



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:10 pm BST

PDB ID : 2O8A
Title : rat PP1cgamma complexed with mouse inhibitor-2
Authors : Hurley, T.D.
Deposited on : 2006-12-12
Resolution : 2.61 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 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	:	2.11
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)	:	2.11

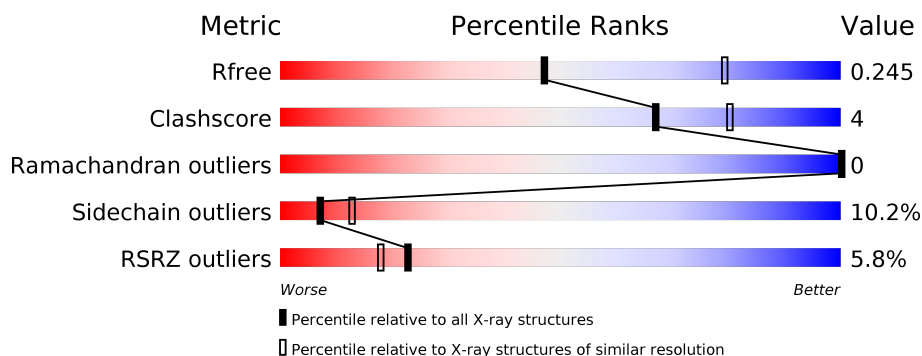
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 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	329	<div> <div>74%</div> <div>13%</div> <div>•</div> <div>10%</div> </div>
1	B	329	<div> <div>%</div> <div>74%</div> <div>15%</div> <div>•</div> <div>10%</div> </div>
2	I	206	<div> <div>11%</div> <div>18%</div> <div>10%</div> <div>71%</div> </div>
2	J	206	<div> <div>7%</div> <div>20%</div> <div>8%</div> <div>72%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5842 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 Serine/threonine-protein phosphatase PP1-gamma catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2380	1527	399	436	18			
1	B	295	Total	C	N	O	S	0	0	0
			2380	1527	399	436	18			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	INITIATING METHIONINE	UNP P63088
A	-4	HIS	-	EXPRESSION TAG	UNP P63088
A	-3	HIS	-	EXPRESSION TAG	UNP P63088
A	-2	HIS	-	EXPRESSION TAG	UNP P63088
A	-1	HIS	-	EXPRESSION TAG	UNP P63088
A	0	HIS	-	EXPRESSION TAG	UNP P63088
A	1	HIS	-	EXPRESSION TAG	UNP P63088
B	-5	MET	-	INITIATING METHIONINE	UNP P63088
B	-4	HIS	-	EXPRESSION TAG	UNP P63088
B	-3	HIS	-	EXPRESSION TAG	UNP P63088
B	-2	HIS	-	EXPRESSION TAG	UNP P63088
B	-1	HIS	-	EXPRESSION TAG	UNP P63088
B	0	HIS	-	EXPRESSION TAG	UNP P63088
B	1	HIS	-	EXPRESSION TAG	UNP P63088

- Molecule 2 is a protein called Protein phosphatase inhibitor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	59	Total	C	N	O	S	0	0	0
			495	309	93	91	2			
2	J	58	Total	C	N	O	S	0	0	0
			487	305	92	88	2			

