



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:39 AM GMT

PDB ID : 2NQK
Title : MoeA D59N mutant
Authors : Nicolas, J.; Xiang, S.; Schindelin, H.; Rajagopalan, K.V.
Deposited on : 2006-10-31
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

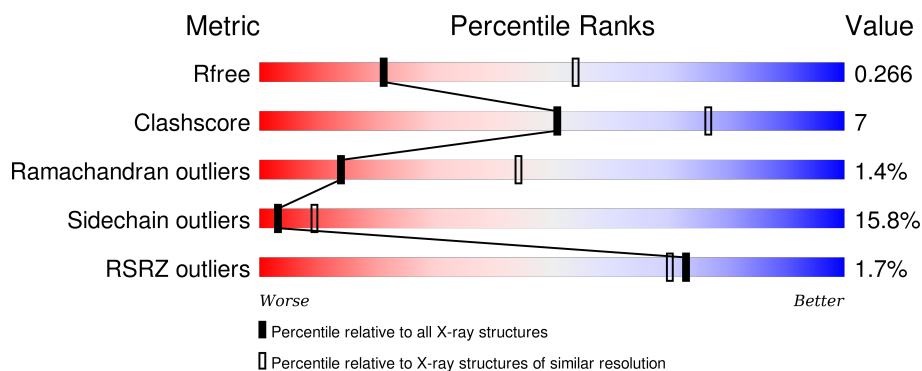
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	411	 72% 23% . .
1	B	411	 72% 24% . .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6080 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 Molybdopterin biosynthesis protein moeA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	0	0
			3040	1918	532	577	13			
1	B	403	Total	C	N	O	S	0	0	0
			3040	1918	532	577	13			

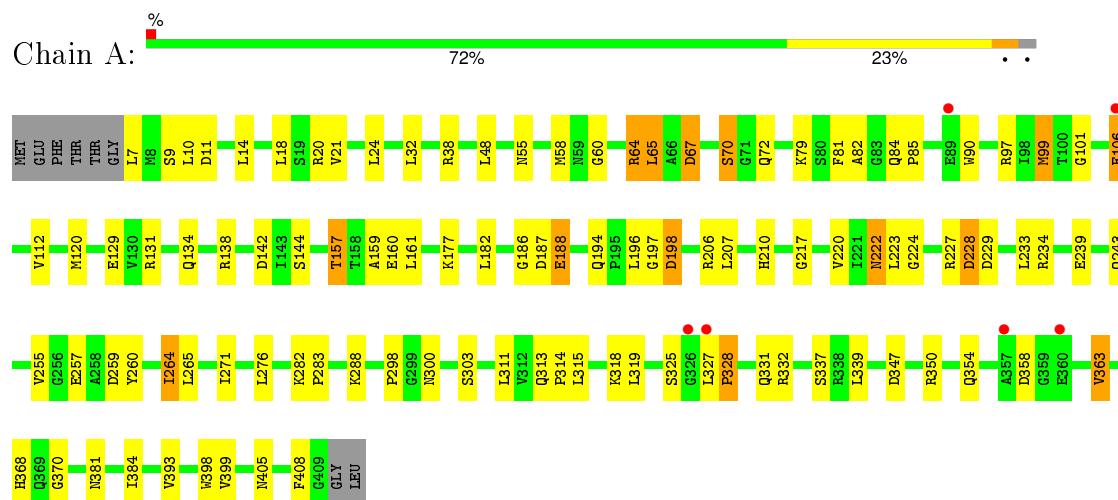
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	ASN	ASP	ENGINEERED	UNP P12281
B	59	ASN	ASP	ENGINEERED	UNP P12281

