



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:35 PM GMT

PDB ID : 4M2T
Title : Corrected Structure of Mouse P-glycoprotein bound to QZ59-SSS
Authors : Li, J.; Jaimes, K.F.; Aller, S.G.
Deposited on : 2013-08-05
Resolution : 4.35 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

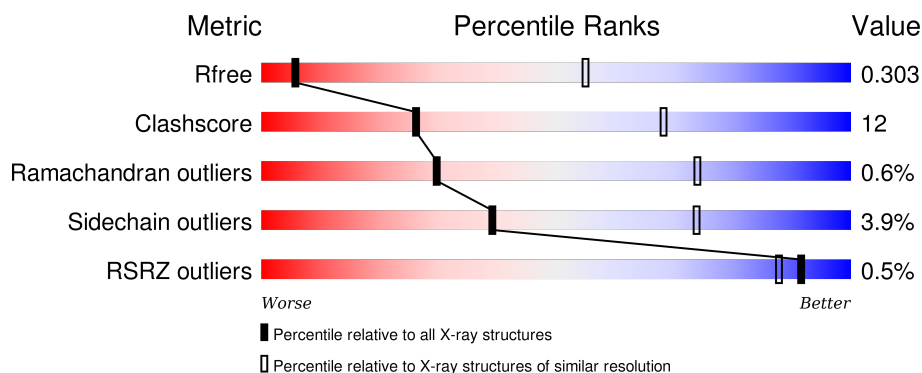
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.35 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	1063 (5.08-3.60)
Clashscore	102246	1171 (5.08-3.60)
Ramachandran outliers	100387	1110 (5.08-3.60)
Sidechain outliers	100360	1093 (5.08-3.60)
RSRZ outliers	91569	1067 (5.08-3.60)

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	1282	<div> <div style="width: 62%; background-color: green;"></div> <div style="width: 29%; background-color: yellow;"></div> <div style="width: 7%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 2%; background-color: grey;"></div> </div> <div>62% 29% • 7%</div>
1	B	1282	<div> <div style="width: 66%; background-color: green;"></div> <div style="width: 24%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 2%; background-color: grey;"></div> </div> <div>66% 24% • 8%</div>

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	2J8	B	6003	-	-	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18473 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.

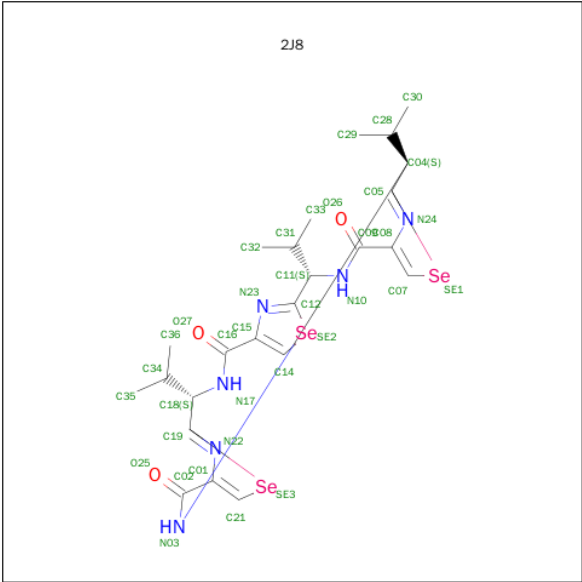
- Molecule 1 is a protein called Multidrug resistance protein 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1188	Total	C	N	O	S	0	0	0
			9214	5923	1559	1694	38			
1	B	1180	Total	C	N	O	S	0	0	0
			9153	5887	1550	1678	38			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	GLN	ASN	CONFLICT	UNP P21447
A	87	GLN	ASN	CONFLICT	UNP P21447
A	90	GLN	ASN	CONFLICT	UNP P21447
A	1277	HIS	-	EXPRESSION TAG	UNP P21447
A	1278	HIS	-	EXPRESSION TAG	UNP P21447
A	1279	HIS	-	EXPRESSION TAG	UNP P21447
A	1280	HIS	-	EXPRESSION TAG	UNP P21447
A	1281	HIS	-	EXPRESSION TAG	UNP P21447
A	1282	HIS	-	EXPRESSION TAG	UNP P21447
B	83	GLN	ASN	CONFLICT	UNP P21447
B	87	GLN	ASN	CONFLICT	UNP P21447
B	90	GLN	ASN	CONFLICT	UNP P21447
B	1277	HIS	-	EXPRESSION TAG	UNP P21447
B	1278	HIS	-	EXPRESSION TAG	UNP P21447
B	1279	HIS	-	EXPRESSION TAG	UNP P21447
B	1280	HIS	-	EXPRESSION TAG	UNP P21447
B	1281	HIS	-	EXPRESSION TAG	UNP P21447
B	1282	HIS	-	EXPRESSION TAG	UNP P21447

- Molecule 2 is (4S,11S,18S)-4,11,18-TRI(PROPAN-2-YL)-6,13,20-TRISELENA-3,10,17,22,23,24-HEXAAZATETRACYCLO[17.2.1.1 5,8 .1 12,15]TETRACOSA-1(21),5(24),7,12(23),14,19(22)-HEXAENE-2,9,16-TRIONE (three-letter code: 2J8) (formula: C₂₄H₃₀N₆O₃Se₃).

