



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:39 AM GMT

PDB ID : 1RC6
Title : Crystal structure of protein Ylba from E. coli, Pfam DUF861
Authors : Fedorov, A.A.; Fedorov, E.V.; Thirumuruhan, R.; Ramagopal, U.A.; Almo, S.C.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2003-11-03
Resolution : 2.60 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

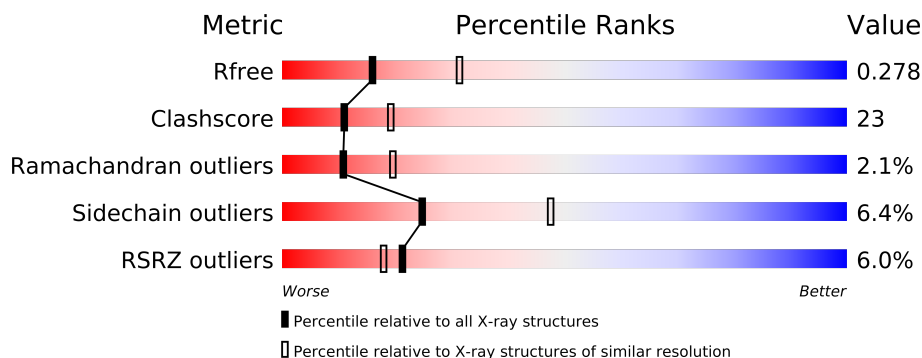
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 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}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	261	
1	B	261	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3760 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

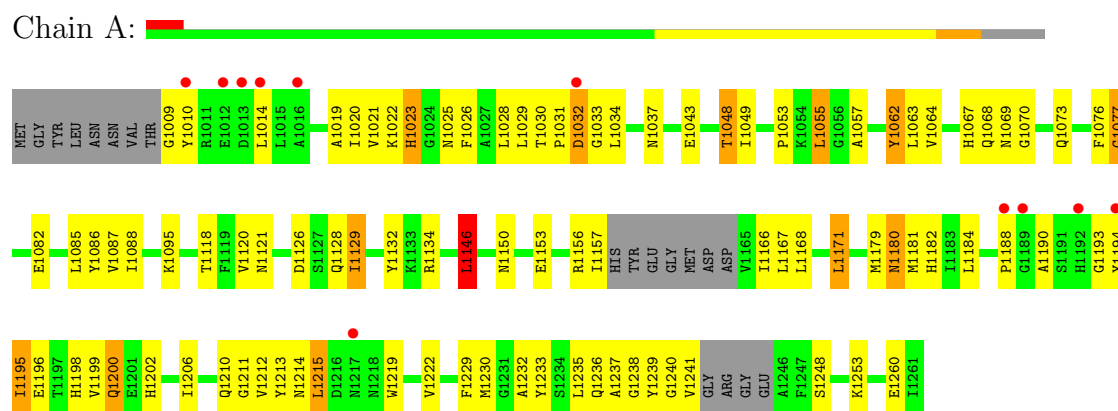
- Molecule 1 is a protein called Hypothetical protein ylbA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1880	1213	306	354	7			
1	B	242	Total	C	N	O	S	0	0	0
			1880	1213	306	354	7			

