Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 12:40 pm BST

PDB ID	:	2CKD
Title	:	Crystal structure of ML2640 from Mycobacterium leprae
Authors	:	Grana, M.; Buschiazzo, A.; Wehenkel, A.; Haouz, A.; Alzari, P.M.
Deposited on	:	2006-04-17
Resolution	:	2.80 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:

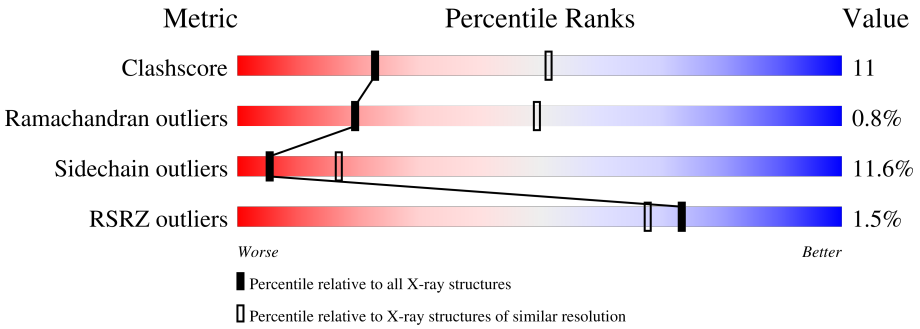
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	310	71% 23%
1	B	310	67% 25%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4692 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 PUTATIVE S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE ML2640.

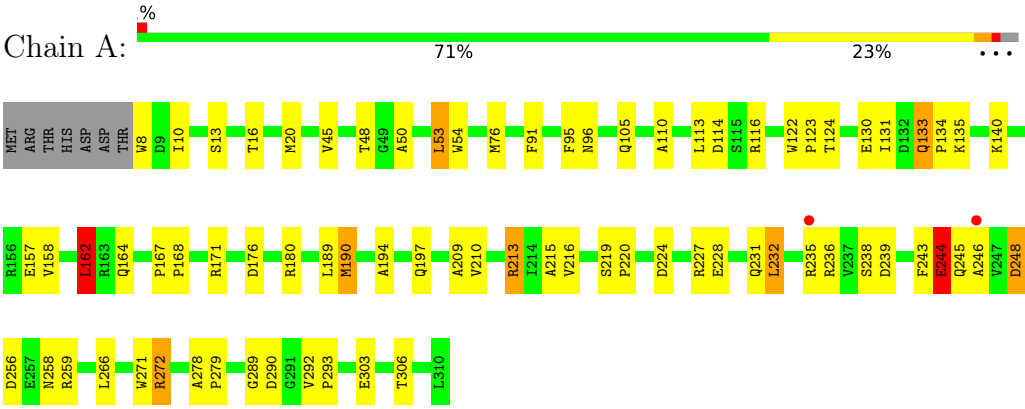
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2369	1489	421	450	9			
1	B	298	Total	C	N	O	S	0	0	0
			2323	1458	414	442	9			

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

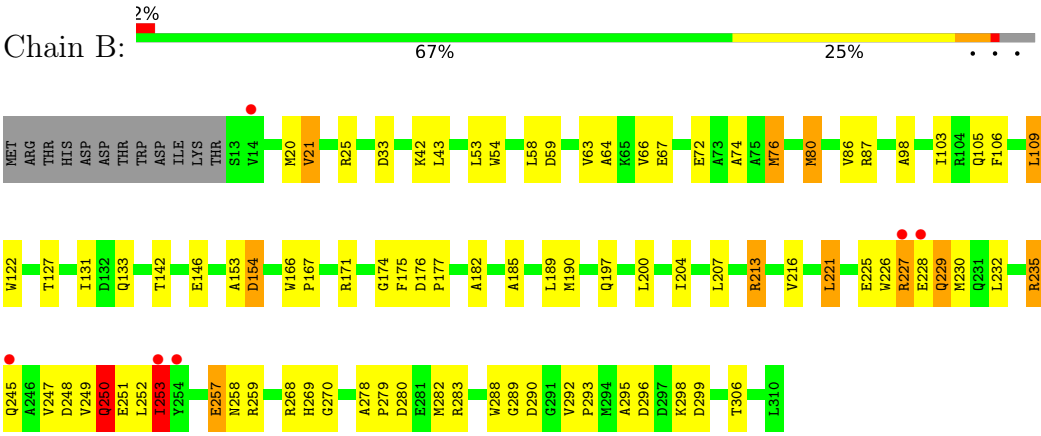
• Molecule 1: PUTATIVE S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE ML2640

