



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2024 – 10:38 PM EST

PDB ID : 4M1M
Title : Corrected Structure of Mouse P-glycoprotein
Authors : Li, J.; Jaimes, K.F.; Aller, S.G.
Deposited on : 2013-08-03
Resolution : 3.80 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

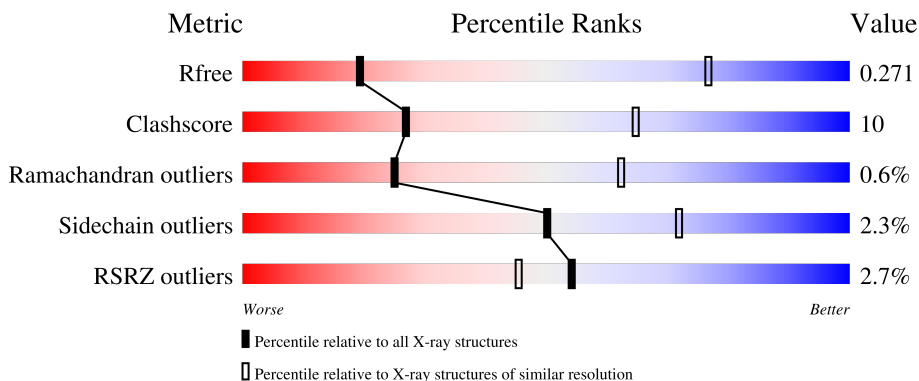
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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}	130704	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	
1	B	1282	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 18378 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
			Total	C	N	O	S			
1	A	1188	9213	5923	1559	1694	37	0	0	0
1	B	1180	9152	5887	1550	1678	37	0	0	0

There are 20 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	952	ALA	CYS	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	952	ALA	CYS	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 MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total 7	Hg 7	0	0
2	B	6	Total 6	Hg 6	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.54Å 115.43Å 378.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.89 – 3.80 42.33 – 3.79	Depositor EDS
% Data completeness (in resolution range)	95.9 (24.89-3.80) 95.5 (42.33-3.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.19 (at 3.76Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.212 , 0.267 0.223 , 0.271	Depositor DCC
R_{free} test set	4245 reflections (10.21%)	wwPDB-VP
Wilson B-factor (Å ²)	132.2	Xtrriage
Anisotropy	0.330	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 87.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18378	wwPDB-VP
Average B, all atoms (Å ²)	155.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.31	0/9382	0.51	0/12684
1	B	0.30	0/9321	0.50	0/12601
All	All	0.31	0/18703	0.51	0/25285

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9213	0	9383	203	0
1	B	9152	0	9333	179	0
2	A	7	0	0	0	0
2	B	6	0	0	0	0
All	All	18378	0	18716	379	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 10.

All (379) 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:A:281:LYS:HZ2	1:A:782:LYS:HA	1.26	0.98
1:A:559:THR:HG22	1:A:584:ARG:HH12	1.39	0.87
1:B:1021:GLY:HA2	1:B:1101:ASN:HB2	1.60	0.81
1:B:433:VAL:HG13	1:B:549:LEU:HD23	1.64	0.80
1:A:1149:ASN:O	1:A:1179:ARG:NH2	2.14	0.79
1:A:433:VAL:HG13	1:A:549:LEU:HD23	1.64	0.79
1:B:257:ILE:HG12	1:B:800:PHE:CE2	2.20	0.77
1:A:966:THR:OG1	1:A:967:PHE:N	2.15	0.77
1:B:1022:LEU:HD11	1:B:1100:LEU:HA	1.67	0.75
1:A:257:ILE:HG12	1:A:800:PHE:CE2	2.22	0.75
1:A:792:MET:HE1	1:A:810:LEU:HB3	1.71	0.73
1:A:396:SER:HB3	1:A:404:GLN:HA	1.70	0.72
1:B:784:LEU:HD22	1:B:821:VAL:HG11	1.72	0.72
1:A:281:LYS:NZ	1:A:785:ARG:HD2	2.05	0.71
1:A:122:LEU:HB3	1:A:943:ALA:HB2	1.72	0.71
1:B:257:ILE:HG12	1:B:800:PHE:HE2	1.54	0.70