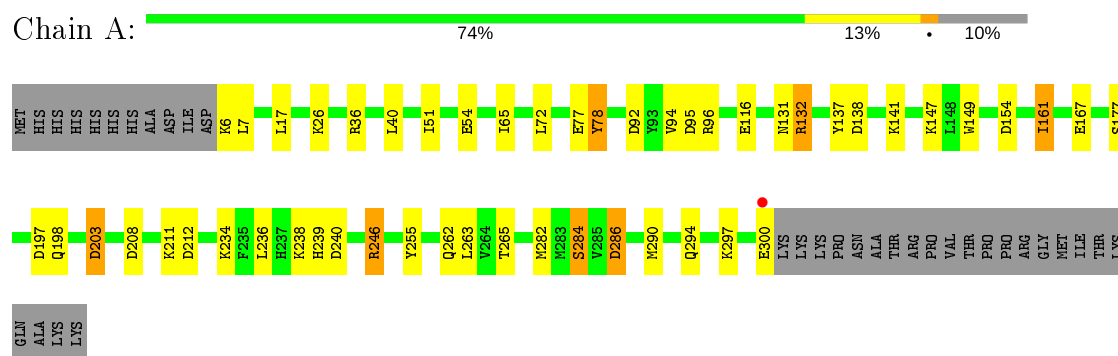
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total 47	O 47	0	0
3	I	5	Total 5	O 5	0	0
3	B	38	Total 38	O 38	0	0
3	J	10	Total 10	O 10	0	0

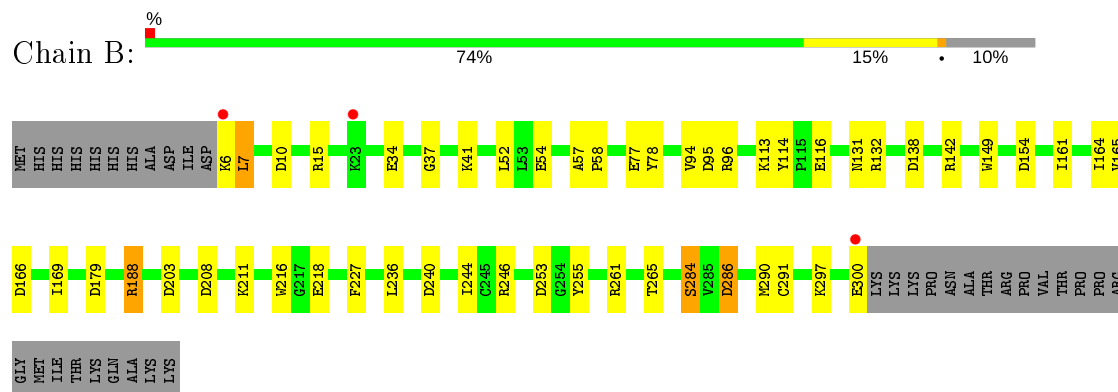
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

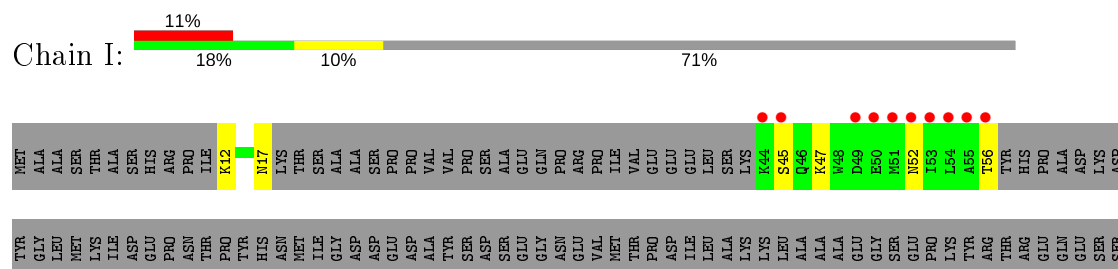
- Molecule 1: Serine/threonine-protein phosphatase PP1-gamma catalytic subunit



