wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 02:16 pm GMT

PDB ID	:	8BWF
Title	:	PTBP1 RRM1 bound to an allosteric inhibitor
Authors	:	Schmeing, S.; Vetter, I.; t Hart, P.; Gasper, R.
Deposited on	:	2022-12-06
Resolution	:	2.90 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 (i) 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 (1)) were used in the production of this report:

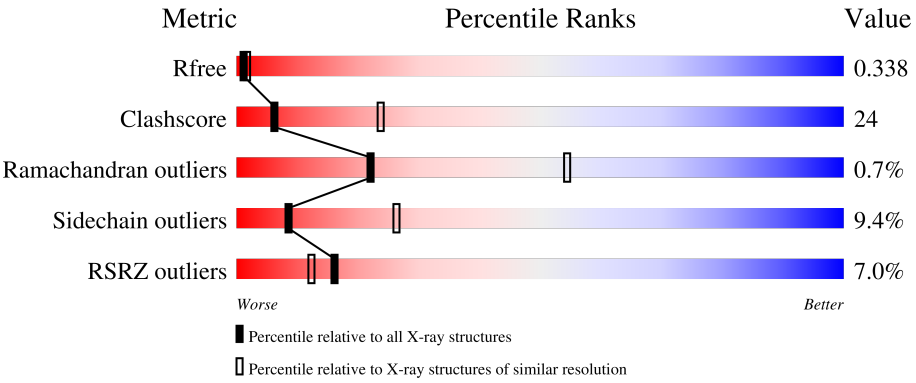
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (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 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	86	55% 34% • 9%
1	B	86	3% 55% 31% • 10%
1	C	86	% 50% 41% • 8%
1	D	86	6% 45% 41% • 10%
1	E	86	7% 41% 45% • 13%

