



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 07:33 PM UTC

PDB ID : 1VDM / pdb_00001vdm
Title : Crystal structure of purine phosphoribosyltransferase from *Pyrococcus horikoshii* Ot3
Authors : Sugahara, M.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2004-03-23
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

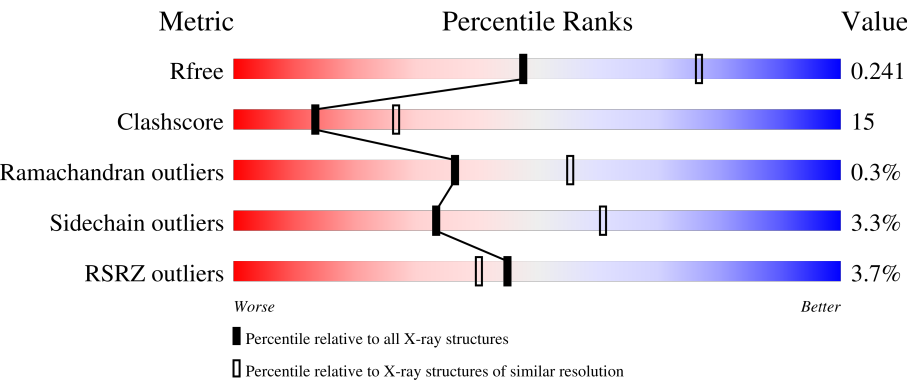
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	153	4% 61% 35% ...
1	B	153	3% 63% 32% ..
1	C	153	4% 66% 27% 7%
1	D	153	6% 65% 30% ..
1	E	153	4% 65% 29% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	153	%81%16%..
1	G	153	7%63%31%5%.
1	H	153	4%62%31%. .
1	I	153	2%69%24%. 5%
1	J	153	2%74%20%. .
1	K	153	5%59%33%. 5%
1	L	153	3%66%29%..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15181 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 purine phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	0	0
			1227	810	199	215	3			
1	B	149	Total	C	N	O	S	0	0	0
			1207	799	194	211	3			
1	C	143	Total	C	N	O	S	0	0	0
			1159	770	187	199	3			
1	D	147	Total	C	N	O	S	0	0	0
			1193	792	192	206	3			
1	E	149	Total	C	N	O	S	0	0	0
			1211	803	194	211	3			
1	F	150	Total	C	N	O	S	0	0	0
			1213	804	195	211	3			
1	G	152	Total	C	N	O	S	0	0	0
			1233	815	200	215	3			
1	H	149	Total	C	N	O	S	0	0	0
			1214	803	197	211	3			
1	I	146	Total	C	N	O	S	0	0	0
			1184	786	190	205	3			
1	J	147	Total	C	N	O	S	0	0	0
			1195	792	194	206	3			
1	K	146	Total	C	N	O	S	0	0	0
			1189	790	191	205	3			
1	L	149	Total	C	N	O	S	0	0	0
			1207	799	194	211	3			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	46	Total	O	0	0
			46	46		
2	B	69	Total	O	0	0
			69	69		

Continued on next page...

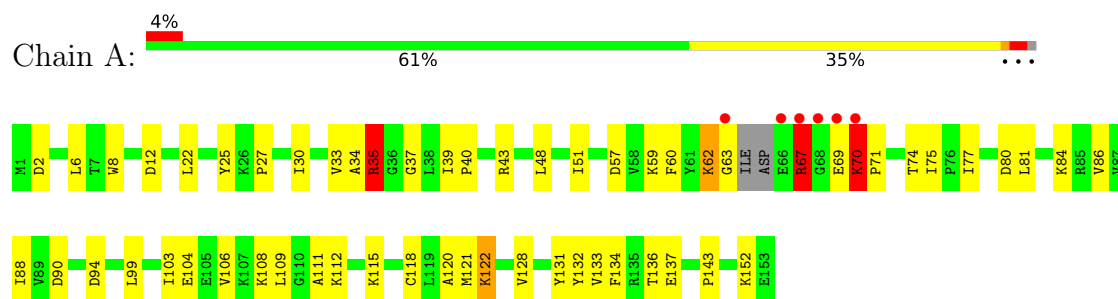
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	52	Total 52	O 52	0	0
2	D	57	Total 57	O 57	0	0
2	E	92	Total 92	O 92	0	0
2	F	98	Total 98	O 98	0	0
2	G	52	Total 52	O 52	0	0
2	H	51	Total 51	O 51	0	0
2	I	52	Total 52	O 52	0	0
2	J	59	Total 59	O 59	0	0
2	K	52	Total 52	O 52	0	0
2	L	69	Total 69	O 69	0	0