1:A:281:LYS:NZ	1:A:782:LYS:HA	2.06	0.70
1:A:208:TRP:HE3	1:A:209:LYS:HG2	1.55	0.70
1:A:854:THR:HG23	1:A:977:ILE:HD11	1.74	0.69
1:A:208:TRP:CE3	1:A:209:LYS:HG2	2.28	0.69
1:A:239:GLU:OE1	1:A:287:LYS:NZ	2.20	0.68
1:A:257:ILE:HG12	1:A:800:PHE:HE2	1.57	0.68
1:B:272:ARG:NH2	1:B:1125:GLU:OE2	2.27	0.68
1:B:966:THR:H	1:B:967:PHE:HA	1.59	0.67
1:A:281:LYS:HZ3	1:A:785:ARG:HD2	1.60	0.66
1:A:59:ILE:HD11	1:A:124:VAL:HG11	1.76	0.66
1:A:384:ILE:HD11	1:A:546:LYS:HB2	1.78	0.66
1:B:484:ILE:HG21	1:B:496:ILE:HG23	1.77	0.66
1:B:160:ASP:OD1	1:B:901:ARG:NH2	2.29	0.66
1:B:396:SER:OG	1:B:403:VAL:O	2.14	0.65
1:A:34:SER:OG	1:A:37:THR:OG1	2.13	0.65
1:B:94:ALA:HB1	1:B:97:ARG:HE	1.62	0.64
1:B:122:LEU:HB3	1:B:943:ALA:HB2	1.78	0.63
1:A:388:LEU:HB2	1:A:413:VAL:HB	1.81	0.63
1:B:282:ARG:HH22	1:B:779:ILE:HA	1.65	0.62
1:A:371:ILE:O	1:A:373:SER:HB3	2.00	0.62
1:A:206:ARG:HE	1:A:206:ARG:HA	1.65	0.61
1:A:794:ARG:HG2	1:A:1012:PRO:HG3	1.82	0.61
1:B:102:LYS:HE3	1:B:106:GLU:OE2	2.00	0.61
1:A:780:LEU:O	1:A:784:LEU:HB2	1.99	0.61
1:A:513:PRO:HB2	1:A:514:HIS:CD2	2.35	0.61
1:A:70:ILE:HD13	1:A:113:TYR:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1033:PHE:HD1	1:B:1036:VAL:HG21	1.67	0.59
1:A:419:VAL:HG22	1:A:593:VAL:HB	1.85	0.59
1:A:784:LEU:HD22	1:A:821:VAL:HG11	1.84	0.59
1:A:1112:VAL:HB	1:A:1195:LEU:HD23	1.84	0.59
1:A:554:THR:HB	1:A:562:GLU:HG3	1.84	0.58
1:A:337:GLY:O	1:A:340:SER:OG	2.21	0.58
1:A:833:PHE:HA	1:A:836:ILE:HG22	1.84	0.58
1:A:1110:GLY:O	1:A:1194:LEU:N	2.33	0.58
1:A:840:GLY:O	1:A:843:ILE:HG22	2.04	0.57
1:A:612:MET:HE1	1:A:622:VAL:HG11	1.86	0.57
1:A:1199:THR:OG1	1:A:1229:ARG:NH2	2.37	0.57
1:A:1036:VAL:H	1:A:1088:GLY:HA3	1.70	0.57
1:B:378:GLY:H	1:B:458:ASN:HB2	1.69	0.57
1:A:1021:GLY:HA3	1:A:1101:ASN:HB2	1.88	0.56
1:A:1204:THR:OG1	1:A:1205:GLU:N	2.38	0.56
1:B:1149:ASN:O	1:B:1179:ARG:NH2	2.38	0.56
1:B:65:PRO:HB2	1:B:202:ILE:HD12	1.87	0.56
1:A:510:MET:SD	1:A:515:GLN:NE2	2.79	0.56
1:B:1096:GLU:OE1	1:B:1098:LYS:N	2.32	0.56
1:B:1065:VAL:HG23	1:B:1241:VAL:HA	1.87	0.56
1:A:123:ILE:O	1:A:127:ILE:HG12	2.05	0.56
1:B:1072:LYS:HD3	1:B:1226:ILE:HG23	1.88	0.56
1:A:1079:LEU:HG	1:A:1109:LEU:HD21	1.89	0.55
1:A:215:LEU:O	1:A:218:SER:OG	2.23	0.55
1:A:281:LYS:HZ2	1:A:782:LYS:CA	2.11	0.55
1:B:510:MET:SD	1:B:515:GLN:NE2	2.80	0.55
1:A:1096:GLU:OE1	1:A:1098:LYS:N	2.36	0.55
1:A:310:PHE:CD2	1:A:755:PHE:HE2	2.24	0.55
1:B:32:ALA:H	1:B:356:GLY:HA2	1.71	0.55
1:A:893:ALA:O	1:A:897:ILE:HG12	2.06	0.55
1:B:289:ILE:HD13	1:B:771:PHE:HE1	1.72	0.55
1:B:292:ASN:ND2	1:B:766:PHE:O	2.41	0.54
1:A:200:PHE:HE2	1:A:215:LEU:HD12	1.72	0.54
1:B:457:ILE:HD11	1:B:462:LEU:HD13	1.88	0.54
1:B:554:THR:HB	1:B:562:GLU:HG3	1.89	0.54
1:B:500:VAL:HG11	1:B:509:ILE:HD12	1.90	0.54
1:A:453:ASP:OD1	1:A:454:ILE:N	2.41	0.53
1:B:393:ILE:H	1:B:445:GLY:HA3	1.73	0.53
1:A:846:SER:HB2	1:A:973:VAL:HG13	1.90	0.53