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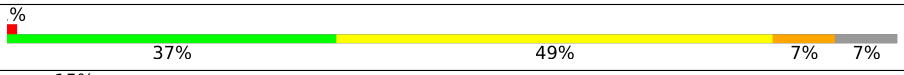
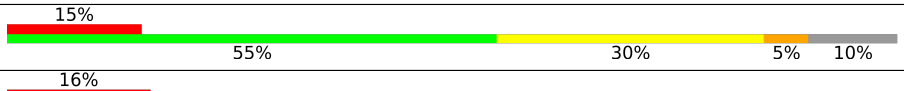
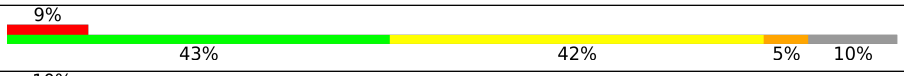
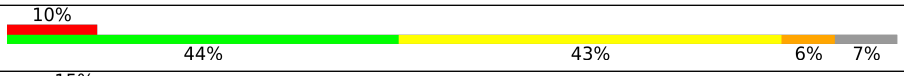
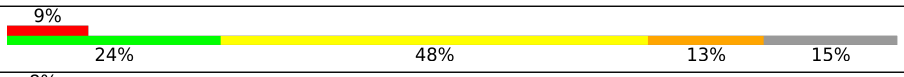
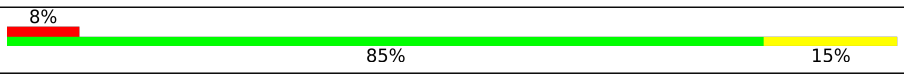
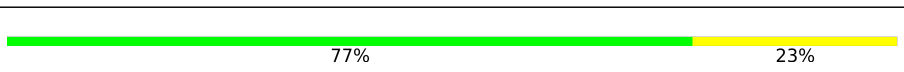
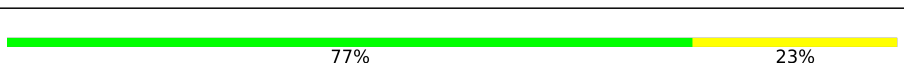
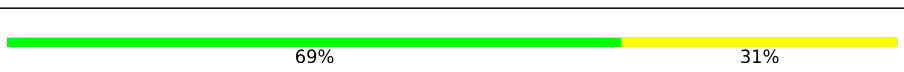
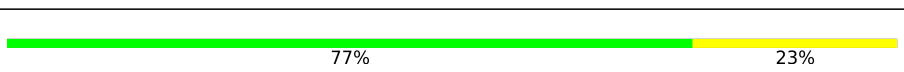
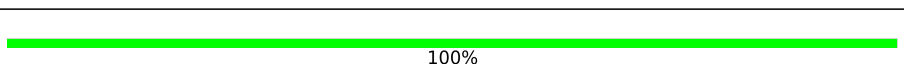
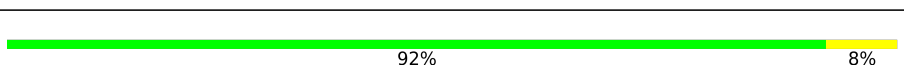
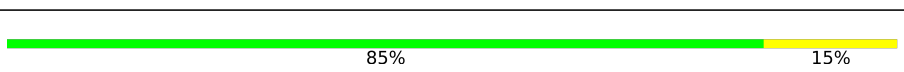
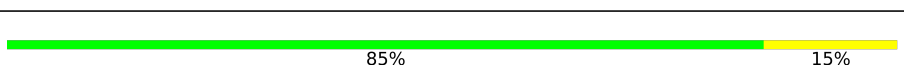
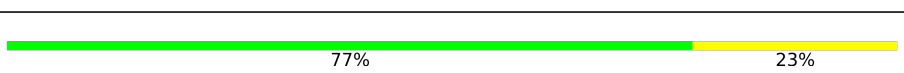
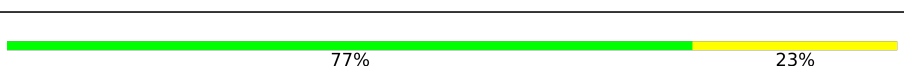
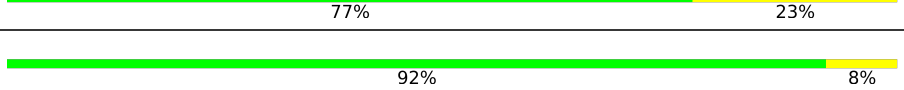
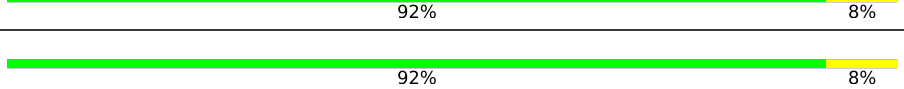
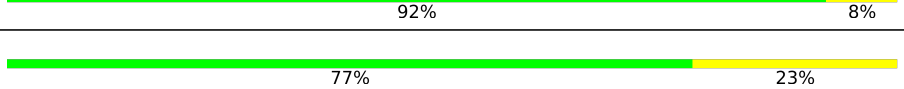
Mol	Chain	Length	Quality of chain
1	F	86	
1	G	86	
1	H	86	
1	I	86	
1	J	86	
1	K	86	
1	L	86	
1	M	86	
1	N	86	
1	O	86	
1	P	86	
2	a	13	
2	b	13	
2	c	13	
2	d	13	
2	e	13	
2	f	13	
2	g	13	
2	h	13	
2	i	13	
2	j	13	
2	k	13	
2	l	13	
2	m	13	
2	n	13	