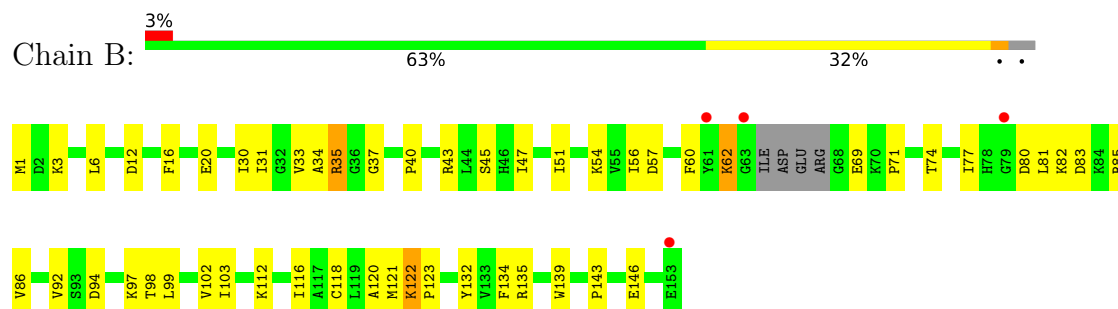
3 Residue-property plots [i](#)

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.

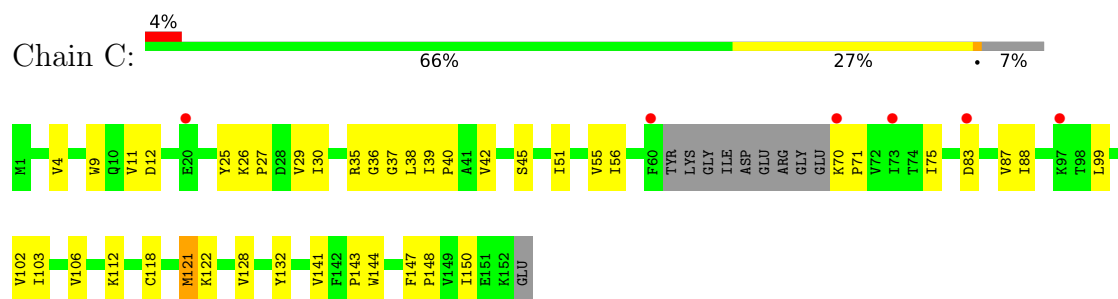
- Molecule 1: purine phosphoribosyltransferase



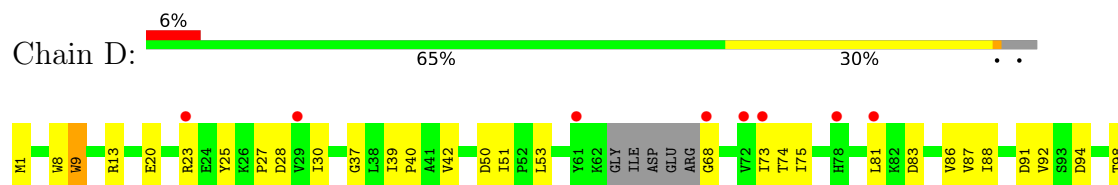
- Molecule 1: purine phosphoribosyltransferase