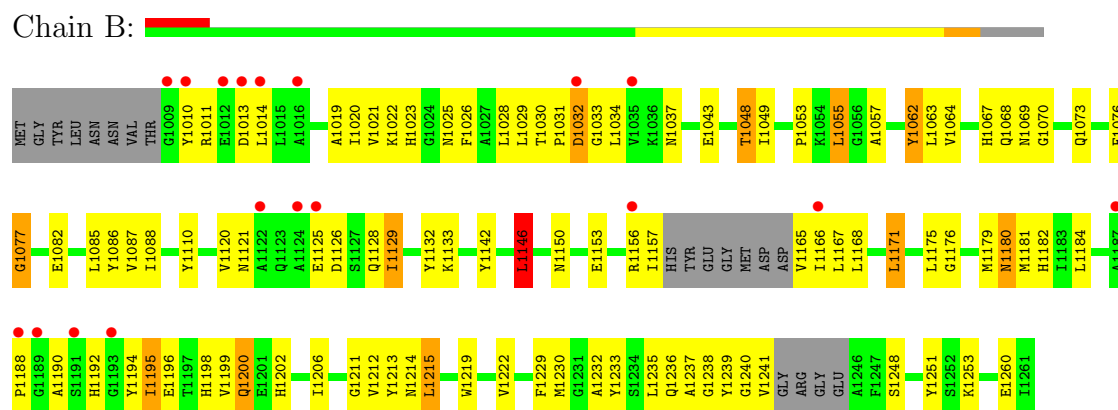
3 Residue-property plots

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: Hypothetical protein ylbA



- Molecule 1: Hypothetical protein ylbA



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	109.03Å 109.03Å 136.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 24.38 – 2.62	Depositor EDS
% Data completeness (in resolution range)	93.6 (20.00-2.60) 95.3 (24.38-2.62)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.60Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.232 , 0.267 0.243 , 0.278	Depositor DCC
R_{free} test set	1100 reflections (4.80%)	DCC
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 29.0	EDS
Estimated twinning fraction	0.025 for -h,k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 23663 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3760	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.44	0/1926	0.64	1/2609 (0.0%)
1	B	0.47	0/1926	0.65	1/2609 (0.0%)
All	All	0.45	0/3852	0.64	2/5218 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1146	LEU	CA-CB-CG	5.53	128.01	115.30
1	B	1146	LEU	CA-CB-CG	5.45	127.84	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1880	0	1818	80	0
1	B	1880	0	1818	90	0
All	All	3760	0	3636	167	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (167) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1156:ARG:HD3	1:A:1166:ILE:HG21	1.64	0.80
1:B:1180:ASN:HD22	1:B:1181:MET:H	1.27	0.79
1:A:1180:ASN:HD22	1:A:1181:MET:H	1.28	0.78
1:A:1037:ASN:ND2	1:A:1049:ILE:H	1.83	0.77
1:B:1087:VAL:HG22	1:B:1129:ILE:HD11	1.67	0.77
1:A:1087:VAL:HG22	1:A:1129:ILE:HD11	1.67	0.77
1:B:1211:GLY:HA2	1:B:1241:VAL:HG12	1.66	0.76
1:B:1230:MET:HB3	1:B:1236:GLN:OE1	1.86	0.74
1:A:1230:MET:HB3	1:A:1236:GLN:OE1	1.87	0.74
1:A:1211:GLY:HA2	1:A:1241:VAL:HG12	1.70	0.72
1:B:1037:ASN:ND2	1:B:1049:ILE:H	1.87	0.72
1:B:1067:HIS:HA	1:B:1126:ASP:OD1	1.89	0.72
1:A:1067:HIS:HA	1:A:1126:ASP:OD1	1.90	0.71
1:A:1171:LEU:H	1:A:1180:ASN:HD21	1.39	0.71
1:A:1037:ASN:HD22	1:A:1049:ILE:H	1.39	0.70
1:A:1020:ILE:HD12	1:A:1021:VAL:H	1.58	0.69
1:B:1020:ILE:HD12	1:B:1021:VAL:H	1.57	0.69
1:B:1171:LEU:H	1:B:1180:ASN:HD21	1.41	0.68
1:B:1180:ASN:HD22	1:B:1181:MET:N	1.91	0.68
1:A:1194:TYR:O	1:A:1237:ALA:HA	1.95	0.67