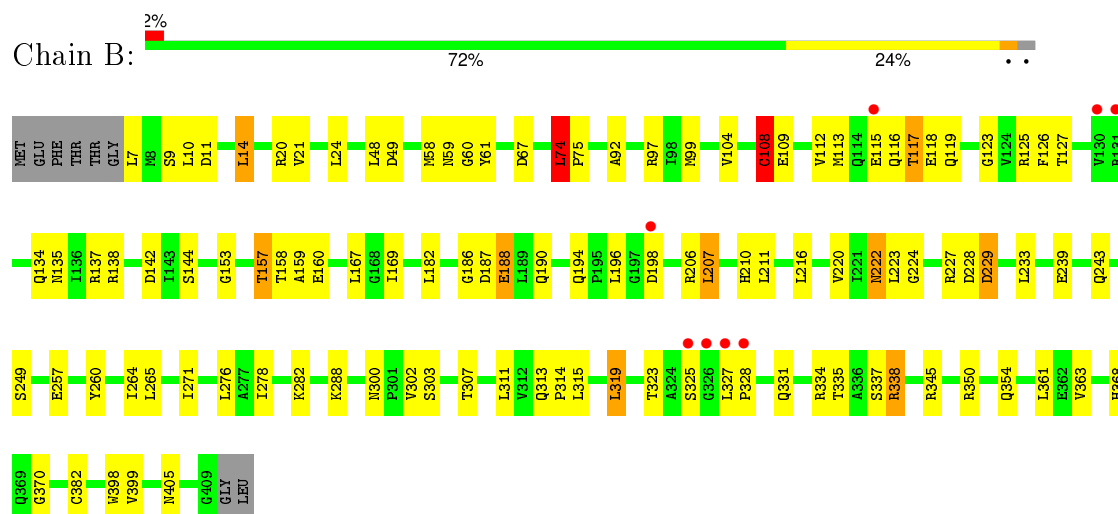
3 Residue-property plots

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: Molybdopterin biosynthesis protein moeA



- Molecule 1: Molybdopterin biosynthesis protein moeA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.19Å 98.22Å 99.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.90 49.87 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.2 (50.00-2.90) 96.2 (49.87-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.198 , 0.266 0.202 , 0.266	Depositor DCC
R_{free} test set	974 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.5	EDS
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 19252 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6080	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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

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	0.72	0/3099	0.88	8/4212 (0.2%)
1	B	0.72	0/3099	0.87	6/4212 (0.1%)
All	All	0.72	0/6198	0.87	14/8424 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	ASP	CB-CG-OD2	8.97	126.38	118.30
1	A	142	ASP	CB-CG-OD2	7.96	125.47	118.30
1	B	187	ASP	CB-CG-OD2	6.32	123.98	118.30
1	A	229	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	358	ASP	CB-CG-OD2	6.21	123.89	118.30
1	B	49	ASP	CB-CG-OD2	5.82	123.53	118.30
1	A	259	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	67	ASP	CB-CG-OD2	5.53	123.27	118.30
1	B	74	LEU	CA-CB-CG	5.42	127.76	115.30
1	A	347	ASP	CB-CG-OD2	5.42	123.17	118.30
1	A	38	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	B	229	ASP	CB-CG-OD2	5.25	123.02	118.30
1	B	142	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	338	ARG	NE-CZ-NH1	5.05	122.82	120.30

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	3040	0	3039	42	0
1	B	3040	0	3039	43	0
All	All	6080	0	6078	84	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 7.