Chain A:



• Molecule 1: PUTATIVE S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE ML2640

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	96.78Å 96.78Å 169.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.92 – 2.80 63.73 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (83.92-2.80) 99.3 (63.73-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.01 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.199 , 0.255 0.205 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	39.3	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 28.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4692	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.85	1/2424 (0.0%)	0.91	3/3302 (0.1%)
1	B	0.85	1/2376 (0.0%)	0.93	5/3236 (0.2%)
All	All	0.85	2/4800 (0.0%)	0.92	8/6538 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	ASN	CB-CG	6.69	1.66	1.51
1	B	270	GLY	CA-C	5.06	1.59	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	270	GLY	N-CA-C	-9.14	90.26	113.10
1	A	213	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	B	213	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	B	154	ASP	CB-CG-OD1	5.65	123.39	118.30
1	B	119	ARG	NE-CZ-NH2	5.51	123.06	120.30
1	A	162	LEU	CA-CB-CG	-5.43	102.80	115.30
1	B	235	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	252	LEU	CA-CB-CG	5.07	126.97	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	269	HIS	Peptide

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	2369	0	2293	56	0
1	B	2323	0	2248	54	0
All	All	4692	0	4541	106	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 11.

All (106) 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:227:ARG:HH11	1:B:227:ARG:HG2	1.14	1.13
1:A:48:THR:HG22	1:A:50:ALA:H	1.01	1.07
1:A:48:THR:HG22	1:A:50:ALA:N	1.83	0.92
1:A:272:ARG:HH11	1:A:272:ARG:HG2	1.38	0.88
1:A:227:ARG:HD3	1:A:251:GLU:HA	1.55	0.87
1:B:226:TRP:HZ3	1:B:293:PRO:O	1.60	0.85
1:B:227:ARG:HG2	1:B:227:ARG:NH1	1.90	0.84
1:B:227:ARG:HH11	1:B:227:ARG:CG	1.90	0.82
1:B:280:ASP:OD1	1:B:283:ARG:NH1	2.18	0.76
1:B:105:GLN:HE22	1:B:176:ASP:H	1.33	0.74
1:A:16:THR:HG21	1:A:248:ASP:OD2	1.87	0.73
1:B:226:TRP:CZ3	1:B:293:PRO:O	2.42	0.73
1:A:232:LEU:HD11	1:A:236:ARG:HH21	1.53	0.71
1:A:272:ARG:HG2	1:A:272:ARG:NH1	2.04	0.70
1:A:8:TRP:HB2	1:A:48:THR:O	1.93	0.69
1:A:292:VAL:HG12	1:A:293:PRO:HD2	1.74	0.68
1:A:45:VAL:O	1:A:48:THR:HB	1.95	0.66
1:A:114:ASP:OD2	1:A:116:ARG:NH1	2.28	0.66
1:A:289:GLY:O	1:A:292:VAL:HG23	1.95	0.66
1:A:227:ARG:CD	1:A:251:GLU:HA	2.26	0.64
1:A:190:MET:HB3	1:A:252:LEU:HD13	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:LEU:HD11	1:B:216:VAL:HG11	1.83	0.59
1:B:227:ARG:O	1:B:230:MET:HB2	2.03	0.58
1:B:109:LEU:HD23	1:B:131:ILE:HD12	1.85	0.58
1:A:105:GLN:HE22	1:A:176:ASP:H	1.53	0.56
1:A:122:TRP:CD1	1:A:153:ALA:HB2	2.41	0.55
1:A:232:LEU:CD1	1:A:236:ARG:HH21	2.18	0.55
1:B:20:MET:HG3	1:B:54:TRP:CE3	2.43	0.54
1:B:292:VAL:HG22	1:B:293:PRO:CD	2.38	0.53
1:A:292:VAL:HG12	1:A:293:PRO:CD	2.38	0.53
1:B:106:PHE:CD1	1:B:182:ALA:HB3	2.44	0.53
1:A:53:LEU:HD13	1:A:238:SER:HB3	1.91	0.53
1:A:272:ARG:HH11	1:A:272:ARG:CG	2.16	0.52
1:B:66:VAL:HG12	1:B:74:ALA:HB2	1.91	0.52
1:A:180:ARG:HD2	1:B:289:GLY:CA	2.39	0.52
1:A:10:ILE:HD11	1:A:135:LYS:HB3	1.92	0.52
1:B:227:ARG:NH1	1:B:227:ARG:CG	2.61	0.51