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Mol	Chain	Length	Quality of chain
2	o	13	92% 8%
2	p	13	92% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	202	-	-	-	X
3	SO4	K	201	-	-	X	-
3	SO4	g	202	-	-	-	X
4	NH2	f	201	-	-	-	X
5	GOL	C	202	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11682 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 Polypyrimidine tract-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	78	Total	C	N	O	S	0	0	0
			614	395	104	112	3			
1	B	77	Total	C	N	O	S	0	0	0
			604	389	101	111	3			
1	C	79	Total	C	N	O	S	0	0	0
			618	397	105	113	3			
1	D	77	Total	C	N	O	S	0	0	0
			609	391	104	111	3			
1	E	75	Total	C	N	O	S	0	0	0
			590	379	99	109	3			
1	F	79	Total	C	N	O	S	0	0	0
			618	397	105	113	3			
1	G	80	Total	C	N	O	S	0	0	0
			632	406	107	116	3			
1	H	77	Total	C	N	O	S	0	0	0
			607	390	103	111	3			
1	I	77	Total	C	N	O	S	0	1	0
			608	391	102	112	3			
1	J	78	Total	C	N	O	S	0	0	0
			611	392	104	112	3			
1	K	83	Total	C	N	O	S	0	0	0
			656	422	111	120	3			
1	L	77	Total	C	N	O	S	0	0	0
			609	391	104	111	3			
1	M	77	Total	C	N	O	S	0	0	0
			604	387	103	111	3			
1	N	80	Total	C	N	O	S	0	0	0
			636	409	108	116	3			
1	O	78	Total	C	N	O	S	0	0	0
			616	396	105	112	3			
1	P	73	Total	C	N	O	S	0	0	0
			576	372	96	105	3			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	GLY	-	expression tag	UNP P26599
A	56	PRO	-	expression tag	UNP P26599
B	55	GLY	-	expression tag	UNP P26599
B	56	PRO	-	expression tag	UNP P26599
C	55	GLY	-	expression tag	UNP P26599
C	56	PRO	-	expression tag	UNP P26599
D	55	GLY	-	expression tag	UNP P26599
D	56	PRO	-	expression tag	UNP P26599
E	55	GLY	-	expression tag	UNP P26599
E	56	PRO	-	expression tag	UNP P26599
F	55	GLY	-	expression tag	UNP P26599
F	56	PRO	-	expression tag	UNP P26599
G	55	GLY	-	expression tag	UNP P26599
G	56	PRO	-	expression tag	UNP P26599
H	55	GLY	-	expression tag	UNP P26599
H	56	PRO	-	expression tag	UNP P26599
I	55	GLY	-	expression tag	UNP P26599
I	56	PRO	-	expression tag	UNP P26599
J	55	GLY	-	expression tag	UNP P26599
J	56	PRO	-	expression tag	UNP P26599
K	55	GLY	-	expression tag	UNP P26599
K	56	PRO	-	expression tag	UNP P26599
L	55	GLY	-	expression tag	UNP P26599
L	56	PRO	-	expression tag	UNP P26599
M	55	GLY	-	expression tag	UNP P26599
M	56	PRO	-	expression tag	UNP P26599
N	55	GLY	-	expression tag	UNP P26599
N	56	PRO	-	expression tag	UNP P26599
O	55	GLY	-	expression tag	UNP P26599
O	56	PRO	-	expression tag	UNP P26599
P	55	GLY	-	expression tag	UNP P26599
P	56	PRO	-	expression tag	UNP P26599

- Molecule 2 is a protein called Ligand.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	a	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	b	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	c	13	Total	C	N	O	0	0	0
			109	70	21	18			

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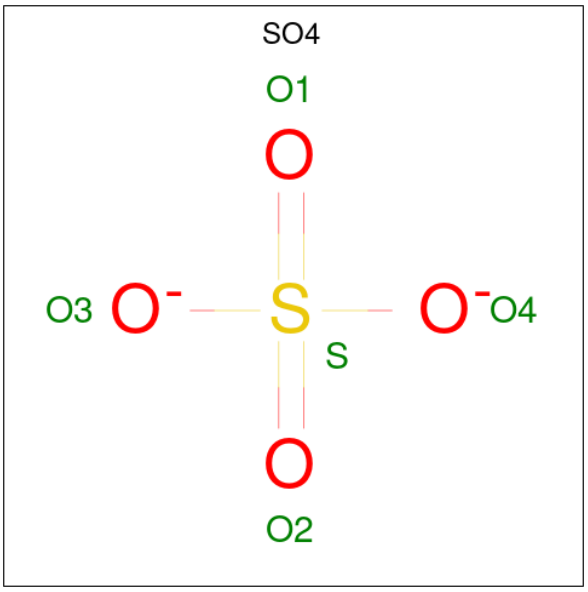
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	d	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	e	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	f	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	g	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	h	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	i	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	j	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	k	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	l	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	m	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	n	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	o	13	Total	C	N	O	0	0	0
			109	70	21	18			
2	p	13	Total	C	N	O	0	0	0
			109	70	21	18			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	G	1	Total O S 5 4 1	0	0
3	g	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0