1:A:1230:LEU:HD23	1:A:1233:ILE:HD12	1.89	0.53
1:B:206:ARG:O	1:B:326:GLN:NE2	2.36	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:475:LEU:HD12	1:B:532:LYS:HG2	1.90	0.53
1:A:373:SER:HB2	1:A:459:VAL:HG11	1.90	0.53
1:B:289:ILE:O	1:B:293:ILE:HG12	2.08	0.53
1:B:1033:PHE:CD1	1:B:1036:VAL:HG21	2.43	0.53
1:A:393:ILE:HB	1:A:409:LEU:HB3	1.89	0.53
1:A:485:ARG:NH2	1:B:914:THR:OG1	2.42	0.53
1:A:175:VAL:HA	1:A:178:ILE:HG22	1.91	0.53
1:B:206:ARG:HG3	1:B:326:GLN:HG3	1.90	0.53
1:A:66:LEU:HD23	1:A:202:ILE:HD11	1.90	0.53
1:A:1020:GLN:HG2	1:A:1021:GLY:N	2.23	0.53
1:A:1049:LEU:HD13	1:A:1052:LEU:HD21	1.91	0.53
1:A:496:ILE:O	1:A:500:VAL:HG23	2.09	0.53
1:A:1234:GLN:HG2	1:A:1253:HIS:CE1	2.44	0.53
1:A:607:ASN:HB3	1:A:610:GLU:OE2	2.08	0.52
1:B:711:ILE:O	1:B:715:ILE:HG13	2.09	0.52
1:B:907:THR:O	1:B:908:ARG:NE	2.42	0.52
1:B:1136:VAL:HG22	1:B:1137:SER:H	1.75	0.52
1:A:316:LEU:HD23	1:A:322:TYR:CD1	2.44	0.52
1:A:728:PHE:CE1	1:A:971:LEU:HD21	2.44	0.52
1:B:695:ARG:HA	1:B:698:LYS:NZ	2.25	0.52
1:B:792:MET:HE1	1:B:810:LEU:HB3	1.92	0.52
1:A:925:ARG:HA	1:B:514:HIS:HD2	1.74	0.52
1:A:46:ASP:OD1	1:A:138:ARG:NH1	2.43	0.52
1:A:360:GLU:O	1:A:364:ILE:HG12	2.10	0.51
1:A:1120:ASP:HB3	1:A:1168:LYS:HD3	1.92	0.51
1:A:33:VAL:HG12	1:A:37:THR:HB	1.91	0.51
1:B:460:ARG:HG3	1:B:907:THR:HG21	1.92	0.51
1:B:300:LEU:HD11	1:B:760:ILE:HD13	1.92	0.51
1:B:317:VAL:HG23	1:B:323:SER:HA	1.92	0.51
1:B:507:ASP:OD1	1:B:508:PHE:N	2.44	0.51
1:B:520:VAL:HG22	1:B:521:GLY:H	1.75	0.51
1:A:831:VAL:HG13	1:A:987:VAL:HG12	1.93	0.51
1:A:937:THR:O	1:A:941:THR:HG23	2.11	0.51
1:B:965:MET:HB3	1:B:966:THR:OG1	2.11	0.51
1:B:1230:LEU:HD23	1:B:1233:ILE:HD12	1.92	0.51
1:A:1033:PHE:HD1	1:A:1036:VAL:HG11	1.76	0.51
1:B:1204:THR:OG1	1:B:1205:GLU:N	2.43	0.50
1:A:170:ARG:HG3	1:A:174:ASP:HB2	1.93	0.50
1:A:175:VAL:O	1:A:178:ILE:HG22	2.11	0.50
1:A:382:ASP:OD1	1:A:382:ASP:N	2.43	0.50
1:B:723:ALA:O	1:B:727:ILE:HG12	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:496:ILE:O	1:B:500:VAL:HG23	2.11	0.50
1:B:849:TYR:HB3	1:B:969:ASN:HB3	1.92	0.50
1:B:1097:ILE:HG23	1:B:1105:LEU:HD22	1.92	0.50
1:A:756:LEU:O	1:A:760:ILE:HG12	2.12	0.50
1:B:379:HIS:H	1:B:457:ILE:HA	1.77	0.50
1:B:94:ALA:HB1	1:B:97:ARG:NE	2.27	0.50
1:A:238:LYS:HG2	1:A:283:LEU:HD11	1.93	0.49
1:B:1110:GLY:HA3	1:B:1193:LEU:HD23	1.94	0.49
1:A:538:ALA:O	1:A:542:VAL:HG23	2.12	0.49
1:A:1150:ILE:HG22	1:A:1179:ARG:HB3	1.94	0.49
1:B:808:GLY:HA2	1:B:811:THR:HG22	1.94	0.49
1:A:723:ALA:O	1:A:727:ILE:HG12	2.13	0.49
1:A:1241:VAL:HB	1:A:1249:GLU:HB2	1.93	0.49
1:B:312:TYR:O	1:B:315:SER:OG	2.21	0.49
1:A:260:VAL:O	1:A:264:GLY:N	2.45	0.49
1:A:424:ASN:H	1:A:429:LYS:HZ1	1.60	0.49
1:B:281:LYS:HD2	1:B:781:THR:HB	1.92	0.49
1:B:879:ALA:O	1:B:883:LYS:HG2	2.12	0.49
1:A:394:HIS:HB2	1:A:444:ASP:HB3	1.94	0.49
1:A:227:ILE:O	1:A:231:ILE:HG13	2.13	0.49