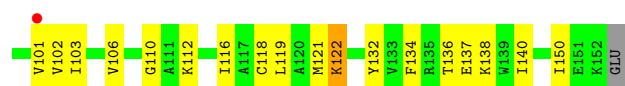


- Molecule 1: purine phosphoribosyltransferase

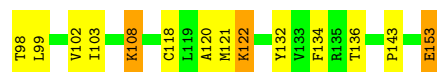


- Molecule 1: purine phosphoribosyltransferase

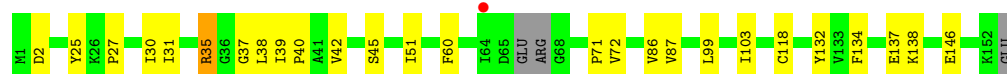
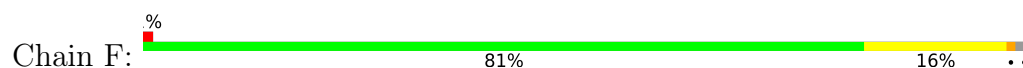




- Molecule 1: purine phosphoribosyltransferase



- Molecule 1: purine phosphoribosyltransferase



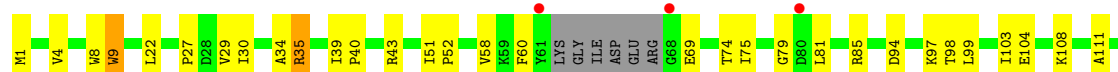
- Molecule 1: purine phosphoribosyltransferase



- Molecule 1: purine phosphoribosyltransferase

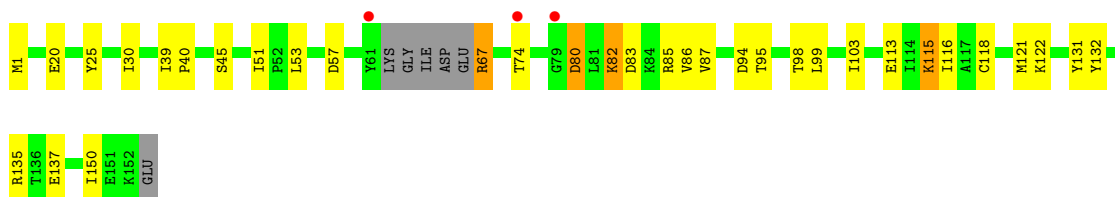
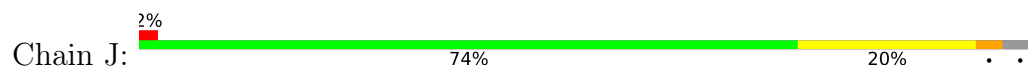


- Molecule 1: purine phosphoribosyltransferase

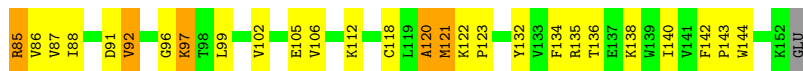
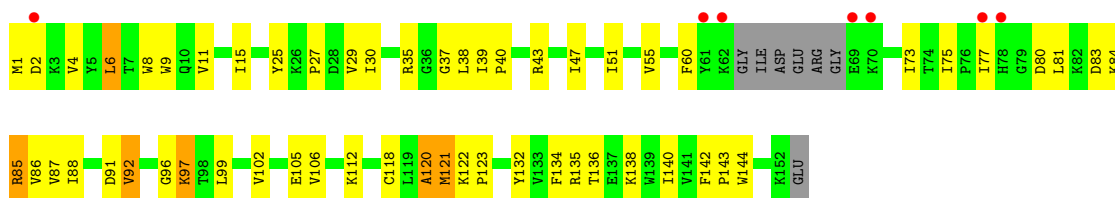