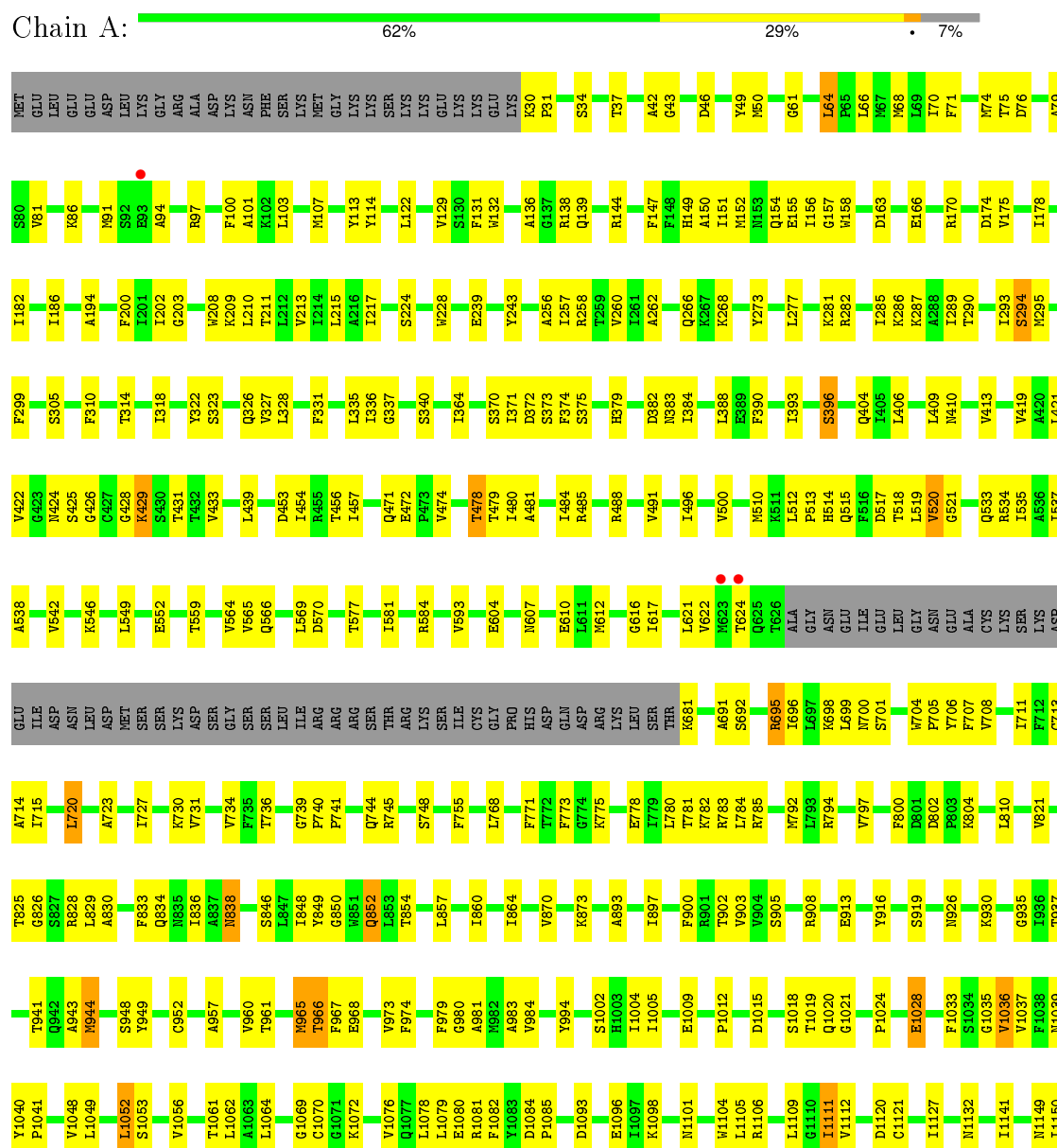


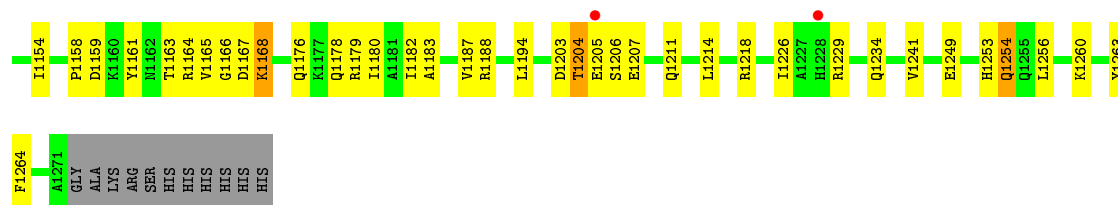
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	Se	0	0
			36	24	6	3	3		
2	A	1	Total	C	N	O	Se	0	0
			17	11	3	1	2		
2	B	1	Total	C	N	O	Se	0	0
			36	24	6	3	3		
2	B	1	Total	C	N	O	Se	0	0
			17	11	3	1	2		

3 Residue-property plots

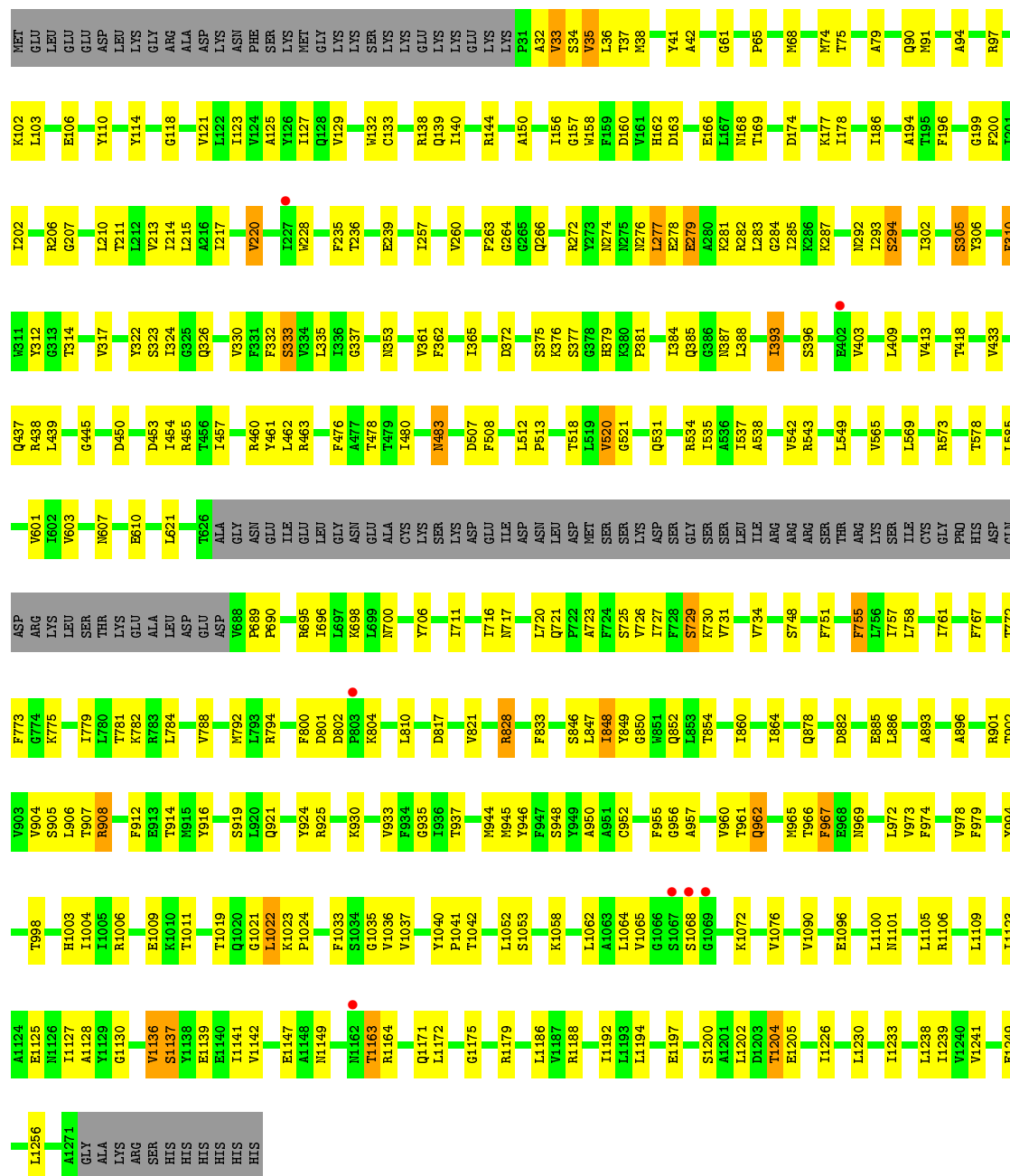
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Multidrug resistance protein 1A





• Molecule 1: Multidrug resistance protein 1A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.74Å 114.98Å 375.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 4.35 19.95 – 4.35	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.95-4.35) 93.2 (19.95-4.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 4.36Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.221 , 0.283 0.254 , 0.303	Depositor DCC
R_{free} test set	2807 reflections (11.77%)	DCC
Wilson B-factor (Å ²)	199.0	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 90.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 28285 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18473	wwPDB-VP
Average B, all atoms (Å ²)	201.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% 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: 2J8

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	0.29	0/9383	0.47	0/12685
1	B	0.29	0/9322	0.46	0/12602
All	All	0.29	0/18705	0.46	0/25287

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	9214	0	9388	249	0
1	B	9153	0	9338	208	0
2	A	53	0	36	6	0
2	B	53	0	36	6	0
All	All	18473	0	18798	457	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 12.

