516:CYS:HA	2:B:336:GLU:OE1	2.20	0.42
2:B:402:LYS:HG2	2:B:403:TYR:CE2	2.55	0.42
1:A:510:SER:C	1:A:512:TYR:H	2.23	0.42
1:A:336:ILE:HG23	1:A:337:PRO:HD2	2.02	0.42
3:C:120:CYS:C	3:C:122:THR:N	2.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:ARG:NE	4:A:614:HOH:O	2.50	0.42
3:C:108:ASN:OD1	3:C:109:TYR:N	2.45	0.42
2:B:288:ASN:HA	2:B:311:THR:HG21	2.02	0.42
2:B:365:GLY:HA2	2:B:391:SER:O	2.20	0.42
3:C:100:LEU:HA	3:C:103:LEU:HD12	2.01	0.41
1:A:340:ARG:NH1	2:B:89:SER:O	2.53	0.41
3:C:89:ASP:C	3:C:91:GLU:N	2.73	0.41
1:A:246:LYS:HE3	1:A:246:LYS:HB3	1.60	0.41
2:B:371:VAL:HG12	2:B:372:SER:O	2.20	0.41
1:A:202:GLU:C	1:A:204:HIS:H	2.24	0.41
1:A:193:MET:O	1:A:197:ARG:HG3	2.20	0.41
1:A:194:GLU:C	1:A:196:CYS:N	2.74	0.41
1:A:451:LEU:HD23	1:A:451:LEU:HA	1.87	0.41
2:B:141:THR:HG21	4:B:554:HOH:O	2.20	0.41
3:C:54:ILE:HA	3:C:57:LYS:HG3	2.01	0.41
3:C:16:VAL:CG2	3:C:17:ASP:N	2.82	0.41
2:B:357:ARG:NH1	2:B:357:ARG:HB3	2.36	0.41
3:C:98:GLY:O	3:C:101:PHE:HB3	2.21	0.41
2:B:120:SER:O	2:B:123:SER:HB2	2.20	0.41
3:C:122:THR:O	3:C:124:ALA:N	2.53	0.41
1:A:47:ARG:O	1:A:196:CYS:CA	2.68	0.41
2:B:44:ILE:HD12	2:B:66:TRP:NE1	2.35	0.41
2:B:45:LEU:O	2:B:49:LYS:HG3	2.21	0.41
1:A:516:CYS:HB3	2:B:336:GLU:CD	2.41	0.41
3:C:30:MET:HG3	3:C:31:LEU:N	2.36	0.41
2:B:178:LYS:CD	2:B:204:LYS:HD2	2.51	0.41
2:B:40:LEU:O	2:B:41:GLN:CB	2.68	0.41
3:C:16:VAL:HG22	3:C:17:ASP:N	2.35	0.41
1:A:510:SER:O	1:A:511:ARG:HB2	2.20	0.41
1:A:348:TRP:HZ2	1:A:379:VAL:HG13	1.84	0.41
3:C:20:ILE:O	3:C:22:LYS:N	2.52	0.41
1:A:95:ARG:CG	1:A:95:ARG:HH11	2.34	0.41
2:B:334:LEU:HA	2:B:334:LEU:HD23	1.80	0.41
1:A:213:LEU:O	1:A:218:PHE:HB2	2.21	0.41
1:A:63:SER:O	1:A:65:VAL:N	2.54	0.40
1:A:426:GLN:HG3	4:A:657:HOH:O	2.20	0.40
2:B:405:LEU:HA	2:B:405:LEU:HD22	1.69	0.40
1:A:499:ILE:HG22	1:A:500:GLU:N	2.35	0.40
2:B:48:PHE:C	2:B:50:TYR:N	2.74	0.40
2:B:251:ARG:HD2	2:B:284:SER:HA	2.03	0.40
1:A:44:ARG:HA	1:A:192:GLN:NE2	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:TRP:HB3	1:A:116:PHE:HB3	2.03	0.40
1:A:465:PRO:HD2	1:A:466:TRP:CZ3	2.55	0.40
3:C:155:LYS:O	3:C:158:GLN:HG2	2.22	0.40
3:C:27:ILE:HG22	3:C:28:LYS:N	2.36	0.40
1:A:337:PRO:HD2	1:A:505:ILE:HD11	2.03	0.40
1:A:390:VAL:HG12	1:A:391:SER:N	2.37	0.40
1:A:374:LEU:HD23	1:A:374:LEU:HA	1.77	0.40
2:B:48:PHE:C	2:B:50:TYR:H	2.24	0.40
1:A:387:ASP:CA	1:A:494:THR:HG21	2.42	0.40
2:B:189:LEU:HA	2:B:189:LEU:HD23	1.64	0.40
1:A:441:ASP:O	1:A:463:TYR:OH	2.22	0.40
1:A:525:VAL:HG13	1:A:525:VAL:O	2.21	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	499/544 (92%)	441 (88%)	44 (9%)	14 (3%)	6	15
2	B	392/428 (92%)	347 (88%)	35 (9%)	10 (3%)	7	16
3	C	124/163 (76%)	80 (64%)	24 (19%)	20 (16%)	0	0
All	All	1015/1135 (89%)	868 (86%)	103 (10%)	44 (4%)	3	7

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	221	GLU
1	A	259	ALA
1	A	297	ASN
1	A	525	VAL
1	A	526	GLU