1:A:604:GLU:OE2	1:A:616:GLY:HA3	2.12	0.49
1:A:981:ALA:O	1:A:984:VAL:HG22	2.13	0.49
1:B:784:LEU:HD21	1:B:1004:ILE:HG21	1.95	0.49
1:A:617:ILE:HD12	1:A:617:ILE:H	1.77	0.48
1:A:794:ARG:NH1	1:A:1015:ASP:OD2	2.46	0.48
1:A:920:LEU:O	1:A:923:PRO:HD2	2.13	0.48
1:A:79:ALA:HB2	1:A:736:THR:HG22	1.95	0.48
1:B:278:GLU:HG3	1:B:282:ARG:HD2	1.95	0.48
1:B:257:ILE:HD12	1:B:260:VAL:HB	1.95	0.48
1:A:388:LEU:HD11	1:A:547:ILE:HD13	1.95	0.48
1:B:966:THR:OG1	1:B:969:ASN:HB2	2.14	0.48
1:B:291:ALA:O	1:B:294:SER:OG	2.22	0.48
1:B:1078:LEU:HD22	1:B:1085:PRO:HD3	1.95	0.48
1:B:388:LEU:HD13	1:B:577:THR:HG21	1.96	0.48
1:A:1178:GLN:O	1:A:1182:ILE:HG12	2.13	0.48
1:B:61:GLY:HA3	1:B:194:ALA:HB3	1.96	0.48
1:B:299:PHE:HA	1:B:302:ILE:HG12	1.95	0.48
1:B:1022:LEU:HD11	1:B:1100:LEU:HD23	1.95	0.48
1:A:1063:ALA:HB3	1:A:1239:ILE:HA	1.96	0.48
1:B:277:LEU:C	1:B:279:GLU:H	2.17	0.48
1:B:1061:THR:HG21	1:B:1218:ARG:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:ILE:O	1:B:220:VAL:HG12	2.13	0.47
1:B:453:ASP:OD1	1:B:454:ILE:N	2.47	0.47
1:B:1045:SER:OG	1:B:1046:ILE:N	2.47	0.47
1:A:158:TRP:HZ2	1:A:364:ILE:HD12	1.79	0.47
1:B:90:GLN:HG2	1:B:91:MET:H	1.79	0.47
1:B:855:LEU:HA	1:B:858:LEU:HG	1.95	0.47
1:B:385:GLN:HB2	1:B:450:ASP:OD2	2.13	0.47
1:B:835:ASN:CG	1:B:984:VAL:HG13	2.35	0.47
1:A:1158:PRO:HA	1:A:1159:ASP:HA	1.62	0.47
1:B:960:VAL:HG21	1:B:967:PHE:HB2	1.96	0.47
1:B:1035:GLY:N	1:B:1053:SER:OG	2.40	0.47
1:B:533:GLN:O	1:B:537:ILE:HG13	2.13	0.47
1:B:1175:GLY:HA2	1:B:1202:LEU:HD11	1.95	0.47
1:B:585:LEU:HD11	1:B:621:LEU:HB3	1.97	0.47
1:B:376:LYS:HA	1:B:377:SER:HA	1.63	0.47
1:A:129:VAL:HG13	1:A:935:GLY:HA2	1.97	0.47
1:B:174:ASP:O	1:B:178:ILE:HG13	2.14	0.47
1:B:689:PRO:HG3	1:B:1003:HIS:CD2	2.50	0.47
1:B:780:LEU:O	1:B:784:LEU:HB2	2.15	0.47
1:A:86:LYS:HZ2	1:A:739:GLY:HA2	1.80	0.46
1:B:714:ALA:HB1	1:B:834:GLN:HG3	1.97	0.46
1:B:1183:ALA:O	1:B:1187:VAL:HG23	2.15	0.46
1:A:562:GLU:OE1	1:A:584:ARG:NH1	2.48	0.46
1:A:702:THR:OG1	1:A:783:ARG:NH2	2.48	0.46
1:A:1024:PRO:HD2	1:A:1104:TRP:CZ2	2.51	0.46
1:B:538:ALA:O	1:B:542:VAL:HG23	2.15	0.46
1:B:122:LEU:HD12	1:B:123:ILE:N	2.30	0.46
1:B:263:PHE:CZ	1:B:1184:ARG:HD3	2.51	0.46
1:A:481:ALA:O	1:A:485:ARG:HG2	2.16	0.46
1:A:488:ARG:HA	1:A:908:ARG:HH11	1.80	0.46
1:B:140:ILE:HD13	1:B:140:ILE:HA	1.84	0.46
1:B:163:ASP:HB3	1:B:166:GLU:HG2	1.97	0.46
1:B:125:ALA:O	1:B:129:VAL:HG12	2.16	0.46
1:A:730:LYS:HB3	1:A:751:PHE:CE2	2.50	0.46
1:A:1183:ALA:O	1:A:1187:VAL:HG23	2.15	0.46
1:A:64:LEU:HD12	1:A:336:ILE:HG21	1.98	0.45
1:A:852:GLN:CD	1:A:852:GLN:H	2.20	0.45
1:A:1159:ASP:OD1	1:A:1159:ASP:N	2.43	0.45
1:A:265:GLY:O	1:A:269:GLU:HG2	2.16	0.45
1:A:957:ALA:HA	1:A:960:VAL:HG12	1.97	0.45
1:B:727:ILE:HD12	1:B:754:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:736:THR:HG21	1:B:967:PHE:HE2	1.80	0.45
1:A:314:THR:HA	1:A:317:VAL:HG12	1.97	0.45