1:A:133:GLN:HG3	1:A:134:PRO:HD2	1.91	0.51
1:B:76:MET:HE1	1:B:226:TRP:CZ2	2.44	0.51
1:A:91:PHE:HE2	1:A:215:ALA:HB1	1.76	0.50
1:B:185:ALA:HB3	1:B:216:VAL:HG22	1.94	0.50
1:A:130:GLU:OE2	1:A:155:ARG:HD2	2.12	0.49
1:A:197:GLN:NE2	1:A:259:ARG:HH11	2.11	0.49
1:A:131:ILE:HG12	1:A:158:VAL:HB	1.94	0.49
1:B:122:TRP:CD1	1:B:153:ALA:HB2	2.48	0.48
1:B:251:GLU:O	1:B:253:ILE:HG12	2.13	0.48
1:B:292:VAL:HG22	1:B:293:PRO:HD2	1.95	0.48
1:A:167:PRO:HB2	1:A:168:PRO:HD3	1.96	0.47
1:B:142:THR:O	1:B:146:GLU:HB2	2.13	0.47
1:B:189:LEU:HD11	1:B:216:VAL:CG1	2.44	0.47
1:A:130:GLU:CD	1:A:155:ARG:HH11	2.17	0.47
1:B:59:ASP:OD1	1:B:59:ASP:C	2.52	0.47
1:A:180:ARG:HD2	1:B:289:GLY:HA2	1.97	0.46
1:A:110:ALA:H	1:A:162:LEU:CD1	2.29	0.46
1:A:194:ALA:O	1:A:197:GLN:HB3	2.15	0.46
1:B:197:GLN:NE2	1:B:259:ARG:HH11	2.13	0.46
1:B:76:MET:CE	1:B:226:TRP:CZ2	2.98	0.46
1:A:53:LEU:CD1	1:A:238:SER:HB3	2.46	0.45
1:A:197:GLN:HE22	1:A:259:ARG:HD3	1.82	0.45
1:B:292:VAL:O	1:B:295:ALA:HB2	2.16	0.45
1:A:232:LEU:C	1:A:232:LEU:HD12	2.37	0.45
1:A:244:GLU:OE1	1:A:245:GLN:HB2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:LEU:HD21	1:B:257:GLU:HB3	1.99	0.45
1:B:21:VAL:HG12	1:B:25:ARG:HH21	1.80	0.45
1:A:189:LEU:HD11	1:A:216:VAL:HG11	1.99	0.45
1:A:105:GLN:HE22	1:A:176:ASP:HB3	1.82	0.45
1:B:288:TRP:HE1	1:B:290:ASP:HB3	1.82	0.45
1:A:20:MET:HG3	1:A:54:TRP:CE3	2.52	0.44
1:B:229:GLN:HE21	1:B:229:GLN:HB2	1.49	0.44
1:A:91:PHE:CE2	1:A:215:ALA:HB1	2.53	0.44
1:A:209:ALA:O	1:A:210:VAL:C	2.56	0.44
1:A:105:GLN:NE2	1:A:176:ASP:H	2.15	0.44
1:B:278:ALA:HB3	1:B:279:PRO:HD3	2.00	0.43
1:B:86:VAL:HG21	1:B:282:MET:HG2	2.00	0.43
1:A:266:LEU:HB3	1:A:271:TRP:HB2	2.01	0.43
1:A:292:VAL:CG1	1:A:293:PRO:HD2	2.44	0.43
1:A:113:LEU:HA	1:A:140:LYS:HD3	2.01	0.43
1:A:155:ARG:NH2	1:A:157:GLU:OE2	2.50	0.43
1:B:175:PHE:CE2	1:B:207:LEU:HB3	2.54	0.43
1:A:224:ASP:O	1:A:228:GLU:HG3	2.18	0.43
1:A:227:ARG:NH1	1:A:231:GLN:HG3	2.34	0.42
1:B:171:ARG:HH11	1:B:171:ARG:HG2	1.84	0.42
1:A:238:SER:HB2	1:A:243:PHE:HB2	2.01	0.42
1:B:174:GLY:O	1:B:175:PHE:C	2.58	0.42
1:B:76:MET:HE1	1:B:226:TRP:CE2	2.55	0.42
1:A:180:ARG:HD2	1:B:289:GLY:HA3	2.00	0.42
1:B:250:GLN:O	1:B:251:GLU:C	2.57	0.42
1:B:127:THR:HG22	1:B:154:ASP:CG	2.39	0.42
1:B:292:VAL:CG2	1:B:293:PRO:CD	2.97	0.42
1:B:80:MET:HE3	1:B:80:MET:HB3	1.80	0.41
1:B:58:LEU:HD21	1:B:80:MET:HE3	2.01	0.41
1:B:175:PHE:O	1:B:177:PRO:HD3	2.19	0.41
1:A:219:SER:HA	1:A:220:PRO:HD3	1.91	0.41
1:A:278:ALA:HB3	1:A:279:PRO:HD3	2.02	0.41
1:B:200:LEU:O	1:B:204:ILE:HG13	2.20	0.41
1:A:190:MET:HA	1:A:219:SER:HB2	2.02	0.41
1:B:53:LEU:HD11	1:B:238:SER:HB3	2.02	0.41
1:B:166:TRP:N	1:B:167:PRO:CD	2.84	0.41
1:A:190:MET:HA	1:A:219:SER:CB	2.50	0.41
1:A:255:HIS:NE2	1:A:256:ASP:OD2	2.54	0.41
1:B:20:MET:HG3	1:B:54:TRP:CZ3	2.56	0.41
1:B:278:ALA:N	1:B:279:PRO:CD	2.84	0.41
1:A:123:PRO:HB2	1:B:67:GLU:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ALA:HB1	1:B:103:ILE:HD12	2.03	0.40
1:B:63:VAL:HG12	1:B:64:ALA:N	2.35	0.40
1:B:296:ASP:OD2	1:B:296:ASP:N	2.49	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	301/310 (97%)	280 (93%)	19 (6%)	2 (1%)	22 53
1	B	296/310 (96%)	270 (91%)	23 (8%)	3 (1%)	15 44
All	All	597/620 (96%)	550 (92%)	42 (7%)	5 (1%)	19 49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	244	GLU
1	B	253	ILE
1	A	246	ALA
1	B	247	VAL
1	B	250	GLN