1:B:1010:TYR:O	1:B:1014:LEU:HD13	1.96	0.66
1:A:1180:ASN:HD22	1:A:1181:MET:N	1.93	0.66
1:B:1167:LEU:HD12	1:B:1168:LEU:H	1.61	0.66
1:B:1194:TYR:O	1:B:1237:ALA:HA	1.96	0.66
1:A:1241:VAL:HG22	1:B:1241:VAL:HG22	1.79	0.65
1:B:1085:LEU:HD23	1:B:1086:TYR:N	2.12	0.64
1:B:1026:PHE:HA	1:B:1229:PHE:O	1.97	0.64
1:A:1082:GLU:HG3	1:A:1179:MET:HE3	1.80	0.64
1:A:1026:PHE:HA	1:A:1229:PHE:O	1.98	0.62
1:B:1142:TYR:CZ	1:B:1175:LEU:HD12	2.34	0.62
1:B:1037:ASN:HD22	1:B:1049:ILE:H	1.47	0.62
1:A:1239:TYR:HD1	1:A:1240:GLY:O	1.83	0.61
1:B:1082:GLU:CD	1:B:1179:MET:HE2	2.21	0.61
1:B:1085:LEU:HD23	1:B:1085:LEU:C	2.21	0.60
1:A:1167:LEU:O	1:A:1168:LEU:HD23	2.02	0.59
1:A:1085:LEU:HD23	1:A:1086:TYR:N	2.17	0.59
1:A:1085:LEU:C	1:A:1085:LEU:HD23	2.23	0.59
1:B:1082:GLU:HG3	1:B:1179:MET:HE3	1.85	0.58
1:B:1150:ASN:O	1:B:1153:GLU:HG3	2.04	0.58
1:A:1193:GLY:HA3	1:B:1014:LEU:HD21	1.85	0.58
1:B:1215:LEU:HD22	1:B:1215:LEU:N	2.19	0.58
1:A:1215:LEU:HD22	1:A:1215:LEU:N	2.18	0.57
1:B:1157:ILE:O	1:B:1157:ILE:HG22	2.05	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:1010:TYR:HB2	1:B:1013:ASP:OD2	2.05	0.57
1:B:1087:VAL:HA	1:B:1129:ILE:HD12	1.86	0.57
1:A:1156:ARG:HD3	1:A:1166:ILE:CG2	2.33	0.57
1:A:1150:ASN:O	1:A:1153:GLU:HG3	2.04	0.57
1:B:1037:ASN:HD22	1:B:1048:THR:HA	1.70	0.56
1:A:1195:ILE:N	1:A:1195:ILE:HD13	2.21	0.55
1:A:1088:ILE:HG21	1:A:1128:GLN:HE21	1.69	0.55
1:B:1195:ILE:HD13	1:B:1195:ILE:N	2.22	0.55
1:B:1167:LEU:HD12	1:B:1168:LEU:N	2.20	0.54
1:A:1239:TYR:CD1	1:A:1240:GLY:O	2.60	0.54
1:B:1235:LEU:HD12	1:B:1236:GLN:N	2.23	0.54
1:B:1088:ILE:HG21	1:B:1128:GLN:HE21	1.73	0.54
1:A:1087:VAL:HA	1:A:1129:ILE:HD12	1.90	0.53
1:A:1132:TYR:HE1	1:A:1179:MET:HE1	1.73	0.53
1:B:1206:ILE:HG13	1:B:1222:VAL:CG1	2.39	0.53
1:A:1235:LEU:HD12	1:A:1236:GLN:N	2.23	0.52
1:A:1206:ILE:HG13	1:A:1222:VAL:CG1	2.40	0.52
1:B:1064:VAL:HB	1:B:1129:ILE:HG22	1.92	0.52
1:B:1073:GLN:NE2	1:B:1120:VAL:HG21	2.25	0.52
1:B:1214:ASN:HB3	1:B:1237:ALA:HB3	1.91	0.52
1:A:1055:LEU:O	1:A:1055:LEU:HD22	2.09	0.52
1:B:1011:ARG:HA	1:B:1014:LEU:HD22	1.92	0.52
1:B:1239:TYR:HD1	1:B:1240:GLY:O	1.92	0.51
1:B:1156:ARG:HD3	1:B:1166:ILE:HD12	1.92	0.51
1:A:1214:ASN:HB3	1:A:1237:ALA:HB3	1.92	0.51
1:B:1167:LEU:O	1:B:1168:LEU:HD23	2.10	0.51
1:A:1037:ASN:HD22	1:A:1048:THR:HA	1.75	0.51