1:A:827:SER:O	1:A:831:VAL:HG23	2.17	0.45
1:B:1151:HIS:ND1	1:B:1154:ILE:HD11	2.31	0.45
1:B:1165:VAL:HA	1:B:1166:GLY:HA2	1.79	0.45
1:A:50:MET:HE1	1:A:139:GLN:HE22	1.81	0.45
1:B:728:PHE:CE2	1:B:971:LEU:HD21	2.52	0.45
1:A:286:LYS:O	1:A:290:THR:HG23	2.16	0.45
1:A:257:ILE:HD12	1:A:260:VAL:HB	1.99	0.45
1:A:471:GLN:HB3	1:A:552:GLU:HB2	1.98	0.45
1:A:478:THR:HB	1:A:482:GLU:HB2	1.98	0.45
1:B:307:ALA:HA	1:B:755:PHE:CE1	2.51	0.45
1:B:38:MET:HA	1:B:362:PHE:HE2	1.81	0.45
1:B:404:GLN:HB3	1:B:407:LYS:NZ	2.32	0.45
1:B:1076:VAL:HG13	1:B:1194:LEU:HD13	1.98	0.45
1:A:217:ILE:O	1:A:220:VAL:HG12	2.17	0.45
1:B:500:VAL:HG21	1:B:516:PHE:HE1	1.82	0.45
1:B:607:ASN:HB3	1:B:610:GLU:OE1	2.16	0.45
1:B:908:ARG:HE	1:B:908:ARG:HA	1.83	0.44
1:A:1061:THR:HG21	1:A:1218:ARG:HD3	1.98	0.44
1:A:784:LEU:HD21	1:A:1004:ILE:HG21	1.99	0.44
1:B:617:ILE:HD12	1:B:617:ILE:H	1.82	0.44
1:A:689:PRO:HG3	1:A:1003:HIS:CD2	2.52	0.44
1:A:741:PRO:HA	1:A:744:GLN:HG3	1.98	0.44
1:A:1165:VAL:HA	1:A:1166:GLY:HA2	1.71	0.44
1:B:407:LYS:O	1:B:601:VAL:HG22	2.17	0.44
1:B:882:ASP:HA	1:B:885:GLU:HG2	2.00	0.44
1:A:38:MET:SD	1:A:355:ARG:HG2	2.58	0.44
1:A:65:PRO:HB2	1:A:202:ILE:HD12	1.99	0.44
1:A:975:SER:O	1:A:979:PHE:HB2	2.18	0.44
1:B:265:GLY:O	1:B:269:GLU:HG2	2.18	0.44
1:B:1081:ARG:HD3	1:B:1097:ILE:CG2	2.47	0.44
1:A:610:GLU:HG3	1:A:613:ARG:HH21	1.83	0.44
1:B:65:PRO:CB	1:B:202:ILE:HD12	2.48	0.44
1:B:273:TYR:CE2	1:B:277:LEU:HD11	2.53	0.44
1:B:283:LEU:HD23	1:B:286:LYS:HD2	2.00	0.44
1:B:1108:GLN:O	1:B:1109:LEU:HD12	2.18	0.44
1:B:692:SER:OG	1:B:695:ARG:HB3	2.18	0.44
1:A:150:ALA:O	1:A:154:GLN:HG2	2.17	0.43
1:A:326:GLN:O	1:A:330:VAL:HG22	2.18	0.43
1:A:692:SER:OG	1:A:695:ARG:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1079:LEU:HD23	1:A:1194:LEU:HD21	2.01	0.43
1:A:1097:ILE:HG23	1:A:1105:LEU:HD22	2.00	0.43
1:A:125:ALA:O	1:A:129:VAL:HG12	2.18	0.43
1:A:808:GLY:HA2	1:A:811:THR:HG22	1.99	0.43
1:B:113:TYR:O	1:B:117:ILE:HG13	2.18	0.43
1:B:1124:ALA:HB2	1:B:1161:TYR:HB2	2.00	0.43
1:A:925:ARG:HG3	1:B:514:HIS:CD2	2.53	0.43
1:B:957:ALA:O	1:B:961:THR:HG23	2.18	0.43
1:B:975:SER:O	1:B:979:PHE:HB2	2.18	0.43
1:B:1040:TYR:HA	1:B:1041:PRO:HD3	1.90	0.43
1:A:289:ILE:O	1:A:293:ILE:HG12	2.18	0.43
1:B:1197:GLU:HB3	1:B:1200:SER:HB3	2.00	0.43
1:A:215:LEU:O	1:A:219:PRO:HD3	2.18	0.43
1:A:726:VAL:O	1:A:730:LYS:HG2	2.18	0.43
1:A:1036:VAL:N	1:A:1088:GLY:HA3	2.31	0.43
1:B:293:ILE:HD12	1:B:767:PHE:HD1	1.83	0.43
1:B:488:ARG:CZ	1:B:491:VAL:HG12	2.49	0.43
1:A:210:LEU:HD21	1:A:327:VAL:HG13	2.01	0.43
1:A:491:VAL:HG11	1:A:542:VAL:CG1	2.48	0.43
1:B:488:ARG:HB3	1:B:491:VAL:HG13	2.00	0.43
1:A:122:LEU:HD12	1:A:123:ILE:N	2.34	0.43
1:A:277:LEU:HD23	1:A:277:LEU:HA	1.86	0.43
1:A:277:LEU:C	1:A:279:GLU:H	2.22	0.43
1:A:1002:SER:HA	1:A:1005:ILE:HG12	2.01	0.43
1:B:422:VAL:HG22	1:B:423:GLY:H	1.83	0.43