All (457) 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:B:1022:LEU:HD11	1:B:1100:LEU:HA	1.56	0.87
1:A:281:LYS:HZ2	1:A:782:LYS:HA	1.40	0.85
1:B:206:ARG:O	1:B:326:GLN:NE2	2.13	0.81
1:B:433:VAL:HG13	1:B:549:LEU:HD23	1.63	0.81
1:A:794:ARG:NH1	1:A:1015:ASP:OD2	2.14	0.81
1:A:433:VAL:HG13	1:A:549:LEU:HD23	1.64	0.79
1:B:930:LYS:HB2	1:B:930:LYS:HZ2	1.49	0.78
1:B:690:PRO:HD2	1:B:1006:ARG:NH1	2.00	0.75
1:A:966:THR:OG1	1:A:967:PHE:N	2.20	0.74
1:B:228:TRP:HB3	1:B:294:SER:HB2	1.69	0.74
1:A:388:LEU:HB2	1:A:413:VAL:HB	1.70	0.73
1:B:206:ARG:HG3	1:B:326:GLN:HG3	1.69	0.72
1:A:281:LYS:HE2	1:A:785:ARG:NH1	2.06	0.71
1:A:1149:ASN:O	1:A:1179:ARG:NH2	2.24	0.71
1:A:784:LEU:HD22	1:A:821:VAL:HG11	1.73	0.70
1:A:406:LEU:HD13	1:A:409:LEU:HD22	1.73	0.70
1:B:1076:VAL:HG13	1:B:1194:LEU:HD13	1.74	0.70
1:B:393:ILE:H	1:B:445:GLY:HA3	1.56	0.70
1:A:794:ARG:HG2	1:A:1012:PRO:HG3	1.74	0.70
1:A:281:LYS:NZ	1:A:782:LYS:HA	2.07	0.68
1:A:34:SER:HG	1:A:37:THR:HG1	1.39	0.68
1:A:559:THR:HG22	1:A:584:ARG:HH12	1.58	0.68
1:A:612:MET:HE1	1:A:622:VAL:HG11	1.74	0.68
1:A:34:SER:OG	1:A:37:THR:OG1	2.11	0.68
1:B:199:GLY:O	1:B:333:SER:OG	2.11	0.67
1:A:1241:VAL:HB	1:A:1249:GLU:HB2	1.75	0.67
1:A:393:ILE:HB	1:A:409:LEU:HB3	1.77	0.67
1:B:846:SER:HB2	1:B:973:VAL:HG13	1.77	0.66
1:A:1069:GLY:HA2	1:A:1072:LYS:HB2	1.77	0.66
1:A:1150:ILE:HG22	1:A:1179:ARG:HB3	1.77	0.65
1:A:1079:LEU:HG	1:A:1109:LEU:HD21	1.79	0.65
1:A:930:LYS:HZ2	1:A:930:LYS:HB2	1.63	0.64
1:A:262:ALA:HB1	1:A:1111:ILE:HG21	1.79	0.64
1:A:86:LYS:NZ	1:A:740:PRO:HD3	2.13	0.64
1:B:94:ALA:HB1	1:B:97:ARG:HE	1.63	0.63
1:B:792:MET:HE1	1:B:810:LEU:HB3	1.79	0.63
1:B:177:LYS:HE2	1:B:353:ASN:HB3	1.81	0.63
1:A:930:LYS:HB2	1:A:930:LYS:NZ	2.14	0.62
1:A:318:ILE:HD12	1:A:745:ARG:HE	1.64	0.62
1:B:129:VAL:HG13	1:B:935:GLY:HA2	1.82	0.62
1:A:780:LEU:O	1:A:784:LEU:HB2	2.00	0.61
1:B:274:ASN:HA	1:B:277:LEU:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:ASN:H	1:A:429:LYS:NZ	1.97	0.61
1:A:730:LYS:HD3	1:A:968:GLU:OE2	2.00	0.61
1:B:689:PRO:HG3	1:B:1003:HIS:CD2	2.35	0.60
1:A:419:VAL:HG22	1:A:593:VAL:HB	1.83	0.60
1:A:916:TYR:O	1:A:919:SER:OG	2.16	0.60
1:B:1136:VAL:HG22	1:B:1137:SER:H	1.67	0.60
1:B:1230:LEU:HD23	1:B:1233:ILE:HD12	1.83	0.60
1:A:698:LYS:O	1:A:701:SER:OG	2.18	0.60
1:A:566:GLN:NE2	1:A:570:ASP:OD1	2.35	0.59
1:B:217:ILE:HG21	1:B:305:SER:HB2	1.84	0.59
1:A:64:LEU:HD12	1:A:336:ILE:HG21	1.84	0.59
1:A:480:ILE:HG23	1:A:535:ILE:HD13	1.84	0.59
1:A:70:ILE:HD13	1:A:113:TYR:HB3	1.84	0.59
1:A:695:ARG:NH1	1:A:1009:GLU:OE2	2.36	0.59
1:B:784:LEU:HD22	1:B:821:VAL:HG11	1.84	0.59
1:A:857:LEU:HD12	1:A:973:VAL:HG12	1.85	0.58
2:A:6001:2J8:H36A	2:A:6002:2J8:H30A	1.84	0.58
1:A:122:LEU:HB3	1:A:943:ALA:HB2	1.85	0.58
1:A:471:GLN:HG3	1:A:472:GLU:HG3	1.85	0.58
1:A:1033:PHE:HD1	1:A:1036:VAL:HG11	1.67	0.58
1:A:902:THR:O	1:A:905:SER:OG	2.21	0.58
1:A:1021:GLY:HA3	1:A:1101:ASN:HB2	1.85	0.58
1:B:901:ARG:O	1:B:905:SER:OG	2.19	0.57
1:B:302:ILE:HD12	2:B:6003:2J8:H35A	1.86	0.57
1:B:1064:LEU:HB2	1:B:1226:ILE:HG13	1.85	0.57
1:B:61:GLY:HA3	1:B:194:ALA:HB3	1.85	0.57
1:A:519:LEU:HD21	1:B:925:ARG:HD3	1.85	0.57
1:B:849:TYR:HB3	1:B:969:ASN:HB3	1.86	0.57
1:A:144:ARG:HB3	1:A:175:VAL:HG11	1.85	0.57
1:A:208:TRP:CE3	1:A:209:LYS:HG2	2.39	0.57
1:B:1175:GLY:HA2	1:B:1202:LEU:HD11	1.86	0.57
1:B:695:ARG:HA	1:B:698:LYS:NZ	2.19	0.57
1:A:1211:GLN:HA	1:A:1214:LEU:HB2	1.87	0.57
1:B:418:THR:HG23	1:B:578:THR:HB	1.85	0.57
1:A:607:ASN:HB3	1:A:610:GLU:OE2	2.04	0.57
1:A:382:ASP:OD1	1:A:382:ASP:N	2.36	0.57
1:A:281:LYS:HZ2	1:A:782:LYS:CA	2.16	0.57
1:A:200:PHE:CE2	1:A:215:LEU:HD12	2.40	0.57
1:A:210:LEU:HD21	1:A:327:VAL:HG13	1.87	0.56
1:A:1234:GLN:HG2	1:A:1253:HIS:CE1	2.40	0.56
1:B:512:LEU:HD13	1:B:518:THR:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:534:ARG:HA	1:B:537:ILE:HD12	1.86	0.56
1:B:916:TYR:O	1:B:919:SER:OG	2.19	0.56
1:B:385:GLN:HB2	1:B:450:ASP:OD2	2.04	0.56
1:A:281:LYS:NZ	1:A:785:ARG:HD2	2.20	0.56
1:A:152:MET:HA	1:A:900:PHE:HE2	1.70	0.56
1:B:438:ARG:NH1	1:B:455:ARG:HA	2.21	0.56
1:A:1064:LEU:HB2	1:A:1226:ILE:HG13	1.88	0.56
1:B:902:THR:O	1:B:906:LEU:HD12	2.05	0.56
1:A:1249:GLU:OE2	1:A:1263:TYR:HB2	2.06	0.56
1:A:1106:ARG:O	1:A:1188:ARG:NH1	2.39	0.56
1:A:421:LEU:HB2	1:A:581:ILE:HG12	1.87	0.55
1:A:846:SER:O	1:A:854:THR:OG1	2.17	0.55
1:A:243:TYR:CD1	1:A:785:ARG:NH1	2.74	0.55
1:A:86:LYS:HD2	1:A:739:GLY:HA2	1.88	0.55
1:B:276:ASN:HA	1:B:279:GLU:HG3	1.87	0.55
1:A:1002:SER:HA	1:A:1005:ILE:HG12	1.89	0.55
1:A:1249:GLU:HB3	1:A:1256:LEU:HD22	1.87	0.55
1:B:696:ILE:HD11	1:B:998:THR:HG23	1.89	0.55
1:A:825:THR:OG1	1:A:826:GLY:N	2.39	0.55
1:A:379:HIS:H	1:A:457:ILE:HA	1.71	0.55
1:A:49:TYR:HA	1:A:131:PHE:HD2	1.71	0.55
1:B:257:ILE:HD12	1:B:260:VAL:HB	1.89	0.55
1:A:371:ILE:O	1:A:373:SER:HB3	2.07	0.54
1:A:699:LEU:HD23	1:A:784:LEU:HD11	1.88	0.54
1:A:208:TRP:HE3	1:A:209:LYS:HG2	1.71	0.54
1:A:1260:LYS:HA	1:A:1264:PHE:HB2	1.90	0.54
1:A:1015:ASP:OD1	1:A:1018:SER:N	2.41	0.54
1:B:1021:GLY:HA2	1:B:1101:ASN:HB2	1.87	0.54
1:A:453:ASP:HB3	1:A:456:THR:HG23	1.90	0.54
1:A:310:PHE:HD2	1:A:755:PHE:HE2	1.55	0.54
1:B:908:ARG:HE	1:B:908:ARG:HA	1.73	0.54