1:A:1195:ILE:O	1:A:1196:GLU:HB2	2.11	0.51
1:B:1062:TYR:N	1:B:1062:TYR:CD1	2.78	0.51
1:B:1195:ILE:O	1:B:1196:GLU:HB2	2.10	0.51
1:B:1120:VAL:HG12	1:B:1121:ASN:O	2.11	0.51
1:A:1009:GLY:N	1:B:1195:ILE:HD11	2.25	0.51
1:A:1053:PRO:HA	1:A:1057:ALA:O	2.11	0.51
1:B:1202:HIS:HB2	1:B:1230:MET:HB2	1.93	0.50
1:B:1076:PHE:O	1:B:1077:GLY:O	2.30	0.50
1:A:1073:GLN:NE2	1:A:1120:VAL:HG21	2.27	0.50
1:A:1028:LEU:HD13	1:A:1028:LEU:C	2.32	0.50
1:B:1011:ARG:O	1:B:1014:LEU:HB2	2.12	0.50
1:B:1199:VAL:HG22	1:B:1233:TYR:CE1	2.46	0.50
1:A:1199:VAL:HG22	1:A:1233:TYR:CE1	2.47	0.49
1:B:1260:GLU:HA	1:B:1260:GLU:OE2	2.12	0.49
1:A:1157:ILE:HG22	1:A:1157:ILE:O	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:1043:GLU:O	1:B:1070:GLY:HA2	2.13	0.49
1:A:1232:ALA:O	1:A:1233:TYR:HB2	2.12	0.49
1:B:1055:LEU:O	1:B:1055:LEU:HD22	2.13	0.49
1:A:1082:GLU:CD	1:A:1179:MET:HE2	2.33	0.49
1:B:1232:ALA:O	1:B:1233:TYR:HB2	2.13	0.49
1:B:1033:GLY:O	1:B:1034:LEU:HD23	2.12	0.49
1:A:1076:PHE:O	1:A:1077:GLY:O	2.31	0.49
1:A:1212:VAL:O	1:A:1238:GLY:HA2	2.13	0.49
1:B:1184:LEU:O	1:B:1248:SER:HA	2.13	0.49
1:A:1212:VAL:HG12	1:A:1219:TRP:HE3	1.79	0.48
1:B:1028:LEU:C	1:B:1028:LEU:HD13	2.34	0.48
1:A:1064:VAL:HB	1:A:1129:ILE:HG22	1.96	0.48
1:A:1202:HIS:HB2	1:A:1230:MET:HB2	1.94	0.48
1:B:1067:HIS:HD2	1:B:1126:ASP:OD1	1.96	0.48
1:B:1212:VAL:HG12	1:B:1219:TRP:HE3	1.79	0.48
1:B:1030:THR:O	1:B:1032:ASP:N	2.47	0.48
1:A:1030:THR:O	1:A:1032:ASP:N	2.47	0.48
1:A:1120:VAL:HG12	1:A:1121:ASN:O	2.14	0.47
1:B:1165:VAL:HG21	1:B:1192:HIS:ND1	2.29	0.47
1:B:1212:VAL:O	1:B:1238:GLY:HA2	2.15	0.47
1:A:1067:HIS:HD2	1:A:1126:ASP:OD1	1.97	0.47
1:B:1048:THR:HG23	1:B:1063:LEU:HB3	1.97	0.47
1:B:1053:PRO:HA	1:B:1057:ALA:O	2.14	0.47
1:A:1062:TYR:CD1	1:A:1062:TYR:N	2.83	0.46
1:A:1195:ILE:HG22	1:A:1237:ALA:HB2	1.98	0.46
1:B:1068:GLN:O	1:B:1069:ASN:HB2	2.15	0.46
1:A:1033:GLY:O	1:A:1034:LEU:HD23	2.15	0.46
1:A:1260:GLU:OE2	1:A:1260:GLU:HA	2.14	0.46
1:A:1068:GLN:O	1:A:1069:ASN:HB2	2.16	0.46
1:B:1082:GLU:HG3	1:B:1179:MET:CE	2.46	0.46
1:A:1043:GLU:O	1:A:1070:GLY:HA2	2.16	0.46
1:B:1198:HIS:HB2	1:B:1200:GLN:NE2	2.30	0.45
1:A:1215:LEU:HD22	1:A:1215:LEU:H	1.80	0.45
1:B:1182:HIS:HE1	1:B:1253:LYS:HD3	1.80	0.45
1:B:1195:ILE:HG22	1:B:1237:ALA:HB2	1.99	0.45
1:A:1184:LEU:O	1:A:1248:SER:HA	2.16	0.45