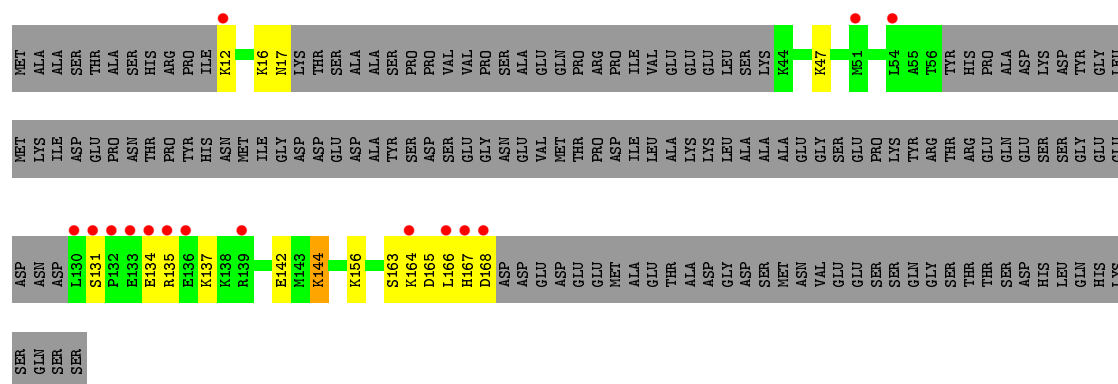
- Molecule 1: Serine/threonine-protein phosphatase PP1-gamma catalytic subunit



- Molecule 2: Protein phosphatase inhibitor 2



- Molecule 2: Protein phosphatase inhibitor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.46Å 103.81Å 151.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.70 – 2.61 41.69 – 2.61	Depositor EDS
% Data completeness (in resolution range)	95.4 (41.70-2.61) 95.4 (41.69-2.61)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.216 , 0.254 0.208 , 0.245	Depositor DCC
R_{free} test set	2248 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5842	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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, 0.333 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	0.47	0/2434	0.76	8/3286 (0.2%)
1	B	0.47	0/2434	0.77	9/3286 (0.3%)
2	I	0.51	0/499	0.71	1/658 (0.2%)
2	J	0.51	0/491	0.75	2/647 (0.3%)
All	All	0.48	0/5858	0.76	20/7877 (0.3%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	ASP	CB-CG-OD2	7.43	124.99	118.30
1	B	208	ASP	CB-CG-OD2	6.32	123.99	118.30
1	B	138	ASP	CB-CG-OD2	6.28	123.96	118.30
1	B	240	ASP	CB-CG-OD2	6.16	123.84	118.30
1	A	138	ASP	CB-CG-OD2	6.03	123.72	118.30
2	J	165	ASP	CB-CG-OD2	6.00	123.70	118.30
1	A	92	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	208	ASP	CB-CG-OD2	5.95	123.66	118.30
1	B	179	ASP	CB-CG-OD2	5.93	123.64	118.30
1	A	240	ASP	CB-CG-OD2	5.89	123.60	118.30
1	B	203	ASP	CB-CG-OD2	5.86	123.58	118.30
1	B	253	ASP	CB-CG-OD2	5.77	123.50	118.30
1	B	286	ASP	CB-CG-OD2	5.75	123.47	118.30
1	B	10	ASP	CB-CG-OD2	5.41	123.17	118.30
1	B	166	ASP	CB-CG-OD2	5.29	123.06	118.30
2	I	165	ASP	CB-CG-OD2	5.28	123.06	118.30
1	A	197	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	203	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	212	ASP	CB-CG-OD2	5.22	123.00	118.30
2	J	168	ASP	CB-CG-OD2	5.14	122.92	118.30

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	2380	0	2351	17	0
1	B	2380	0	2351	16	0
2	I	495	0	507	8	0
2	J	487	0	503	7	0
3	A	47	0	0	1	0
3	B	38	0	0	0	0
3	I	5	0	0	0	0
3	J	10	0	0	2	0
All	All	5842	0	5712	45	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 4.