1:B:846:SER:HA	1:B:973:VAL:HG22	1.90	0.54
1:A:534:ARG:NH1	1:A:564:VAL:HG11	2.22	0.54
1:B:91:MET:SD	1:B:97:ARG:NH2	2.66	0.53
1:A:852:GLN:CD	1:A:852:GLN:H	2.11	0.53
1:A:91:MET:HB3	1:A:94:ALA:HB3	1.88	0.53
1:A:893:ALA:O	1:A:897:ILE:HG12	2.09	0.53
1:B:585:LEU:HD11	1:B:621:LEU:HB3	1.91	0.53
1:B:38:MET:HA	1:B:362:PHE:HE2	1.72	0.53
1:A:979:PHE:HZ	2:A:6002:2J8:C21	2.21	0.53
1:A:286:LYS:O	1:A:290:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:GLY:C	1:A:211:THR:HG21	2.28	0.53
1:A:66:LEU:HD23	1:A:202:ILE:HD11	1.90	0.53
1:B:317:VAL:HG23	1:B:323:SER:HA	1.91	0.53
1:B:1058:LYS:HB3	1:B:1058:LYS:NZ	2.24	0.53
1:A:406:LEU:HD22	1:A:409:LEU:HD13	1.90	0.53
1:A:512:LEU:HD13	1:A:518:THR:HG21	1.91	0.53
1:A:481:ALA:O	1:A:485:ARG:HG2	2.09	0.52
1:B:102:LYS:HE3	1:B:106:GLU:OE2	2.08	0.52
1:A:621:LEU:HA	1:A:624:THR:HG22	1.91	0.52
1:A:1028:GLU:HB3	1:A:1093:ASP:OD2	2.09	0.52
1:A:1096:GLU:OE1	1:A:1098:LYS:N	2.38	0.52
1:A:46:ASP:OD1	1:A:138:ARG:NH1	2.42	0.52
1:A:833:PHE:HA	1:A:836:ILE:HG22	1.92	0.52
1:B:272:ARG:NH2	1:B:1125:GLU:OE2	2.43	0.52
1:A:79:ALA:HA	1:A:736:THR:HA	1.92	0.52
1:B:979:PHE:CE1	2:B:6004:2J8:H29B	2.44	0.52
1:B:758:LEU:HA	1:B:761:ILE:HD12	1.92	0.52
1:A:1035:GLY:N	1:A:1053:SER:OG	2.42	0.52
1:B:385:GLN:OE1	1:B:387:ASN:ND2	2.43	0.52
1:B:388:LEU:HB2	1:B:413:VAL:HB	1.92	0.52
1:B:507:ASP:OD1	1:B:508:PHE:N	2.41	0.52
1:B:1090:VAL:N	1:B:1096:GLU:OE2	2.35	0.52
1:B:957:ALA:O	1:B:961:THR:HG23	2.10	0.52
1:B:1109:LEU:HD12	1:B:1192:ILE:HB	1.91	0.51
1:A:1036:VAL:HG23	1:A:1085:PRO:HB3	1.92	0.51
1:B:65:PRO:HB2	1:B:202:ILE:HD12	1.92	0.51
1:A:496:ILE:O	1:A:500:VAL:HG23	2.11	0.51
1:A:86:LYS:HZ2	1:A:740:PRO:HD3	1.75	0.51
1:A:299:PHE:HZ	2:A:6001:2J8:C07	2.24	0.51
1:B:437:GLN:HG3	1:B:439:LEU:HG	1.92	0.51
1:B:966:THR:H	1:B:967:PHE:HA	1.74	0.51
1:B:538:ALA:O	1:B:542:VAL:HG23	2.11	0.51
1:A:1204:THR:OG1	1:A:1205:GLU:N	2.43	0.51
1:A:604:GLU:OE2	1:A:616:GLY:HA3	2.11	0.51
1:A:1061:THR:HG21	1:A:1218:ARG:HD3	1.91	0.51
1:A:485:ARG:NH2	1:B:914:THR:OG1	2.41	0.51
1:B:847:LEU:HG	1:B:854:THR:HG21	1.93	0.51
1:A:372:ASP:HA	1:A:373:SER:HB3	1.91	0.51
1:B:956:GLY:O	1:B:960:VAL:HG23	2.11	0.51
1:A:175:VAL:HA	1:A:178:ILE:HG22	1.92	0.51
1:A:484:ILE:HG23	1:A:542:VAL:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:711:ILE:HG12	1:B:833:PHE:CE2	2.45	0.50
1:A:299:PHE:CE2	2:A:6001:2J8:H33B	2.47	0.50
1:B:160:ASP:OD1	1:B:901:ARG:NH2	2.43	0.50
1:B:1204:THR:OG1	1:B:1205:GLU:N	2.42	0.50
1:B:979:PHE:HZ	2:B:6004:2J8:C01	2.24	0.50
1:B:965:MET:HB3	1:B:966:THR:OG1	2.10	0.50
1:A:1049:LEU:HD22	1:A:1052:LEU:HD22	1.93	0.50
1:A:792:MET:HE1	1:A:810:LEU:HB3	1.93	0.50
1:B:74:MET:HA	1:B:110:TYR:CE2	2.46	0.50
1:B:94:ALA:HB1	1:B:97:ARG:NE	2.27	0.50
1:A:1078:LEU:HD22	1:A:1085:PRO:HD3	1.92	0.50
1:B:460:ARG:HG3	1:B:907:THR:HG21	1.94	0.50
1:A:699:LEU:O	1:A:783:ARG:NH2	2.35	0.49
1:A:314:THR:OG1	1:A:748:SER:OG	2.25	0.49
1:B:960:VAL:HG21	1:B:967:PHE:HB2	1.93	0.49
1:B:285:ILE:HD12	1:B:775:LYS:HG2	1.94	0.49
1:B:132:TRP:CZ3	1:B:186:ILE:HD11	2.48	0.49
1:A:257:ILE:HG12	1:A:800:PHE:CE2	2.47	0.49
1:B:322:TYR:O	1:B:326:GLN:HB3	2.13	0.49
1:A:424:ASN:HB2	1:A:621:LEU:HD21	1.95	0.49
1:A:538:ALA:O	1:A:542:VAL:HG23	2.12	0.49
1:B:282:ARG:HH22	1:B:779:ILE:HA	1.77	0.49
1:B:896:ALA:HB2	1:B:912:PHE:CD2	2.48	0.49
1:A:76:ASP:OD1	1:A:323:SER:OG	2.25	0.49
1:B:1149:ASN:O	1:B:1179:ARG:NH2	2.46	0.49
1:A:1101:ASN:HB3	1:A:1104:TRP:HB3	1.95	0.49
1:B:695:ARG:NH2	1:B:1009:GLU:OE2	2.46	0.49
1:A:1076:VAL:HG13	1:A:1194:LEU:HB3	1.93	0.48
1:A:937:THR:O	1:A:941:THR:HG23	2.13	0.48
1:B:381:PRO:O	1:B:461:TYR:OH	2.24	0.48
1:B:772:THR:OG1	1:B:773:PHE:N	2.46	0.48
1:A:281:LYS:NZ	1:A:781:THR:HG22	2.28	0.48
1:B:1123:ILE:HG12	1:B:1163:THR:HG23	1.95	0.48
1:A:692:SER:OG	1:A:695:ARG:HB3	2.13	0.48
1:A:741:PRO:HA	1:A:744:GLN:HG3	1.95	0.48
1:B:960:VAL:HG21	1:B:967:PHE:CB	2.43	0.48
1:A:158:TRP:HZ2	1:A:364:ILE:HD12	1.77	0.48
1:A:129:VAL:HG13	1:A:935:GLY:HA2	1.95	0.48
1:A:268:LYS:HZ1	1:A:1132:ASN:HA	1.78	0.48
1:B:123:ILE:O	1:B:127:ILE:HG12	2.13	0.48
1:B:1106:ARG:O	1:B:1188:ARG:NH1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:SER:HB3	1:A:404:GLN:HA	1.95	0.48
1:B:848:ILE:HG22	1:B:849:TYR:CD2	2.48	0.48
1:B:42:ALA:HB2	1:B:139:GLN:NE2	2.28	0.48
1:A:1024:PRO:HD2	1:A:1104:TRP:CH2	2.49	0.48
1:B:1065:VAL:HG23	1:B:1241:VAL:HA	1.94	0.48
1:B:1233:ILE:HG22	1:B:1239:ILE:HG12	1.94	0.48
1:A:900:PHE:HA	1:A:903:VAL:HG12	1.96	0.48
1:B:68:MET:HE3	1:B:332:PHE:HB3	1.95	0.48
1:A:42:ALA:HB2	1:A:139:GLN:OE1	2.12	0.48
1:A:75:THR:HG22	1:A:967:PHE:HZ	1.79	0.48
1:B:379:HIS:HB2	1:B:457:ILE:HG22	1.95	0.48
1:A:323:SER:HB3	1:A:326:GLN:HG3	1.96	0.48
1:B:730:LYS:HB3	1:B:751:PHE:CE2	2.48	0.47
1:A:797:VAL:HG21	1:A:1082:PHE:CG	2.49	0.47
1:A:100:PHE:CD1	1:A:961:THR:HB	2.49	0.47
1:B:376:LYS:HA	1:B:377:SER:HA	1.65	0.47
1:B:784:LEU:HD21	1:B:1004:ILE:HG21	1.96	0.47
1:B:908:ARG:HA	1:B:908:ARG:NE	2.28	0.47
1:A:704:TRP:CG	1:A:705:PRO:HD3	2.49	0.47
1:A:213:VAL:O	1:A:217:ILE:HG12	2.14	0.47
1:B:952:CYS:SG	1:B:974:PHE:HD1	2.38	0.47
1:A:1056:VAL:HG21	1:A:1062:LEU:HB2	1.96	0.47
1:A:691:ALA:HB1	1:A:692:SER:HB2	1.97	0.47
2:A:6002:2J8:H30B	2:A:6002:2J8:SE1	2.64	0.47