1:A:1198:HIS:HB2	1:A:1200:GLN:NE2	2.31	0.45
1:A:1048:THR:HG23	1:A:1063:LEU:HB3	1.99	0.44
1:A:1195:ILE:HG22	1:A:1237:ALA:CB	2.47	0.44
1:A:1082:GLU:HG3	1:A:1179:MET:CE	2.46	0.44
1:A:1022:LYS:O	1:A:1025:ASN:HB2	2.18	0.44
1:A:1210:GLN:O	1:A:1241:VAL:HG12	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:1087:VAL:HA	1:B:1129:ILE:CD1	2.47	0.44
1:B:1142:TYR:CD2	1:B:1175:LEU:HB2	2.52	0.44
1:A:1188:PRO:C	1:A:1190:ALA:H	2.22	0.44
1:B:1022:LYS:O	1:B:1025:ASN:HB2	2.18	0.43
1:B:1188:PRO:C	1:B:1190:ALA:H	2.22	0.43
1:A:1182:HIS:HE1	1:A:1253:LYS:HD3	1.82	0.43
1:B:1110:TYR:C	1:B:1110:TYR:CD1	2.92	0.43
1:B:1062:TYR:OH	1:B:1133:LYS:HE2	2.18	0.43
1:B:1067:HIS:CD2	1:B:1126:ASP:OD1	2.71	0.43
1:B:1215:LEU:H	1:B:1215:LEU:HD22	1.81	0.43
1:B:1195:ILE:HG22	1:B:1237:ALA:CB	2.48	0.43
1:B:1142:TYR:CE2	1:B:1175:LEU:HB2	2.54	0.43
1:B:1120:VAL:HG12	1:B:1121:ASN:N	2.34	0.43
1:B:1167:LEU:C	1:B:1168:LEU:HD23	2.38	0.42
1:B:1146:LEU:C	1:B:1146:LEU:CD1	2.88	0.42
1:A:1156:ARG:O	1:A:1157:ILE:C	2.58	0.42
1:B:1142:TYR:HB3	1:B:1176:GLY:HA2	2.01	0.42
1:A:1146:LEU:CD1	1:A:1146:LEU:C	2.88	0.42
1:B:1240:GLY:O	1:B:1241:VAL:HB	2.20	0.42
1:B:1020:ILE:HG13	1:B:1021:VAL:N	2.34	0.42
1:A:1067:HIS:CD2	1:A:1126:ASP:OD1	2.72	0.42
1:A:1120:VAL:HG12	1:A:1121:ASN:N	2.35	0.42
1:A:1095:LYS:HB2	1:A:1118:THR:OG1	2.20	0.42
1:B:1156:ARG:O	1:B:1157:ILE:C	2.58	0.42
1:A:1020:ILE:HG13	1:A:1021:VAL:N	2.35	0.41
1:B:1020:ILE:CG1	1:B:1021:VAL:N	2.83	0.41
1:B:1120:VAL:CG1	1:B:1121:ASN:N	2.83	0.41
1:B:1182:HIS:HB2	1:B:1251:TYR:CE1	2.55	0.41
1:B:1132:TYR:HE1	1:B:1179:MET:HE1	1.85	0.41
1:B:1146:LEU:C	1:B:1146:LEU:HD12	2.41	0.41
1:A:1156:ARG:HD2	1:A:1166:ILE:HD13	2.03	0.41
1:A:1087:VAL:HA	1:A:1129:ILE:CD1	2.50	0.41
1:A:1010:TYR:O	1:A:1014:LEU:HD13	2.21	0.41
1:A:1134:ARG:HD3	1:A:1179:MET:HE2	2.02	0.41
1:A:1020:ILE:CG1	1:A:1021:VAL:N	2.84	0.41
1:B:1082:GLU:CD	1:B:1179:MET:CE	2.88	0.40
1:A:1022:LYS:O	1:A:1023:HIS:C	2.59	0.40
1:A:1020:ILE:HD12	1:A:1021:VAL:N	2.32	0.40
1:A:1020:ILE:CD1	1:A:1021:VAL:H	2.31	0.40
1:B:1020:ILE:CD1	1:B:1021:VAL:H	2.30	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	236/261 (90%)	211 (89%)	20 (8%)	5 (2%)	11	19
1	B	236/261 (90%)	214 (91%)	17 (7%)	5 (2%)	11	19
All	All	472/522 (90%)	425 (90%)	37 (8%)	10 (2%)	11	19