All (45) 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)
2:J:131:SER:HB3	2:J:134:GLU:HB2	1.73	0.69
1:B:286:ASP:OD1	1:B:290:MET:HB3	1.97	0.65
1:A:284:SER:HB2	1:A:294:GLN:HE22	1.61	0.64
2:I:131:SER:HB2	2:I:134:GLU:HB2	1.78	0.64
2:I:52:ASN:O	2:I:56:THR:HG23	1.99	0.61
2:I:131:SER:HB3	2:I:134:GLU:H	1.65	0.61
2:I:131:SER:O	2:I:135:ARG:HB2	2.05	0.56
1:B:236:LEU:HD21	1:B:244:ILE:HG13	1.88	0.55
1:A:131:ASN:HB3	1:A:149:TRP:HE1	1.73	0.54
1:B:15:ARG:NH2	1:B:34:GLU:OE2	2.42	0.53
2:I:136:GLU:OE1	2:I:139:ARG:NH1	2.37	0.53
2:I:131:SER:CB	2:I:134:GLU:HB2	2.39	0.52
2:J:47:LYS:HD3	3:J:216:HOH:O	2.09	0.52
1:B:15:ARG:HH22	1:B:34:GLU:CD	2.13	0.51
2:J:131:SER:HB3	2:J:134:GLU:H	1.75	0.51
1:B:131:ASN:HB3	1:B:149:TRP:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:131:SER:CB	2:J:134:GLU:HB2	2.41	0.49
1:A:132:ARG:NH2	1:A:137:TYR:CE2	2.82	0.48
1:A:286:ASP:OD1	1:A:290:MET:HB3	2.13	0.48
1:B:113:LYS:HG2	1:B:114:TYR:CE1	2.49	0.47
1:B:94:VAL:O	1:B:95:ASP:HB2	2.14	0.47
1:B:57:ALA:HB1	1:B:58:PRO:HA	1.97	0.46
1:A:65:ILE:HD13	1:A:72:LEU:HD13	1.99	0.45
1:A:94:VAL:O	1:A:95:ASP:HB2	2.15	0.45
1:A:54:GLU:HG3	2:I:17:ASN:ND2	2.31	0.45
1:A:36:ARG:O	1:A:40:LEU:HG	2.17	0.45
1:A:239:HIS:HE1	3:A:326:HOH:O	2.00	0.45
1:B:188:ARG:HD3	1:B:188:ARG:HA	1.74	0.45
1:A:177:SER:HB2	1:A:203:ASP:HB2	2.00	0.44
1:B:255:TYR:HA	1:B:265:THR:O	2.16	0.44
1:A:284:SER:HB2	1:A:294:GLN:NE2	2.29	0.44
1:B:54:GLU:HG3	2:J:17:ASN:ND2	2.34	0.43
1:B:216:TRP:CZ3	1:B:227:PHE:HB3	2.54	0.43
1:A:255:TYR:HA	1:A:265:THR:O	2.19	0.43
1:A:246:ARG:HD2	1:A:263:LEU:HD21	2.00	0.43
1:A:132:ARG:NH1	2:I:161:LEU:HD13	2.35	0.42
1:A:78:TYR:CE2	1:A:294:GLN:HG2	2.54	0.42
1:A:236:LEU:CD1	1:A:262:GLN:HB3	2.50	0.42
1:B:165:VAL:HB	1:B:169:ILE:HB	2.03	0.41
2:J:144:LYS:HD2	3:J:208:HOH:O	2.19	0.41
1:A:51:ILE:HD11	1:A:161:ILE:CD1	2.51	0.41
2:J:131:SER:O	2:J:135:ARG:HB2	2.21	0.41
1:B:284:SER:O	1:B:291:CYS:HA	2.20	0.41
1:B:52:LEU:HD11	1:B:164:ILE:HG13	2.03	0.41
1:B:7:LEU:HD13	1:B:37:GLY:HA3	2.03	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	293/329 (89%)	277 (94%)	16 (6%)	0	100	100
1	B	293/329 (89%)	276 (94%)	17 (6%)	0	100	100
2	I	53/206 (26%)	51 (96%)	2 (4%)	0	100	100
2	J	52/206 (25%)	52 (100%)	0	0	100	100
All	All	691/1070 (65%)	656 (95%)	35 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	261/291 (90%)	238 (91%)	23 (9%)	10	18
1	B	261/291 (90%)	242 (93%)	19 (7%)	14	27
2	I	54/181 (30%)	42 (78%)	12 (22%)	1	1
2	J	53/181 (29%)	43 (81%)	10 (19%)	1	2
All	All	629/944 (67%)	565 (90%)	64 (10%)	7	13