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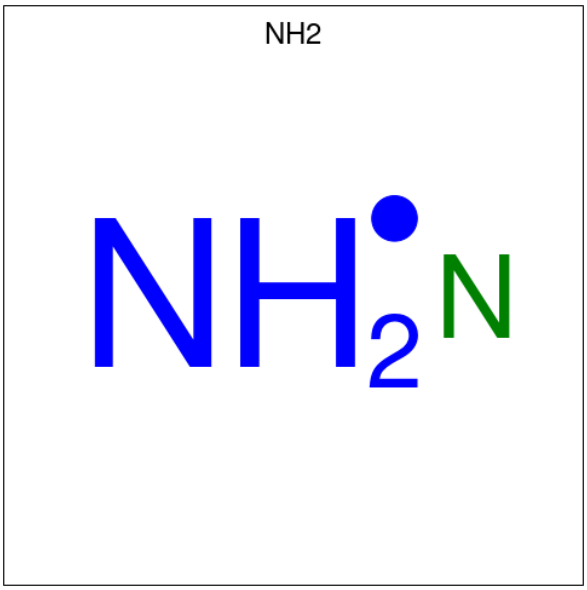
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	O	1	Total O S 5 4 1	0	0

- Molecule 4 is AMINO GROUP (three-letter code: NH2) (formula: H_2N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	a	1	Total N 1 1	0	0
4	b	1	Total N 1 1	0	0
4	c	1	Total N 1 1	0	0
4	d	1	Total N 1 1	0	0
4	e	1	Total N 1 1	0	0
4	f	1	Total N 1 1	0	0
4	g	1	Total N 1 1	0	0

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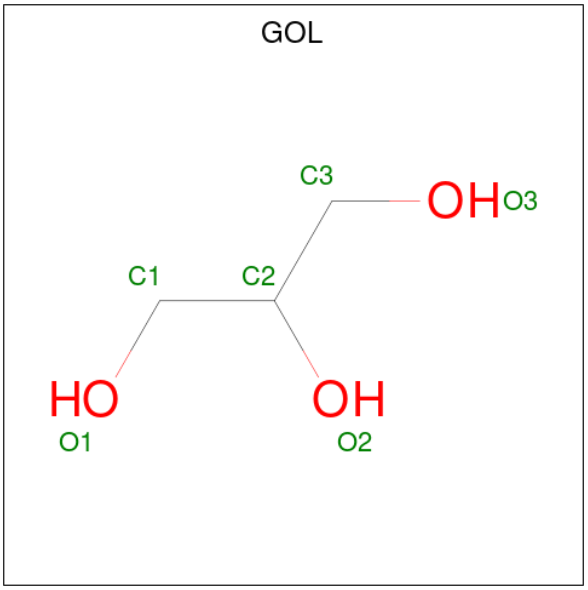
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	h	1	Total N 1 1	0	0
4	i	1	Total N 1 1	0	0
4	j	1	Total N 1 1	0	0
4	k	1	Total N 1 1	0	0
4	l	1	Total N 1 1	0	0
4	m	1	Total N 1 1	0	0
4	n	1	Total N 1 1	0	0
4	o	1	Total N 1 1	0	0
4	p	1	Total N 1 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 6 3 3	0	0
5	F	1	Total C O 6 3 3	0	0

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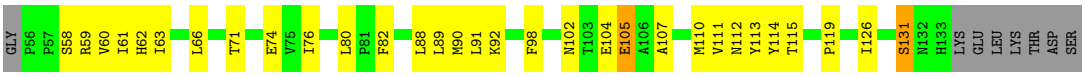
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	I	1	Total	C	O	0	0
			6	3	3		
5	i	1	Total	C	O	0	0
			6	3	3		

3 Residue-property plots

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.