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1023	HIS
1	A	1077	GLY
1	B	1023	HIS
1	B	1077	GLY
1	A	1019	ALA
1	A	1031	PRO
1	A	1215	LEU
1	B	1019	ALA
1	B	1031	PRO
1	B	1215	LEU

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	196/211 (93%)	184 (94%)	12 (6%)	26	50
1	B	196/211 (93%)	183 (93%)	13 (7%)	24	45
All	All	392/422 (93%)	367 (94%)	25 (6%)	25	47

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1029	LEU
1	A	1032	ASP
1	A	1048	THR
1	A	1055	LEU
1	A	1062	TYR
1	A	1129	ILE
1	A	1146	LEU
1	A	1171	LEU
1	A	1180	ASN
1	A	1195	ILE
1	A	1200	GLN
1	A	1213	TYR
1	B	1029	LEU
1	B	1032	ASP
1	B	1048	THR
1	B	1055	LEU
1	B	1062	TYR
1	B	1125	GLU
1	B	1129	ILE
1	B	1146	LEU
1	B	1171	LEU
1	B	1180	ASN
1	B	1195	ILE
1	B	1200	GLN
1	B	1213	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1025	ASN
1	A	1037	ASN
1	A	1067	HIS
1	A	1123	GLN
1	A	1180	ASN
1	A	1182	HIS
1	A	1200	GLN
1	A	1217	ASN
1	B	1025	ASN
1	B	1037	ASN
1	B	1067	HIS
1	B	1123	GLN
1	B	1180	ASN
1	B	1182	HIS

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Mol	Chain	Res	Type
1	B	1200	GLN
1	B	1217	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	242/261 (92%)	0.10	11 (4%) 32 28	19, 40, 90, 109	0
1	B	242/261 (92%)	0.42	18 (7%) 14 12	23, 55, 94, 109	0
All	All	484/522 (92%)	0.26	29 (5%) 21 18	19, 48, 93, 109	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1010	TYR	5.6
1	B	1189	GLY	5.4
1	B	1010	TYR	5.1
1	B	1013	ASP	4.9
1	B	1188	PRO	4.4
1	A	1013	ASP	4.4
1	B	1009	GLY	3.2
1	B	1187	ALA	3.2
1	B	1032	ASP	3.2
1	B	1166	ILE	3.0
1	A	1188	PRO	3.0
1	B	1014	LEU	2.9
1	A	1189	GLY	2.9
1	B	1012	GLU	2.9
1	B	1125	GLU	2.8
1	A	1194	TYR	2.8
1	B	1124	ALA	2.8
1	A	1014	LEU	2.7
1	B	1122	ALA	2.6
1	B	1156	ARG	2.5
1	B	1191	SER	2.5
1	A	1192	HIS	2.5
1	A	1012	GLU	2.4
1	A	1016	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	1193	GLY	2.4
1	B	1016	ALA	2.3
1	B	1035	VAL	2.3
1	A	1032	ASP	2.2
1	A	1217	ASN	2.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.