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	7	LEU
1	A	17	LEU
1	A	26	LYS
1	A	77	GLU
1	A	78	TYR
1	A	96	ARG
1	A	116	GLU
1	A	132	ARG
1	A	141	LYS
1	A	147	LYS
1	A	154	ASP
1	A	161	ILE

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Mol	Chain	Res	Type
1	A	167	GLU
1	A	198	GLN
1	A	211	LYS
1	A	234	LYS
1	A	238	LYS
1	A	246	ARG
1	A	282	MET
1	A	284	SER
1	A	297	LYS
1	A	300	GLU
2	I	12	LYS
2	I	45	SER
2	I	47	LYS
2	I	131	SER
2	I	137	LYS
2	I	138	LYS
2	I	142	GLU
2	I	143	MET
2	I	163	SER
2	I	166	LEU
2	I	167	HIS
2	I	168	ASP
1	B	6	LYS
1	B	7	LEU
1	B	41	LYS
1	B	77	GLU
1	B	78	TYR
1	B	96	ARG
1	B	116	GLU
1	B	132	ARG
1	B	142	ARG
1	B	154	ASP
1	B	161	ILE
1	B	188	ARG
1	B	211	LYS
1	B	218	GLU
1	B	246	ARG
1	B	261	ARG
1	B	284	SER
1	B	297	LYS
1	B	300	GLU
2	J	12	LYS

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Mol	Chain	Res	Type
2	J	16	LYS
2	J	137	LYS
2	J	142	GLU
2	J	144	LYS
2	J	156	LYS
2	J	163	SER
2	J	164	LYS
2	J	166	LEU
2	J	167	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	HIS
1	B	99	GLN
1	B	239	HIS
2	J	140	GLN

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 carbohydrates 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 ⓘ

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	295/329 (89%)	-0.24	1 (0%) 94 93	30, 42, 59, 73	0
1	B	295/329 (89%)	-0.38	3 (1%) 82 80	30, 42, 59, 73	0
2	I	59/206 (28%)	1.45	22 (37%) 0 0	36, 62, 82, 85	0
2	J	58/206 (28%)	1.01	15 (25%) 0 0	35, 63, 82, 85	0
All	All	707/1070 (66%)	-0.05	41 (5%) 23 18	30, 44, 71, 85	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	167	HIS	5.8
2	J	168	ASP	5.6
2	I	51	MET	5.5
2	I	167	HIS	5.5
2	I	54	LEU	5.4
2	I	168	ASP	5.0
2	I	56	THR	4.7
2	I	55	ALA	4.7
2	J	132	PRO	4.7
2	J	134	GLU	4.6
2	I	166	LEU	4.4
2	I	132	PRO	4.2
2	I	165	ASP	4.0
2	J	135	ARG	3.8
2	I	169	ASP	3.6
2	J	133	GLU	3.5
2	I	135	ARG	3.5
2	J	166	LEU	3.3
1	B	6	LYS	3.1
2	I	134	GLU	3.0
1	B	23	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
2	J	12	LYS	3.0
2	I	52	ASN	3.0
2	I	136	GLU	3.0
2	I	45	SER	3.0
2	I	53	ILE	2.9
2	I	133	GLU	2.9
2	J	130	LEU	2.9
1	A	300	GLU	2.9
2	I	164	LYS	2.9
2	J	54	LEU	2.6
2	I	44	LYS	2.5
2	I	131	SER	2.4
2	J	136	GLU	2.4
1	B	300	GLU	2.3
2	J	164	LYS	2.3
2	J	139	ARG	2.3
2	J	131	SER	2.2
2	I	50	GLU	2.1
2	J	51	MET	2.1
2	I	49	ASP	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.