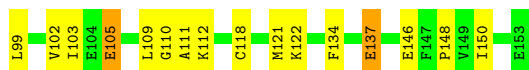
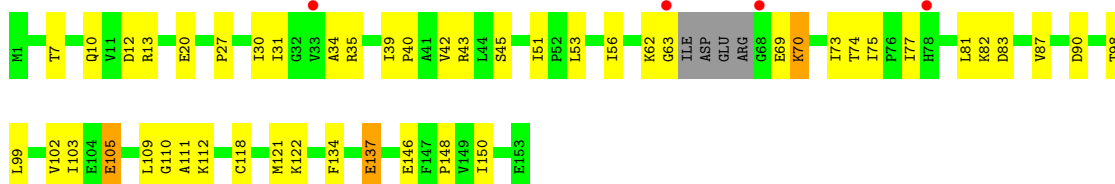
- Molecule 1: purine phosphoribosyltransferase



- Molecule 1: purine phosphoribosyltransferase



- Molecule 1: purine phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.60Å 157.35Å 170.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.55 – 2.50 39.55 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.55-2.50) 100.0 (39.55-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.48Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.241 0.209 , 0.241	Depositor DCC
R_{free} test set	4967 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15181	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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](#)

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	0.52	0/1256	1.07	7/1701 (0.4%)
1	B	0.53	0/1236	0.95	3/1675 (0.2%)
1	C	0.46	0/1187	1.02	6/1612 (0.4%)
1	D	0.63	2/1222 (0.2%)	0.94	5/1658 (0.3%)
1	E	0.51	0/1240	1.01	2/1681 (0.1%)
1	F	0.49	0/1242	0.94	1/1685 (0.1%)
1	G	0.49	0/1263	1.03	8/1714 (0.5%)
1	H	0.49	0/1243	0.99	5/1684 (0.3%)
1	I	0.47	0/1213	0.99	3/1647 (0.2%)
1	J	0.53	0/1224	0.96	1/1661 (0.1%)
1	K	0.56	0/1218	1.02	4/1653 (0.2%)
1	L	0.46	0/1236	0.92	7/1675 (0.4%)
All	All	0.51	2/14780 (0.0%)	0.99	52/20046 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	9	TRP	NE1-CE2	10.44	1.49	1.37
1	D	8	TRP	NE1-CE2	10.41	1.49	1.37

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	122	LYS	CA-C-N	7.25	126.78	119.24
1	C	122	LYS	C-N-CA	7.25	126.78	119.24
1	D	137	GLU	N-CA-C	-6.24	105.61	113.72
1	E	122	LYS	CA-C-N	6.22	127.61	119.84
1	E	122	LYS	C-N-CA	6.22	127.61	119.84

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	1227	0	1284	48	0
1	B	1207	0	1265	37	0
1	C	1159	0	1225	37	0
1	D	1193	0	1256	42	0
1	E	1211	0	1273	42	0
1	F	1213	0	1274	20	0
1	G	1233	0	1294	51	0
1	H	1214	0	1275	45	0
1	I	1184	0	1243	34	0
1	J	1195	0	1256	25	0
1	K	1189	0	1253	50	0
1	L	1207	0	1265	39	0
2	A	46	0	0	0	0
2	B	69	0	0	1	0
2	C	52	0	0	0	0
2	D	57	0	0	1	0
2	E	92	0	0	2	0
2	F	98	0	0	0	0
2	G	52	0	0	1	0
2	H	51	0	0	0	0
2	I	52	0	0	1	0
2	J	59	0	0	1	0
2	K	52	0	0	1	0
2	L	69	0	0	0	0
All	All	15181	0	15163	435	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 15.