1:B:1062:LEU:HD11	1:B:1240:VAL:HG23	2.01	0.43
1:A:488:ARG:NH2	1:A:491:VAL:HG12	2.34	0.43
1:B:156:ILE:HD11	1:B:439:LEU:O	2.17	0.43
1:B:281:LYS:HG3	1:B:782:LYS:HB2	2.01	0.43
1:B:707:PHE:O	1:B:711:ILE:HG13	2.19	0.43
1:B:896:ALA:HB2	1:B:912:PHE:CD2	2.54	0.43
1:B:1022:LEU:O	1:B:1024:PRO:HD3	2.19	0.43
1:B:1061:THR:HG22	1:B:1223:CYS:HB3	2.00	0.43
1:A:211:THR:HG22	1:A:334:VAL:HG21	2.00	0.43
1:A:727:ILE:HB	1:A:755:PHE:HE1	1.84	0.43
1:A:1118:LEU:HD12	1:A:1165:VAL:HG11	2.01	0.43
1:B:691:ALA:HB1	1:B:692:SER:HA	2.01	0.43
1:A:86:LYS:NZ	1:A:739:GLY:HA2	2.33	0.42
1:A:784:LEU:CD2	1:A:821:VAL:HG11	2.48	0.42
1:B:488:ARG:NH2	1:B:491:VAL:HG12	2.34	0.42
1:B:1033:PHE:CE2	1:B:1075:VAL:HG13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1081:ARG:HD3	1:B:1097:ILE:HG22	2.01	0.42
1:A:54:THR:CG2	1:A:132:TRP:HZ2	2.32	0.42
1:B:828:ARG:HA	1:B:831:VAL:HG22	1.99	0.42
1:A:848:ILE:HG13	1:A:849:TYR:CD1	2.53	0.42
1:B:730:LYS:HB3	1:B:751:PHE:CE2	2.54	0.42
1:B:792:MET:CE	1:B:810:LEU:HB3	2.49	0.42
1:B:1064:LEU:HB2	1:B:1226:ILE:HG13	2.01	0.42
1:A:303:TYR:HE1	1:A:758:LEU:HD23	1.84	0.42
1:A:980:GLY:O	1:A:984:VAL:HG13	2.19	0.42
1:A:1070:CYS:HA	1:A:1071:GLY:HA2	1.56	0.42
1:B:169:THR:O	1:B:173:ASP:HB2	2.19	0.42
1:B:603:VAL:HG13	1:B:604:GLU:H	1.84	0.42
1:A:132:TRP:CZ3	1:A:186:ILE:HD11	2.55	0.42
1:A:372:ASP:HA	1:A:373:SER:HB3	2.01	0.42
1:A:424:ASN:H	1:A:429:LYS:NZ	2.17	0.42
1:A:436:MET:HB3	1:A:549:LEU:HD21	2.02	0.42
1:B:123:ILE:O	1:B:127:ILE:HG12	2.19	0.42
1:B:221:LEU:HD12	1:B:222:GLY:N	2.35	0.42
1:A:604:GLU:OE1	1:A:617:ILE:N	2.52	0.42
1:A:1064:LEU:HD22	1:A:1242:ILE:HD11	2.00	0.42
1:A:482:GLU:HA	1:A:485:ARG:HG2	2.01	0.42
1:B:286:LYS:O	1:B:290:THR:HG23	2.20	0.42
1:B:1181:ALA:O	1:B:1184:ARG:HB3	2.20	0.42
1:B:610:GLU:OE1	1:B:610:GLU:N	2.52	0.42
1:A:1040:TYR:HA	1:A:1041:PRO:HD3	1.73	0.42
1:B:257:ILE:HG13	1:B:261:ILE:HG13	2.02	0.42
1:B:1160:LYS:HB3	1:B:1161:TYR:H	1.65	0.42
1:A:922:ILE:HB	1:A:923:PRO:HD3	2.01	0.42
1:B:703:GLU:HB3	1:B:706:TYR:HD2	1.84	0.42
1:A:282:ARG:HE	1:A:282:ARG:N	2.17	0.41
1:A:484:ILE:HG21	1:A:496:ILE:HG23	2.01	0.41
1:B:508:PHE:O	1:B:512:LEU:HG	2.20	0.41
1:A:335:LEU:HD12	1:A:335:LEU:HA	1.87	0.41
1:A:156:ILE:HD11	1:A:439:LEU:O	2.19	0.41
1:A:200:PHE:CE2	1:A:215:LEU:HD12	2.54	0.41
1:A:390:PHE:O	1:A:410:ASN:HA	2.19	0.41
1:B:46:ASP:OD1	1:B:138:ARG:NH1	2.54	0.41
1:B:289:ILE:HD13	1:B:771:PHE:CE1	2.54	0.41
1:A:484:ILE:HG23	1:A:542:VAL:HG21	2.03	0.41
1:A:54:THR:HG23	1:A:132:TRP:HZ2	1.85	0.41
1:A:136:ALA:HB2	1:A:183:GLY:HA2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:ALA:O	1:A:294:SER:OG	2.27	0.41
1:B:404:GLN:HB3	1:B:407:LYS:HZ3	1.86	0.41
1:B:1100:LEU:HD13	1:B:1105:LEU:HD13	2.02	0.41
1:A:54:THR:O	1:A:58:ILE:HG12	2.21	0.41
1:A:594:ILE:HB	1:A:611:LEU:HD22	2.02	0.41
1:A:719:GLY:C	1:A:722:PRO:HD2	2.40	0.41
1:A:1049:LEU:HD21	1:A:1071:GLY:HA3	2.02	0.41