All (84) 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:206:ARG:HH11	1:B:222:ASN:HD21	1.13	0.91
1:A:157:THR:HG22	1:A:159:ALA:H	1.37	0.90
1:A:206:ARG:HH11	1:A:222:ASN:HD21	1.21	0.87
1:B:300:ASN:HD22	1:B:303:SER:H	1.36	0.73
1:B:313:GLN:HE22	1:B:405:ASN:HD21	1.38	0.70
1:A:368:HIS:HD2	1:A:370:GLY:H	1.41	0.67
1:B:368:HIS:HD2	1:B:370:GLY:H	1.41	0.65
1:A:300:ASN:HD22	1:A:303:SER:H	1.44	0.65
1:B:157:THR:HG22	1:B:159:ALA:H	1.62	0.64
1:A:206:ARG:HH11	1:A:222:ASN:ND2	1.94	0.62
1:B:14:LEU:HD11	1:B:327:LEU:HD21	1.82	0.62
1:A:313:GLN:HB3	1:A:314:PRO:HD3	1.82	0.61
1:A:106:GLU:H	1:A:106:GLU:CD	2.04	0.61
1:A:260:TYR:O	1:A:264:ILE:HD12	2.02	0.59
1:A:55:ASN:HD22	1:A:101:GLY:HA2	1.67	0.59
1:B:104:VAL:HG13	1:B:108:CYS:SG	2.43	0.58
1:B:265:LEU:HD22	1:B:271:ILE:HD13	1.86	0.57
1:A:55:ASN:ND2	1:A:101:GLY:HA2	2.21	0.55
1:B:61:TYR:CE1	1:B:117:THR:HG21	2.40	0.55
1:A:313:GLN:HE22	1:A:405:ASN:HD21	1.53	0.55
1:A:197:GLY:O	1:A:198:ASP:C	2.45	0.55
1:B:206:ARG:HH11	1:B:222:ASN:ND2	1.95	0.54
1:B:313:GLN:HE22	1:B:405:ASN:ND2	2.02	0.54
1:A:283:PRO:HG2	1:A:298:PRO:HB3	1.88	0.54
1:A:381:ASN:C	1:A:381:ASN:OD1	2.45	0.53
1:B:21:VAL:HG21	1:B:315:LEU:CD1	2.40	0.52
1:A:206:ARG:NH1	1:A:224:GLY:HA2	2.24	0.52
1:B:157:THR:HB	1:B:160:GLU:OE2	2.09	0.52
1:A:210:HIS:HD2	1:A:222:ASN:OD1	1.93	0.52
1:A:70:SER:HB3	1:A:72:GLN:OE1	2.10	0.52
1:A:313:GLN:HE22	1:A:405:ASN:ND2	2.08	0.51
1:B:153:GLY:HA3	1:B:323:THR:HG23	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:ASN:HD22	1:A:224:GLY:H	1.58	0.50
1:B:74:LEU:HD21	1:B:126:PHE:CE1	2.46	0.50
1:B:260:TYR:O	1:B:264:ILE:HD12	2.11	0.50
1:A:186:GLY:HA3	1:A:188:GLU:OE1	2.11	0.50
1:B:206:ARG:NH1	1:B:222:ASN:HD21	1.95	0.50
1:B:313:GLN:HB3	1:B:314:PRO:HD3	1.94	0.49
1:B:104:VAL:HG13	1:B:108:CYS:CB	2.43	0.49
1:B:61:TYR:HE1	1:B:117:THR:HG21	1.78	0.48
1:B:207:LEU:HD22	1:B:211:LEU:HG	1.95	0.48
1:A:157:THR:HB	1:A:160:GLU:OE2	2.14	0.47
1:B:300:ASN:HD21	1:B:302:VAL:HB	1.79	0.47
1:A:339:LEU:HB2	1:A:393:VAL:HB	1.96	0.47
1:B:167:LEU:HB2	1:B:169:ILE:HD12	1.97	0.47
1:A:64:ARG:HD2	1:A:90:TRP:CZ2	2.50	0.47
1:B:21:VAL:HG21	1:B:315:LEU:HD12	1.96	0.46
1:A:234:ARG:HG3	1:A:264:ILE:HG12	1.97	0.46
1:A:81:PHE:CD2	1:A:99:MET:HG3	2.51	0.46
1:A:311:LEU:C	1:A:314:PRO:HD2	2.36	0.45
1:B:67:ASP:HB3	1:B:74:LEU:HD12	1.98	0.45
1:A:363:VAL:HG11	1:A:384:ILE:HG12	1.97	0.45
1:A:64:ARG:HD3	1:A:67:ASP:OD1	2.17	0.45
1:A:18:LEU:O	1:A:318:LYS:NZ	2.45	0.45
1:B:300:ASN:HD22	1:B:303:SER:N	2.10	0.45
1:A:21:VAL:HG21	1:A:315:LEU:CD1	2.47	0.45
1:B:319:LEU:HD23	1:B:319:LEU:HA	1.88	0.45
1:B:67:ASP:OD2	1:B:92:ALA:O	2.34	0.44
1:B:210:HIS:CD2	1:B:220:VAL:HG11	2.52	0.44
1:B:186:GLY:HA3	1:B:188:GLU:OE1	2.17	0.44
1:A:210:HIS:CD2	1:A:220:VAL:HG11	2.53	0.44
1:B:210:HIS:HD2	1:B:222:ASN:OD1	2.01	0.44
1:B:222:ASN:HD22	1:B:224:GLY:H	1.65	0.44
1:B:368:HIS:HD2	1:B:370:GLY:N	2.12	0.43
1:B:60:GLY:HA3	1:B:112:VAL:O	2.17	0.43
1:A:32:LEU:HB3	1:A:161:LEU:HD22	2.00	0.43
1:A:81:PHE:HB2	1:A:84:GLN:HG3	2.00	0.43
1:A:60:GLY:HA3	1:A:112:VAL:O	2.19	0.43
1:A:405:ASN:C	1:A:405:ASN:OD1	2.57	0.42
1:B:278:ILE:O	1:B:345:ARG:HD2	2.18	0.42
1:A:327:LEU:O	1:A:328:PRO:C	2.58	0.42
1:A:408:PHE:HA	1:B:157:THR:HG23	2.00	0.42
1:B:157:THR:CG2	1:B:158:THR:N	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:ARG:HG3	1:B:398:TRP:CZ3	2.54	0.42
1:A:265:LEU:HD23	1:A:265:LEU:HA	1.88	0.42
1:A:65:LEU:HD13	1:A:65:LEU:HA	1.92	0.42
1:A:332:ARG:HG2	1:A:398:TRP:CE3	2.56	0.41
1:A:177:LYS:HD3	1:A:217:GLY:O	2.21	0.41
1:B:307:THR:O	1:B:311:LEU:HB2	2.21	0.41
1:B:75:PRO:HA	1:B:123:GLY:HA2	2.04	0.40
1:B:265:LEU:HD23	1:B:265:LEU:HA	1.97	0.40
1:B:216:LEU:HD11	1:B:313:GLN:HG3	2.04	0.40
1:B:58:MET:SD	1:B:135:ASN:ND2	2.95	0.40
1:A:131:ARG:O	1:A:134:GLN:HG2	2.22	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	401/411 (98%)	380 (95%)	15 (4%)	6 (2%)	13	42
1	B	401/411 (98%)	381 (95%)	15 (4%)	5 (1%)	16	48
All	All	802/822 (98%)	761 (95%)	30 (4%)	11 (1%)	14	44