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	240/247 (97%)	217 (90%)	23 (10%)	8 24
1	B	235/247 (95%)	203 (86%)	32 (14%)	3 11
All	All	475/494 (96%)	420 (88%)	55 (12%)	5 17

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	53	LEU
1	A	76	MET
1	A	95	PHE
1	A	124	THR
1	A	133	GLN
1	A	150	THR
1	A	162	LEU
1	A	164	GLN
1	A	171	ARG
1	A	190	MET
1	A	213	ARG
1	A	232	LEU
1	A	235	ARG
1	A	239	ASP
1	A	244	GLU
1	A	248	ASP
1	A	252	LEU
1	A	258	ASN
1	A	272	ARG
1	A	290	ASP
1	A	303	GLU
1	A	306	THR
1	B	21	VAL
1	B	33	ASP
1	B	42	LYS
1	B	43	LEU
1	B	72	GLU
1	B	76	MET
1	B	80	MET
1	B	87	ARG
1	B	109	LEU
1	B	120	LEU
1	B	133	GLN
1	B	190	MET

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Mol	Chain	Res	Type
1	B	213	ARG
1	B	221	LEU
1	B	225	GLU
1	B	227	ARG
1	B	228	GLU
1	B	229	GLN
1	B	232	LEU
1	B	235	ARG
1	B	245	GLN
1	B	248	ASP
1	B	249	VAL
1	B	250	GLN
1	B	252	LEU
1	B	253	ILE
1	B	257	GLU
1	B	258	ASN
1	B	268	ARG
1	B	298	LYS
1	B	299	ASP
1	B	306	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	GLN
1	A	133	GLN
1	A	147	HIS
1	A	197	GLN
1	B	47	ASN
1	B	105	GLN
1	B	147	HIS
1	B	197	GLN
1	B	229	GLN
1	B	258	ASN

5.3.3 RNA

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)

There are no ligands in this entry.

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, 95^{th} 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	303/310 (97%)	-0.21	2 (0%)	87 84	2, 10, 26, 36	0
1	B	298/310 (96%)	-0.13	7 (2%)	60 51	2, 10, 34, 51	0
All	All	601/620 (96%)	-0.18	9 (1%)	73 68	2, 10, 28, 51	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	ALA	3.3
1	B	244	GLU	3.1
1	B	245	GLN	3.0
1	B	228	GLU	3.0
1	B	254	TYR	2.5
1	B	227	ARG	2.3
1	B	14	VAL	2.1
1	B	253	ILE	2.0
1	A	235	ARG	2.0

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 monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.