1:A:1076:VAL:HG13	1:A:1194:LEU:HB3	2.02	0.41
1:A:1157:LEU:HD12	1:A:1158:PRO:HD2	2.03	0.41
1:B:322:TYR:O	1:B:326:GLN:HB3	2.21	0.41
1:A:113:TYR:O	1:A:117:ILE:HG13	2.21	0.41
1:B:150:ALA:O	1:B:154:GLN:HG2	2.20	0.41
1:B:1023:LYS:HA	1:B:1024:PRO:HD3	1.82	0.41
1:B:1089:SER:HB3	1:B:1096:GLU:HG2	2.03	0.41
1:B:1217:ALA:O	1:B:1221:ARG:HD2	2.20	0.41
1:A:64:LEU:HB3	1:A:65:PRO:HD3	2.02	0.41
1:A:67:MET:HE3	1:A:946:TYR:CD2	2.56	0.41
1:A:550:LEU:HD23	1:A:569:LEU:HD13	2.02	0.41
1:B:257:ILE:HG21	1:B:800:PHE:CD2	2.55	0.41
1:B:388:LEU:HB2	1:B:413:VAL:HB	2.02	0.41
1:A:39:PHE:CD1	1:A:50:MET:HE1	2.56	0.41
1:A:203:GLY:C	1:A:211:THR:HG21	2.41	0.41
1:A:828:ARG:HA	1:A:828:ARG:HD2	1.88	0.41
1:A:955:PHE:O	1:A:959:LEU:HG	2.20	0.41
1:A:1004:ILE:O	1:A:1008:ILE:HG13	2.20	0.41
1:B:825:THR:OG1	1:B:826:GLY:N	2.53	0.41
1:B:833:PHE:HD1	1:B:836:ILE:HD11	1.86	0.41
1:A:519:LEU:HD22	1:A:519:LEU:H	1.85	0.41
1:A:1076:VAL:HG13	1:A:1194:LEU:HD13	2.02	0.41
1:B:156:ILE:H	1:B:156:ILE:HG13	1.59	0.41
1:B:314:THR:HA	1:B:317:VAL:HG12	2.02	0.41
1:B:956:GLY:O	1:B:960:VAL:HG23	2.21	0.41
1:A:1243:GLN:OE1	1:A:1248:LYS:HD2	2.20	0.40
1:B:983:ALA:O	1:B:987:VAL:HG23	2.22	0.40
1:A:140:ILE:HD13	1:A:140:ILE:HA	1.85	0.40
1:A:156:ILE:HG12	1:A:439:LEU:HB3	2.03	0.40
1:A:310:PHE:HD2	1:A:755:PHE:HE2	1.63	0.40
1:A:828:ARG:HG2	1:A:994:TYR:CE2	2.55	0.40
1:A:845:ILE:HG22	1:A:972:LEU:HD21	2.03	0.40
1:B:147:PHE:O	1:B:151:ILE:HG13	2.21	0.40
1:A:729:SER:OG	1:A:972:LEU:HD12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:SER:O	1:A:795:GLN:HG2	2.20	0.40
1:A:1175:GLY:O	1:A:1179:ARG:HG3	2.22	0.40
1:B:1090:VAL:O	1:B:1097:ILE:HG13	2.20	0.40
1:B:1096:GLU:OE1	1:B:1097:ILE:N	2.54	0.40
1:A:107:MET:SD	1:A:110:TYR:HD2	2.44	0.40
1:A:139:GLN:O	1:A:143:ILE:HG13	2.22	0.40
1:B:1189:GLN:OE1	1:B:1221:ARG:NH2	2.55	0.40
1:B:728:PHE:HE2	1:B:971:LEU:HD21	1.87	0.40
1:B:829:LEU:O	1:B:832:ILE:HG22	2.21	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%)	1124 (95%)	54 (5%)	6 (0%)	29 66
1	B	1176/1282 (92%)	1111 (94%)	57 (5%)	8 (1%)	22 60
All	All	2360/2564 (92%)	2235 (95%)	111 (5%)	14 (1%)	25 62

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1036	VAL
1	B	32	ALA
1	B	1136	VAL
1	A	1070	CYS
1	A	1120	ASP
1	B	393	ILE
1	A	278	GLU
1	A	838	ASN
1	B	278	GLU

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Mol	Chain	Res	Type
1	B	383	ASN
1	B	1172	LEU
1	B	128	GLN
1	B	33	VAL
1	A	1046	ILE

5.3.2 Protein sidechains [i](#)

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	978/1062 (92%)	953 (97%)	25 (3%)	46	69
1	B	972/1062 (92%)	953 (98%)	19 (2%)	55	75
All	All	1950/2124 (92%)	1906 (98%)	44 (2%)	50	72

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	206	ARG
1	A	258	ARG
1	A	283	LEU
1	A	310	PHE
1	A	374	PHE
1	A	383	ASN
1	A	396	SER
1	A	435	LEU
1	A	478	THR
1	A	520	VAL
1	A	681	LYS