1:A:273:TYR:CE2	1:A:277:LEU:HD11	2.49	0.47
1:B:1033:PHE:HD1	1:B:1036:VAL:HG21	1.79	0.47
1:B:306:TYR:HE1	2:B:6003:2J8:H35B	1.80	0.47
1:B:125:ALA:O	1:B:129:VAL:HG12	2.14	0.47
1:A:517:ASP:O	1:B:925:ARG:NH1	2.40	0.47
1:B:200:PHE:CE2	1:B:215:LEU:HD12	2.49	0.47
1:A:239:GLU:HB2	1:A:287:LYS:NZ	2.28	0.47
1:A:114:TYR:CE1	1:A:949:TYR:HB3	2.49	0.47
1:A:425:SER:OG	1:A:426:GLY:N	2.48	0.47
1:A:965:MET:HA	1:A:966:THR:HA	1.70	0.47
1:B:457:ILE:HD11	1:B:462:LEU:HD13	1.97	0.47
1:A:155:GLU:OE1	1:A:370:SER:OG	2.32	0.47
1:B:1197:GLU:HB3	1:B:1200:SER:HB3	1.97	0.47
1:B:1127:ILE:HG21	1:B:1141:ILE:HG23	1.97	0.47
1:B:607:ASN:HB3	1:B:610:GLU:OE1	2.15	0.46
1:A:136:ALA:HB2	1:A:182:ILE:O	2.16	0.46
1:B:933:VAL:O	1:B:937:THR:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:453:ASP:OD2	1:B:455:ARG:NH2	2.48	0.46
1:A:170:ARG:HG3	1:A:174:ASP:HB2	1.96	0.46
1:A:43:GLY:H	1:A:46:ASP:HB2	1.80	0.46
1:A:723:ALA:O	1:A:727:ILE:HG12	2.16	0.46
1:A:860:ILE:O	1:A:864:ILE:HG13	2.14	0.46
1:A:714:ALA:HB1	1:A:834:GLN:HG3	1.97	0.46
1:A:1158:PRO:HA	1:A:1159:ASP:HA	1.42	0.46
1:A:850:GLY:O	1:A:854:THR:OG1	2.34	0.46
1:B:726:VAL:HA	1:B:972:LEU:HD23	1.97	0.46
1:B:278:GLU:HB2	1:B:782:LYS:NZ	2.31	0.46
1:B:196:PHE:HD1	1:B:337:GLY:O	1.99	0.46
1:A:510:MET:HA	1:A:515:GLN:HE22	1.80	0.46
1:A:61:GLY:HA3	1:A:194:ALA:HB3	1.97	0.46
1:A:68:MET:HE1	2:A:6002:2J8:O25	2.16	0.46
1:B:257:ILE:HG12	1:B:800:PHE:CE2	2.51	0.46
1:A:802:ASP:OD1	1:A:804:LYS:HG2	2.16	0.46
1:A:156:ILE:HD12	1:A:157:GLY:N	2.31	0.46
1:B:314:THR:HA	1:B:317:VAL:HG12	1.98	0.46
1:A:1154:ILE:HD13	1:A:1161:TYR:CE2	2.50	0.46
1:B:361:VAL:O	1:B:365:ILE:HG13	2.16	0.46
1:B:788:VAL:O	1:B:792:MET:HG3	2.16	0.45
1:B:893:ALA:HB2	1:B:916:TYR:CE1	2.51	0.45
1:B:281:LYS:HD2	1:B:781:THR:HB	1.98	0.45
1:B:1164:ARG:O	1:B:1171:GLN:NE2	2.49	0.45
1:B:33:VAL:HB	1:B:34:SER:H	1.46	0.45
1:B:34:SER:HG	1:B:37:THR:HG1	1.61	0.45
1:A:71:PHE:HE1	1:A:328:LEU:HD13	1.81	0.45
1:B:1100:LEU:HD13	1:B:1105:LEU:HD13	1.98	0.45
1:A:210:LEU:HB2	1:A:322:TYR:HE1	1.80	0.45
1:B:281:LYS:O	1:B:285:ILE:HG12	2.17	0.45
1:B:1023:LYS:HA	1:B:1024:PRO:HD3	1.74	0.45
1:A:147:PHE:O	1:A:151:ILE:HG13	2.16	0.45
1:A:838:ASN:ND2	1:A:983:ALA:HB3	2.30	0.45
1:A:1178:GLN:O	1:A:1182:ILE:HG12	2.16	0.45
1:A:981:ALA:O	1:A:984:VAL:HG22	2.16	0.45
1:A:707:PHE:O	1:A:711:ILE:HG12	2.16	0.45
1:A:1081:ARG:HH11	1:A:1081:ARG:HG2	1.81	0.45
1:A:156:ILE:HG12	1:A:439:LEU:HB3	1.98	0.45
1:B:236:THR:O	1:B:239:GLU:HB3	2.17	0.45
1:A:471:GLN:HB3	1:A:552:GLU:HB2	1.98	0.45
1:B:921:GLN:HB3	1:B:925:ARG:NH2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:726:VAL:HG22	1:B:972:LEU:HD21	1.97	0.45
1:A:1183:ALA:O	1:A:1187:VAL:HG23	2.17	0.45
1:A:513:PRO:HB2	1:A:514:HIS:CD2	2.51	0.45
1:A:163:ASP:HB3	1:A:166:GLU:HG2	1.99	0.45
1:B:852:GLN:HG2	1:B:955:PHE:HZ	1.82	0.45
1:B:1022:LEU:HD11	1:B:1100:LEU:HD23	1.98	0.45
1:A:30:LYS:HA	1:A:31:PRO:HD3	1.72	0.45
1:B:114:TYR:HB3	1:B:950:ALA:HB2	1.97	0.45
1:B:848:ILE:HA	1:B:848:ILE:HD12	1.83	0.45
1:A:731:VAL:O	1:A:734:VAL:HG12	2.16	0.45
1:B:235:PHE:HB3	1:B:287:LYS:HB2	1.99	0.45
1:A:1040:TYR:HA	1:A:1041:PRO:HD3	1.72	0.45
1:A:1260:LYS:HA	1:A:1264:PHE:CB	2.46	0.44
1:B:711:ILE:HG12	1:B:833:PHE:HE2	1.82	0.44
1:A:980:GLY:O	1:A:984:VAL:HG13	2.17	0.44
1:B:284:GLY:O	1:B:287:LYS:HB3	2.16	0.44
1:B:802:ASP:OD2	1:B:804:LYS:HG2	2.17	0.44
1:B:121:VAL:HG21	1:B:946:TYR:CE1	2.52	0.44
1:B:210:LEU:O	1:B:214:ILE:HG13	2.17	0.44
1:A:372:ASP:CA	1:A:373:SER:HB3	2.47	0.44
1:A:256:ALA:O	1:A:260:VAL:HG23	2.17	0.44
1:A:773:PHE:CE2	1:A:830:ALA:HB2	2.52	0.44
1:B:794:ARG:HH12	1:B:1011:THR:HA	1.83	0.44
1:B:1035:GLY:N	1:B:1053:SER:OG	2.27	0.44
1:A:784:LEU:CD2	1:A:821:VAL:HG11	2.46	0.44
1:B:1147:GLU:CD	1:B:1186:LEU:HD21	2.38	0.44
1:A:784:LEU:HD21	1:A:1004:ILE:HG21	1.99	0.44
1:A:1165:VAL:HA	1:A:1166:GLY:HA2	1.62	0.44
1:A:149:HIS:HA	1:A:913:GLU:OE2	2.18	0.44
1:A:81:VAL:HG21	1:A:103:LEU:HD11	1.99	0.44
1:B:1062:LEU:HD12	1:B:1238:LEU:O	2.16	0.44
1:A:828:ARG:HG2	1:A:994:TYR:CE2	2.53	0.44
1:B:207:GLY:HA3	1:B:330:VAL:HG21	2.00	0.44
1:B:1139:GLU:HA	1:B:1142:VAL:HG12	2.00	0.44
1:B:543:ARG:NH1	1:B:906:LEU:HD23	2.33	0.44
1:A:1080:GLU:HG3	1:A:1106:ARG:HD3	1.99	0.44
1:B:520:VAL:HG22	1:B:521:GLY:H	1.82	0.44
1:A:870:VAL:HA	1:A:873:LYS:HB3	1.98	0.44
1:A:1203:ASP:O	1:A:1206:SER:OG	2.32	0.44
1:B:79:ALA:HB2	1:B:324:ILE:HG21	2.00	0.44
1:A:1076:VAL:HG13	1:A:1194:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:512:LEU:HA	1:B:513:PRO:HD3	1.87	0.43
1:A:228:TRP:HB3	1:A:294:SER:HB2	1.98	0.43
1:A:696:ILE:H	1:A:696:ILE:HG13	1.60	0.43
1:A:1079:LEU:HD23	1:A:1194:LEU:HD21	2.00	0.43
1:B:978:VAL:HG12	1:B:979:PHE:CD1	2.53	0.43
1:B:476:PHE:H	1:B:483:ASN:HD21	1.67	0.43
1:A:696:ILE:HA	1:A:699:LEU:HD13	1.99	0.43
1:A:1121:CYS:O	1:A:1164:ARG:NH1	2.52	0.43
1:A:533:GLN:O	1:A:537:ILE:HG13	2.17	0.43
1:A:1254:GLN:NE2	1:A:1254:GLN:H	2.17	0.43
1:A:952:CYS:HG	1:A:974:PHE:HD1	1.65	0.43
1:B:168:ASN:OD1	1:B:169:THR:N	2.51	0.43
1:A:1207:GLU:HB2	1:A:1229:ARG:HH22	1.84	0.43
1:A:149:HIS:CD2	1:A:913:GLU:OE2	2.72	0.43
1:A:565:VAL:O	1:A:569:LEU:HG	2.19	0.43
1:B:293:ILE:HD12	1:B:767:PHE:HD1	1.84	0.43
1:B:882:ASP:HA	1:B:885:GLU:HG2	2.01	0.43