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Mol	Chain	Res	Type
2	B	39	LEU
2	B	41	GLN
2	B	263	ASN
2	B	298	GLU
3	C	28	LYS
3	C	49	ASN
3	C	89	ASP
3	C	109	TYR
3	C	111	ASP
1	A	138	ALA
1	A	249	VAL
3	C	26	THR
3	C	46	PRO
3	C	48	PRO
3	C	61	TRP
3	C	94	LYS
3	C	146	THR
3	C	147	GLU
1	A	44	ARG
1	A	64	SER
1	A	191	GLN
1	A	264	ALA
1	A	453	LYS
2	B	246	SER
2	B	266	GLN
3	C	53	ALA
2	B	226	LEU
2	B	297	GLU
2	B	348	ASP
2	B	384	GLY
3	C	112	ILE
3	C	113	LYS
3	C	123	VAL
3	C	139	PHE
1	A	47	ARG
3	C	4	ILE
3	C	50	VAL
1	A	103	PRO
3	C	25	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	432/460 (94%)	377 (87%)	55 (13%)	5	13
2	B	360/390 (92%)	312 (87%)	48 (13%)	5	11
3	C	119/150 (79%)	102 (86%)	17 (14%)	4	10
All	All	911/1000 (91%)	791 (87%)	120 (13%)	5	12

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	VAL
1	A	44	ARG
1	A	47	ARG
1	A	52	VAL
1	A	59	PHE
1	A	64	SER
1	A	65	VAL
1	A	67	ILE
1	A	71	ARG
1	A	80	LEU
1	A	104	ARG
1	A	112	THR
1	A	125	LYS
1	A	134	MET
1	A	137	GLU
1	A	150	LEU
1	A	153	LEU
1	A	155	ARG
1	A	180	LEU
1	A	193	MET
1	A	200	ILE
1	A	207	THR
1	A	221	GLU
1	A	223	LEU
1	A	246	LYS
1	A	256	ARG

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Mol	Chain	Res	Type
1	A	257	MET
1	A	260	ASN
1	A	262	LEU
1	A	274	ARG
1	A	279	SER
1	A	287	LEU
1	A	288	TRP
1	A	292	LYS
1	A	304	LEU
1	A	319	THR
1	A	340	ARG
1	A	350	GLU
1	A	379	VAL
1	A	403	LEU
1	A	409	SER
1	A	439	ARG
1	A	440	THR
1	A	449	ARG
1	A	471	SER
1	A	488	ILE
1	A	496	ARG
1	A	497	LEU
1	A	499	ILE
1	A	503	LYS
1	A	509	LEU
1	A	513	ARG
1	A	517	LEU
1	A	520	SER
1	A	525	VAL
2	B	35	ASP
2	B	38	ASN
2	B	39	LEU
2	B	41	GLN
2	B	44	ILE
2	B	92	LYS
2	B	98	LEU
2	B	108	ASN
2	B	120	SER
2	B	121	LYS
2	B	138	SER
2	B	164	LEU
2	B	179	ILE

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Mol	Chain	Res	Type
2	B	182	THR
2	B	202	LEU
2	B	203	LEU
2	B	206	SER
2	B	216	ILE
2	B	217	LEU
2	B	227	ARG
2	B	240	LEU
2	B	241	LEU
2	B	246	SER
2	B	247	GLU
2	B	250	VAL
2	B	256	ARG
2	B	267	THR
2	B	275	SER
2	B	281	ILE
2	B	297	GLU
2	B	298	GLU
2	B	308	ILE
2	B	311	THR
2	B	317	ARG
2	B	319	VAL
2	B	330	THR
2	B	342	ASN
2	B	344	LEU
2	B	349	GLU
2	B	356	GLU
2	B	360	ASN
2	B	361	LEU
2	B	362	SER
2	B	364	ILE
2	B	383	CYS
2	B	388	SER
2	B	405	LEU
2	B	418	ARG
3	C	6	LEU
3	C	19	GLU
3	C	33	ASP
3	C	45	VAL
3	C	51	ASN
3	C	54	ILE
3	C	55	LEU

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Mol	Chain	Res	Type
3	C	57	LYS
3	C	63	THR
3	C	64	HIS
3	C	88	TRP
3	C	89	ASP
3	C	109	TYR
3	C	111	ASP
3	C	117	ASP
3	C	118	VAL
3	C	141	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	426	GLN
1	A	429	HIS
1	A	491	HIS
2	B	266	GLN
2	B	312	HIS
3	C	7	GLN
3	C	64	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	503/544 (92%)	-0.28	4 (0%)	87 88	20, 38, 83, 119	0
2	B	394/428 (92%)	-0.43	1 (0%)	94 95	23, 42, 68, 95	0
3	C	130/163 (79%)	1.03	31 (23%)	1 1	44, 87, 139, 160	0
All	All	1027/1135 (90%)	-0.17	36 (3%)	48 48	20, 43, 101, 160	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	30	MET	7.9
3	C	20	ILE	5.9
3	C	33	ASP	5.3
3	C	31	LEU	5.2
3	C	4	ILE	4.5
3	C	18	VAL	3.9
3	C	12	GLU	3.9
3	C	23	GLN	3.8
3	C	22	LYS	3.7
3	C	62	CYS	3.6
3	C	47	LEU	3.5
3	C	7	GLN	3.4
3	C	6	LEU	3.4
3	C	46	PRO	3.3
3	C	50	VAL	3.2
3	C	44	PRO	3.1
3	C	27	ILE	3.1
3	C	45	VAL	3.0
1	A	201	GLN	2.9
3	C	29	THR	2.8
2	B	265	GLY	2.6
3	C	15	GLU	2.6
1	A	63	SER	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	49	ASN	2.5
1	A	202	GLU	2.5
3	C	5	LYS	2.4
3	C	24	SER	2.4
3	C	10	ASP	2.4
3	C	19	GLU	2.3
3	C	9	SER	2.3
3	C	11	GLY	2.3
3	C	55	LEU	2.2
3	C	115	LEU	2.2
1	A	204	HIS	2.2
3	C	48	PRO	2.1
3	C	16	VAL	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.