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ALA
1	A	198	ASP
1	A	282	LYS
1	B	198	ASP
1	B	282	LYS
1	A	228	ASP
1	A	328	PRO

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Mol	Chain	Res	Type
1	B	328	PRO
1	B	109	GLU
1	B	108	CYS
1	A	85	PRO

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	325/331 (98%)	278 (86%)	47 (14%)	4	12
1	B	325/331 (98%)	269 (83%)	56 (17%)	2	7
All	All	650/662 (98%)	547 (84%)	103 (16%)	3	9

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	9	SER
1	A	10	LEU
1	A	11	ASP
1	A	14	LEU
1	A	20	ARG
1	A	24	LEU
1	A	48	LEU
1	A	58	MET
1	A	64	ARG
1	A	65	LEU
1	A	70	SER
1	A	79	LYS
1	A	97	ARG
1	A	99	MET
1	A	106	GLU
1	A	120	MET
1	A	129	GLU
1	A	138	ARG

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Mol	Chain	Res	Type
1	A	144	SER
1	A	157	THR
1	A	182	LEU
1	A	188	GLU
1	A	194	GLN
1	A	196	LEU
1	A	207	LEU
1	A	222	ASN
1	A	223	LEU
1	A	227	ARG
1	A	228	ASP
1	A	233	LEU
1	A	239	GLU
1	A	243	GLN
1	A	255	VAL
1	A	257	GLU
1	A	264	ILE
1	A	271	ILE
1	A	276	LEU
1	A	288	LYS
1	A	319	LEU
1	A	325	SER
1	A	331	GLN
1	A	337	SER
1	A	350	ARG
1	A	354	GLN
1	A	363	VAL
1	A	399	VAL
1	B	7	LEU
1	B	9	SER
1	B	10	LEU
1	B	11	ASP
1	B	14	LEU
1	B	20	ARG
1	B	24	LEU
1	B	48	LEU
1	B	59	ASN
1	B	74	LEU
1	B	97	ARG
1	B	99	MET
1	B	108	CYS
1	B	113	MET

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Mol	Chain	Res	Type
1	B	115	GLU
1	B	116	GLN
1	B	117	THR
1	B	118	GLU
1	B	119	GLN
1	B	125	ARG
1	B	127	THR
1	B	134	GLN
1	B	137	ARG
1	B	138	ARG
1	B	144	SER
1	B	157	THR
1	B	182	LEU
1	B	188	GLU
1	B	190	GLN
1	B	194	GLN
1	B	196	LEU
1	B	207	LEU
1	B	222	ASN
1	B	223	LEU
1	B	227	ARG
1	B	228	ASP
1	B	229	ASP
1	B	233	LEU
1	B	239	GLU
1	B	243	GLN
1	B	249	SER
1	B	257	GLU
1	B	276	LEU
1	B	288	LYS
1	B	319	LEU
1	B	325	SER
1	B	331	GLN
1	B	335	THR
1	B	337	SER
1	B	338	ARG
1	B	350	ARG
1	B	354	GLN
1	B	361	LEU
1	B	363	VAL
1	B	382	CYS
1	B	399	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	34	GLN
1	A	55	ASN
1	A	59	ASN
1	A	114	GLN
1	A	194	GLN
1	A	210	HIS
1	A	222	ASN
1	A	243	GLN
1	A	300	ASN
1	A	313	GLN
1	A	368	HIS
1	B	87	HIS
1	B	134	GLN
1	B	194	GLN
1	B	210	HIS
1	B	222	ASN
1	B	300	ASN
1	B	313	GLN
1	B	368	HIS

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 ⓘ

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 [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	403/411 (98%)	-0.27	6 (1%) 76 74	12, 28, 58, 79	0
1	B	403/411 (98%)	-0.10	8 (1%) 68 64	15, 31, 68, 85	0
All	All	806/822 (98%)	-0.19	14 (1%) 73 70	12, 29, 65, 85	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	326	GLY	3.6
1	B	325	SER	3.6
1	B	328	PRO	3.4
1	B	327	LEU	3.2
1	B	115	GLU	2.8
1	A	327	LEU	2.7
1	A	357	ALA	2.6
1	B	198	ASP	2.5
1	A	106	GLU	2.5
1	A	89	GLU	2.4
1	A	326	GLY	2.4
1	A	360	GLU	2.2
1	B	131	ARG	2.2
1	B	130	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.