1:A:285:ILE:HD12	1:A:775:LYS:HG2	2.00	0.43
1:A:74:MET:HG3	1:A:107:MET:HE1	2.01	0.43
1:A:488:ARG:NH2	1:A:491:VAL:HG12	2.34	0.43
1:B:480:ILE:HD12	1:B:535:ILE:HD13	2.00	0.42
1:B:731:VAL:O	1:B:734:VAL:HG22	2.19	0.42
1:A:287:LYS:HE2	1:A:287:LYS:HB3	1.69	0.42
1:B:35:VAL:HG13	1:B:36:LEU:H	1.84	0.42
1:B:372:ASP:HB3	1:B:375:SER:HB3	2.00	0.42
1:B:690:PRO:HD2	1:B:1006:ARG:HH11	1.82	0.42
1:B:757:ILE:O	1:B:761:ILE:HG13	2.20	0.42
1:A:1159:ASP:OD1	1:A:1159:ASP:N	2.52	0.42
1:A:1112:VAL:HG21	1:A:1182:ILE:HD13	2.01	0.42
1:A:706:TYR:HE1	1:A:775:LYS:HD2	1.85	0.42
1:B:463:ARG:NH1	1:B:904:VAL:HG22	2.34	0.42
1:A:337:GLY:O	1:A:340:SER:OG	2.36	0.42
1:B:846:SER:O	1:B:854:THR:OG1	2.37	0.42
1:A:926:ASN:O	1:A:930:LYS:NZ	2.52	0.42
1:A:1176:GLN:O	1:A:1180:ILE:HG13	2.19	0.42
1:A:150:ALA:O	1:A:154:GLN:HG2	2.18	0.42
1:B:210:LEU:HB2	1:B:322:TYR:HE2	1.83	0.42
1:A:699:LEU:HD21	1:A:1005:ILE:HG22	2.01	0.42
1:B:543:ARG:HH11	1:B:906:LEU:HD23	1.84	0.42
1:A:838:ASN:HD21	1:A:983:ALA:HB3	1.85	0.42
1:B:1249:GLU:HG2	1:B:1256:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:944:MET:HE3	1:A:944:MET:HB2	1.93	0.42
1:A:132:TRP:CZ3	1:A:186:ILE:HD11	2.55	0.42
1:B:850:GLY:O	1:B:854:THR:OG1	2.23	0.42
1:A:453:ASP:OD1	1:A:454:ILE:N	2.52	0.42
1:A:848:ILE:HG13	1:A:849:TYR:CD1	2.55	0.42
1:B:213:VAL:HG21	1:B:312:TYR:CE2	2.54	0.42
1:A:314:THR:O	1:A:318:ILE:HG13	2.19	0.42
1:B:1202:LEU:HA	1:B:1202:LEU:HD12	1.84	0.42
1:A:520:VAL:HB	1:A:521:GLY:H	1.65	0.42
1:B:140:ILE:HD13	1:B:140:ILE:HA	1.92	0.42
1:A:429:LYS:HB3	1:A:581:ILE:HD13	2.02	0.42
1:A:1084:ASP:HA	1:A:1085:PRO:HD2	1.88	0.42
1:B:965:MET:HA	1:B:966:THR:HA	1.94	0.42
1:B:960:VAL:HG22	1:B:966:THR:N	2.34	0.42
1:A:908:ARG:HA	1:A:908:ARG:HD3	1.78	0.42
1:B:1040:TYR:HA	1:B:1041:PRO:HD3	1.81	0.42
1:B:758:LEU:HD12	1:B:761:ILE:HD12	2.01	0.42
1:A:704:TRP:O	1:A:708:VAL:HG23	2.20	0.42
1:B:930:LYS:NZ	1:B:930:LYS:HB2	2.26	0.42
1:A:519:LEU:H	1:A:519:LEU:HD22	1.84	0.42
1:B:418:THR:HG21	1:B:573:ARG:HD2	2.02	0.42
2:B:6004:2J8:SE1	2:B:6004:2J8:H30B	2.70	0.42
1:B:706:TYR:O	1:B:772:THR:HB	2.20	0.42
1:A:510:MET:SD	1:A:515:GLN:NE2	2.93	0.42
1:B:878:GLN:HE22	1:B:930:LYS:HA	1.84	0.41
1:B:1076:VAL:HG13	1:B:1194:LEU:CD1	2.47	0.41
1:B:156:ILE:HD12	1:B:157:GLY:N	2.35	0.41
1:A:388:LEU:HD13	1:A:577:THR:HG21	2.01	0.41
1:A:1105:LEU:O	1:A:1109:LEU:HD13	2.20	0.41
1:B:721:GLN:HB2	2:B:6003:2J8:H32A	2.02	0.41
1:A:720:LEU:O	1:A:723:ALA:HB3	2.20	0.41
1:A:707:PHE:HD2	1:A:829:LEU:HD12	1.84	0.41
1:B:264:GLY:C	1:B:266:GLN:H	2.24	0.41
1:B:565:VAL:O	1:B:569:LEU:HG	2.20	0.41
1:B:310:PHE:HD2	1:B:755:PHE:HZ	1.68	0.41
1:A:784:LEU:CD2	1:A:1004:ILE:HG21	2.50	0.41
1:B:531:GLN:O	1:B:535:ILE:HG13	2.20	0.41
1:A:944:MET:HG3	1:A:944:MET:H	1.50	0.41
1:B:716:ILE:HG13	1:B:717:ASN:N	2.35	0.41
1:A:289:ILE:O	1:A:293:ILE:HG12	2.20	0.41
1:B:381:PRO:O	1:B:384:ILE:HD11	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1154:ILE:HD13	1:A:1161:TYR:CZ	2.56	0.41
1:B:41:TYR:OH	1:B:365:ILE:HG21	2.19	0.41
1:A:384:ILE:HD11	1:A:546:LYS:HB2	2.02	0.41
1:B:217:ILE:O	1:B:220:VAL:HG12	2.21	0.41
1:B:158:TRP:CE2	1:B:162:HIS:CE1	3.08	0.41
1:B:263:PHE:CD1	1:B:1130:GLY:HA2	2.56	0.41
1:B:174:ASP:O	1:B:178:ILE:HG13	2.21	0.41
1:B:828:ARG:HG3	1:B:994:TYR:CD2	2.56	0.41
1:B:138:ARG:HA	1:B:924:TYR:HE1	1.86	0.41
1:A:97:ARG:O	1:A:101:ALA:HB3	2.20	0.41
1:A:286:LYS:HA	1:A:289:ILE:HD12	2.03	0.41
1:B:103:LEU:HB2	1:B:961:THR:HG22	2.02	0.41
1:A:1127:ILE:HG21	1:A:1141:ILE:HG23	2.02	0.41
1:A:1019:THR:O	1:A:1019:THR:OG1	2.37	0.41
1:B:396:SER:OG	1:B:403:VAL:O	2.38	0.41
1:B:453:ASP:OD1	1:B:454:ILE:N	2.54	0.41
1:A:46:ASP:O	1:A:50:MET:HG3	2.21	0.41
1:B:1068:SER:O	1:B:1072:LYS:HD2	2.20	0.41
1:B:163:ASP:O	1:B:166:GLU:HG2	2.21	0.41
1:A:331:PHE:O	1:A:335:LEU:HB2	2.21	0.41
1:B:1175:GLY:CA	1:B:1202:LEU:HD11	2.51	0.41
1:B:281:LYS:HG3	1:B:782:LYS:HB2	2.02	0.41
1:A:711:ILE:O	1:A:715:ILE:HG13	2.21	0.41
1:B:689:PRO:HA	1:B:690:PRO:HD2	1.93	0.41
1:B:91:MET:HB3	1:B:94:ALA:HB3	2.03	0.41
1:B:729:SER:OG	1:B:972:LEU:HD23	2.20	0.41
1:A:510:MET:HA	1:A:515:GLN:NE2	2.36	0.41
1:B:801:ASP:O	1:B:1042:THR:HG21	2.21	0.41
1:B:723:ALA:O	1:B:727:ILE:HG12	2.21	0.41
1:B:277:LEU:HD23	1:B:277:LEU:HA	1.87	0.41
1:B:1128:ALA:HB1	1:B:1136:VAL:HG11	2.03	0.41
1:A:979:PHE:CD1	1:A:979:PHE:N	2.90	0.40
1:B:150:ALA:CB	1:B:365:ILE:HA	2.52	0.40
1:A:428:GLY:O	1:A:431:THR:HB	2.21	0.40
1:A:713:CYS:HB2	1:A:768:LEU:HD23	2.02	0.40
1:B:118:GLY:O	1:B:121:VAL:HB	2.20	0.40
1:A:224:SER:O	1:A:228:TRP:HD1	2.04	0.40
1:A:478:THR:HB	1:A:479:THR:H	1.65	0.40
1:A:390:PHE:O	1:A:410:ASN:HA	2.21	0.40
1:B:860:ILE:O	1:B:864:ILE:HG13	2.21	0.40
1:A:604:GLU:OE1	1:A:617:ILE:N	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1120:ASP:HB3	1:A:1168:LYS:HD2	2.03	0.40
1:A:422:VAL:C	1:A:429:LYS:NZ	2.74	0.40
1:A:480:ILE:HG12	1:A:480:ILE:H	1.70	0.40
1:B:961:THR:OG1	1:B:962:GLN:N	2.54	0.40
1:A:957:ALA:HA	1:A:960:VAL:HG12	2.04	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	1184/1282 (92%)	1096 (93%)	82 (7%)	6 (0%)	34	77
1	B	1176/1282 (92%)	1077 (92%)	91 (8%)	8 (1%)	26	71
All	All	2360/2564 (92%)	2173 (92%)	173 (7%)	14 (1%)	30	74