1	A	688	VAL
1	A	695	ARG
1	A	700	ASN
1	A	817	ASP
1	A	852	GLN
1	A	942	GLN
1	A	965	MET

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Mol	Chain	Res	Type
1	A	966	THR
1	A	1020	GLN
1	A	1037	VAL
1	A	1111	ILE
1	A	1163	THR
1	A	1167	ASP
1	A	1168	LYS
1	B	258	ARG
1	B	310	PHE
1	B	335	LEU
1	B	373	SER
1	B	383	ASN
1	B	435	LEU
1	B	478	THR
1	B	603	VAL
1	B	755	PHE
1	B	817	ASP
1	B	828	ARG
1	B	886	LEU
1	B	908	ARG
1	B	944	MET
1	B	966	THR
1	B	967	PHE
1	B	1022	LEU
1	B	1111	ILE
1	B	1163	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	139	GLN
1	A	514	HIS
1	A	515	GLN
1	A	608	HIS
1	A	852	GLN
1	B	347	ASN
1	B	514	HIS
1	B	515	GLN
1	B	838	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1188/1282 (92%)	-0.16	29 (2%) 59 50	83, 141, 236, 375	0
1	B	1180/1282 (92%)	-0.02	36 (3%) 49 40	86, 152, 247, 420	0
All	All	2368/2564 (92%)	-0.09	65 (2%) 54 45	83, 146, 241, 420	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	598	ASP	5.2
1	B	423	GLY	4.9
1	B	1114	GLN	4.9
1	A	963	GLN	4.3
1	B	1196	ASP	4.1
1	B	1020	GLN	3.9
1	A	1046	ILE	3.6
1	B	1156	SER	3.6
1	B	1068	SER	3.4
1	A	1123	ILE	3.4
1	B	1159	ASP	3.3
1	B	1229	ARG	3.3
1	B	878	GLN	3.3
1	B	1113	SER	3.2
1	B	1227	ALA	3.2
1	A	1227	ALA	3.1
1	A	36	LEU	3.1
1	A	1045	SER	3.0
1	B	1162	ASN	3.0
1	A	1244	ASN	3.0
1	B	1230	LEU	3.0
1	B	1164	ARG	2.9
1	B	1233	ILE	2.9
1	A	1124	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	965	MET	2.8
1	A	1226	ILE	2.8
1	B	1158	PRO	2.8
1	B	1212	GLU	2.7
1	B	876	SER	2.7
1	B	1021	GLY	2.7
1	A	796	ASP	2.7
1	B	875	LEU	2.6
1	A	443	LEU	2.6
1	B	1169	GLY	2.6
1	B	874	MET	2.5
1	A	383	ASN	2.5
1	A	964	LEU	2.5
1	B	1178	GLN	2.5
1	A	1228	HIS	2.5
1	A	108	THR	2.4
1	B	105	GLU	2.4
1	A	1172	LEU	2.4
1	A	1063	ALA	2.4
1	A	278	GLU	2.4
1	B	108	THR	2.4
1	B	597	PHE	2.3
1	A	279	GLU	2.3
1	A	1241	VAL	2.3
1	B	425	SER	2.3
1	A	1162	ASN	2.2
1	A	1171	GLN	2.2
1	A	359	TYR	2.2
1	A	423	GLY	2.2
1	B	1127	ILE	2.2
1	B	989	SER	2.2
1	B	402	GLU	2.2
1	B	1226	ILE	2.2
1	A	526	GLN	2.1
1	B	97	ARG	2.1
1	B	1172	LEU	2.1
1	A	690	PRO	2.1
1	B	109	THR	2.1
1	B	1199	THR	2.0
1	A	1161	TYR	2.0
1	A	489	GLU	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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	HG	B	1302	1/1	0.75	0.23	189,189,189,189	1
2	HG	A	1307	1/1	0.81	0.82	138,138,138,138	1
2	HG	A	1302	1/1	0.85	0.48	71,71,71,71	1
2	HG	A	1306	1/1	0.90	0.50	96,96,96,96	1
2	HG	B	1306	1/1	0.90	0.27	71,71,71,71	1
2	HG	B	1303	1/1	0.93	0.09	198,198,198,198	1
2	HG	A	1304	1/1	0.95	0.33	38,38,38,38	1
2	HG	A	1305	1/1	0.96	0.44	65,65,65,65	1
2	HG	A	1303	1/1	0.96	0.33	102,102,102,102	1
2	HG	B	1304	1/1	0.98	0.25	107,107,107,107	1
2	HG	B	1305	1/1	0.98	0.62	46,46,46,46	1
2	HG	A	1301	1/1	0.98	0.13	164,164,164,164	1
2	HG	B	1301	1/1	0.99	0.18	129,129,129,129	1

6.5 Other polymers [i](#)

There are no such residues in this entry.