The worst 5 of 435 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:70:LYS:HB3	1:A:71:PRO:HD2	1.28	1.07
1:C:70:LYS:HB2	1:C:71:PRO:HD3	1.43	1.00
1:J:30:ILE:HG13	1:J:51:ILE:HD11	1.45	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:66:GLU:HG2	1:G:67:ARG:N	1.82	0.94
1:C:39:ILE:HB	1:C:40:PRO:HD3	1.49	0.92

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	147/153 (96%)	135 (92%)	10 (7%)	2 (1%)	9	17
1	B	145/153 (95%)	139 (96%)	6 (4%)	0	100	100
1	C	139/153 (91%)	129 (93%)	10 (7%)	0	100	100
1	D	143/153 (94%)	133 (93%)	8 (6%)	2 (1%)	9	17
1	E	145/153 (95%)	138 (95%)	7 (5%)	0	100	100
1	F	146/153 (95%)	143 (98%)	3 (2%)	0	100	100
1	G	150/153 (98%)	144 (96%)	5 (3%)	1 (1%)	18	34
1	H	145/153 (95%)	139 (96%)	6 (4%)	0	100	100
1	I	142/153 (93%)	135 (95%)	7 (5%)	0	100	100
1	J	143/153 (94%)	138 (96%)	5 (4%)	0	100	100
1	K	142/153 (93%)	135 (95%)	7 (5%)	0	100	100
1	L	145/153 (95%)	140 (97%)	5 (3%)	0	100	100
All	All	1732/1836 (94%)	1648 (95%)	79 (5%)	5 (0%)	36	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	LYS
1	G	112	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	70	LYS
1	D	110	GLY
1	D	73	ILE

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	134/136 (98%)	128 (96%)	6 (4%)	24	49
1	B	132/136 (97%)	129 (98%)	3 (2%)	44	72
1	C	128/136 (94%)	126 (98%)	2 (2%)	55	79
1	D	131/136 (96%)	129 (98%)	2 (2%)	57	80
1	E	133/136 (98%)	127 (96%)	6 (4%)	24	49
1	F	133/136 (98%)	131 (98%)	2 (2%)	57	80
1	G	135/136 (99%)	130 (96%)	5 (4%)	30	57
1	H	133/136 (98%)	127 (96%)	6 (4%)	24	49
1	I	130/136 (96%)	125 (96%)	5 (4%)	29	56
1	J	131/136 (96%)	124 (95%)	7 (5%)	20	42
1	K	131/136 (96%)	126 (96%)	5 (4%)	29	56
1	L	132/136 (97%)	129 (98%)	3 (2%)	44	72
All	All	1583/1632 (97%)	1531 (97%)	52 (3%)	33	61

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	70	LYS
1	I	115	LYS
1	L	20	GLU
1	H	80	ASP
1	I	9	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	46	HIS
1	F	78	HIS

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 oligosaccharides 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 [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	151/153 (98%)	0.34	6 (3%) 42 38	24, 46, 75, 104	0
1	B	149/153 (97%)	0.12	4 (2%) 56 51	23, 41, 69, 91	0
1	C	143/153 (93%)	0.44	6 (4%) 40 36	24, 51, 81, 85	0
1	D	147/153 (96%)	0.42	9 (6%) 27 23	25, 48, 87, 97	0
1	E	149/153 (97%)	0.09	6 (4%) 42 38	23, 40, 68, 88	0
1	F	150/153 (98%)	-0.07	1 (0%) 84 81	22, 38, 59, 82	0
1	G	152/153 (99%)	0.38	10 (6%) 24 21	22, 48, 78, 89	0
1	H	149/153 (97%)	0.25	6 (4%) 42 38	23, 44, 80, 86	0
1	I	146/153 (95%)	0.11	3 (2%) 63 59	20, 42, 64, 79	0
1	J	147/153 (96%)	0.01	3 (2%) 65 61	22, 37, 62, 75	0
1	K	146/153 (95%)	0.19	7 (4%) 35 31	23, 40, 73, 84	0
1	L	149/153 (97%)	0.25	4 (2%) 56 51	23, 46, 79, 89	0
All	All	1778/1836 (96%)	0.21	65 (3%) 45 40	20, 44, 78, 104	0

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	66	GLU	7.3
1	E	64	ILE	5.9
1	B	63	GLY	5.7
1	A	63	GLY	4.8
1	B	61	TYR	4.0

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 oligosaccharides 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.