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	962	GLN
1	A	1028	GLU
1	A	1036	VAL
1	A	1204	THR
1	B	33	VAL
1	B	1136	VAL
1	B	32	ALA
1	A	838	ASN
1	A	1070	CYS
1	B	1172	LEU
1	B	1204	THR
1	A	429	LYS
1	B	393	ILE

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Mol	Chain	Res	Type
1	B	520	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	979/1063 (92%)	944 (96%)	35 (4%)	42	76
1	B	973/1063 (92%)	931 (96%)	42 (4%)	35	72
All	All	1952/2126 (92%)	1875 (96%)	77 (4%)	39	74

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	LEU
1	A	258	ARG
1	A	266	GLN
1	A	282	ARG
1	A	294	SER
1	A	295	MET
1	A	305	SER
1	A	374	PHE
1	A	375	SER
1	A	383	ASN
1	A	396	SER
1	A	474	VAL
1	A	478	THR
1	A	520	VAL
1	A	681	LYS
1	A	695	ARG
1	A	700	ASN
1	A	720	LEU
1	A	771	PHE
1	A	778	GLU
1	A	852	GLN
1	A	944	MET

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Mol	Chain	Res	Type
1	A	948	SER
1	A	965	MET
1	A	966	THR
1	A	1020	GLN
1	A	1037	VAL
1	A	1039	ASN
1	A	1048	VAL
1	A	1052	LEU
1	A	1111	ILE
1	A	1163	THR
1	A	1167	ASP
1	A	1168	LYS
1	A	1254	GLN
1	B	35	VAL
1	B	75	THR
1	B	90	GLN
1	B	133	CYS
1	B	144	ARG
1	B	211	THR
1	B	220	VAL
1	B	277	LEU
1	B	279	GLU
1	B	283	LEU
1	B	292	ASN
1	B	294	SER
1	B	305	SER
1	B	310	PHE
1	B	333	SER
1	B	335	LEU
1	B	409	LEU
1	B	478	THR
1	B	483	ASN
1	B	601	VAL
1	B	603	VAL
1	B	700	ASN
1	B	720	LEU
1	B	725	SER
1	B	729	SER
1	B	748	SER
1	B	755	PHE
1	B	817	ASP
1	B	828	ARG

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Mol	Chain	Res	Type
1	B	848	ILE
1	B	886	LEU
1	B	908	ARG
1	B	944	MET
1	B	945	MET
1	B	948	SER
1	B	967	PHE
1	B	1019	THR
1	B	1022	LEU
1	B	1037	VAL
1	B	1052	LEU
1	B	1137	SER
1	B	1163	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	HIS
1	A	266	GLN
1	A	515	GLN
1	A	834	GLN
1	A	838	ASN
1	A	852	GLN
1	B	191	GLN
1	B	292	ASN
1	B	387	ASN
1	B	394	HIS
1	B	515	GLN
1	B	608	HIS
1	B	942	GLN

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 ⓘ

4 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	2J8	A	6001	-	27,39,39	1.81	7 (25%)	24,57,57	2.96	11 (45%)
2	2J8	A	6002	-	10,18,39	1.72	2 (20%)	9,24,57	3.67	4 (44%)
2	2J8	B	6003	-	27,39,39	2.06	7 (25%)	24,57,57	3.42	11 (45%)
2	2J8	B	6004	-	10,18,39	1.19	1 (10%)	9,24,57	3.09	4 (44%)

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	2J8	A	6001	-	-	0/24/48/48	0/0/4/4
2	2J8	A	6002	-	-	0/8/16/48	0/0/2/4
2	2J8	B	6003	-	-	0/24/48/48	0/0/4/4
2	2J8	B	6004	-	-	0/8/16/48	0/0/2/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	6001	2J8	C18-N17	-2.06	1.41	1.46
2	A	6001	2J8	C28-C04	2.03	1.60	1.54
2	B	6004	2J8	C02-N03	2.27	1.39	1.34
2	B	6003	2J8	C16-N17	2.42	1.39	1.34
2	A	6001	2J8	C31-C11	2.58	1.62	1.54
2	A	6002	2J8	C02-N03	2.63	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6003	2J8	C09-N10	2.64	1.40	1.34
2	B	6003	2J8	C02-N03	2.89	1.40	1.34
2	B	6003	2J8	C28-C04	2.92	1.63	1.54
2	A	6001	2J8	C09-N10	2.95	1.40	1.34
2	A	6001	2J8	C02-N03	3.10	1.41	1.34
2	A	6001	2J8	C05-C04	3.19	1.55	1.51
2	A	6002	2J8	C05-C04	3.83	1.55	1.51
2	B	6003	2J8	C05-C04	3.88	1.55	1.51
2	B	6003	2J8	C19-C18	4.04	1.55	1.51
2	A	6001	2J8	C12-C11	5.35	1.57	1.51
2	B	6003	2J8	C12-C11	5.85	1.57	1.51

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6003	2J8	C01-C02-N03	2.03	119.62	115.10
2	A	6001	2J8	C08-C09-N10	2.04	119.64	115.10
2	B	6003	2J8	C08-C09-N10	2.28	120.19	115.10
2	B	6004	2J8	C07-C08-N24	2.83	116.64	109.36
2	A	6001	2J8	C01-C02-N03	3.10	122.00	115.10
2	A	6001	2J8	C29-C28-C04	3.15	114.18	111.30
2	A	6001	2J8	C04-N03-C02	3.21	127.42	122.02
2	A	6002	2J8	C07-C08-N24	3.22	117.64	109.36
2	B	6003	2J8	C32-C31-C11	3.30	114.32	111.30
2	B	6003	2J8	C18-N17-C16	3.37	127.69	122.02
2	B	6003	2J8	C11-N10-C09	3.38	127.70	122.02
2	A	6001	2J8	C36-C34-C18	3.52	114.52	111.30
2	A	6001	2J8	C11-N10-C09	3.73	128.30	122.02
2	A	6001	2J8	C32-C31-C11	3.81	114.78	111.30
2	A	6002	2J8	C29-C28-C04	4.03	114.98	111.30
2	B	6004	2J8	C04-N03-C02	4.39	129.41	122.02
2	B	6003	2J8	C36-C34-C18	4.71	115.60	111.30
2	B	6004	2J8	C30-C28-C04	4.95	115.82	111.30
2	A	6001	2J8	C33-C31-C11	4.99	115.86	111.30
2	B	6003	2J8	C04-N03-C02	5.10	130.59	122.02
2	A	6001	2J8	C35-C34-C18	5.32	116.16	111.30
2	B	6003	2J8	C35-C34-C18	5.48	116.31	111.30
2	B	6004	2J8	C29-C28-C04	5.51	116.33	111.30
2	A	6002	2J8	C04-N03-C02	5.90	131.94	122.02
2	A	6001	2J8	C30-C28-C04	5.94	116.73	111.30
2	A	6001	2J8	C18-N17-C16	6.14	132.36	122.02
2	B	6003	2J8	C30-C28-C04	6.20	116.97	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	6003	2J8	C33-C31-C11	7.13	117.82	111.30
2	A	6002	2J8	C30-C28-C04	7.35	118.02	111.30
2	B	6003	2J8	C29-C28-C04	7.62	118.27	111.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	6001	2J8	3	0
2	A	6002	2J8	4	0
2	B	6003	2J8	3	0
2	B	6004	2J8	3	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	1188/1282 (92%)	-0.51	5 (0%) 93 90	115, 186, 284, 381	0
1	B	1180/1282 (92%)	-0.48	7 (0%) 90 86	120, 197, 296, 512	0
All	All	2368/2564 (92%)	-0.49	12 (0%) 91 88	115, 191, 291, 512	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1068	SER	4.6
1	B	1067	SER	3.1
1	A	1228	HIS	3.0
1	A	1205	GLU	2.8
1	B	227	ILE	2.4
1	B	803	PRO	2.4
1	B	1162	ASN	2.3
1	A	93	GLU	2.3
1	A	624	THR	2.2
1	A	623	MET	2.1
1	B	402	GLU	2.1
1	B	1069	GLY	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	2J8	A	6002	17/36	0.78	0.37	1.46	234,240,512,514	0
2	2J8	B	6003	36/36	0.75	0.45	1.45	191,311,336,550	0
2	2J8	A	6001	36/36	0.87	0.28	0.50	149,241,277,497	0
2	2J8	B	6004	17/36	0.85	0.26	0.41	149,240,316,443	0

6.5 Other polymers [i](#)

There are no such residues in this entry.