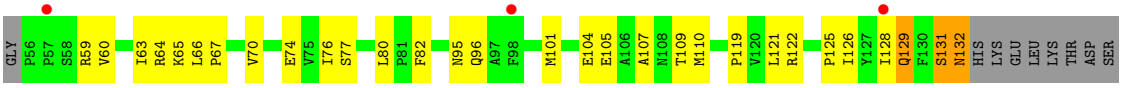
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain A:



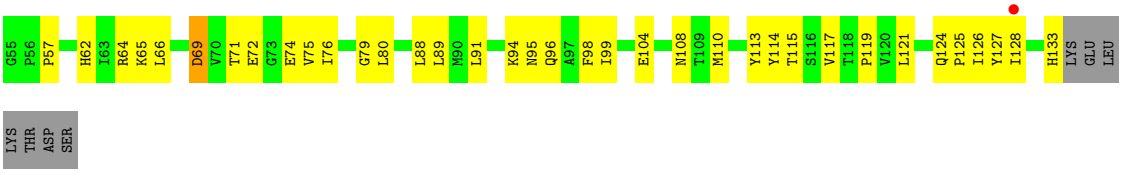
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain B:



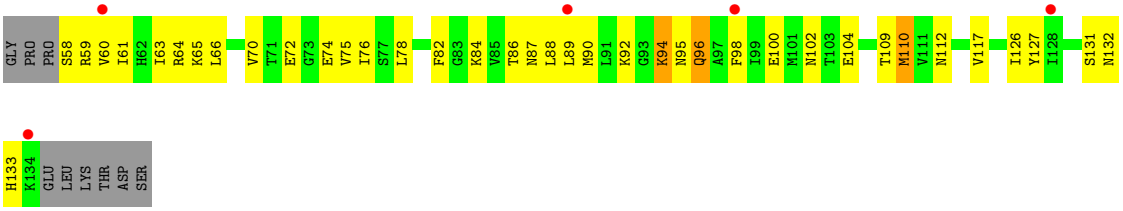
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain C:



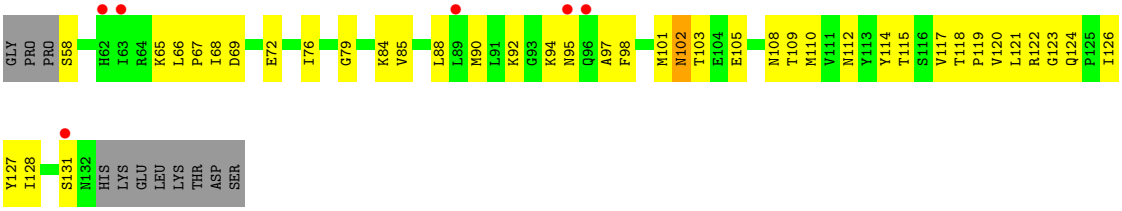
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain D:

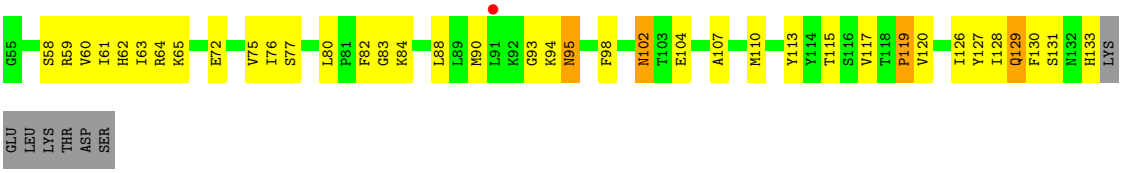


• Molecule 1: Polypyrimidine tract-binding protein 1

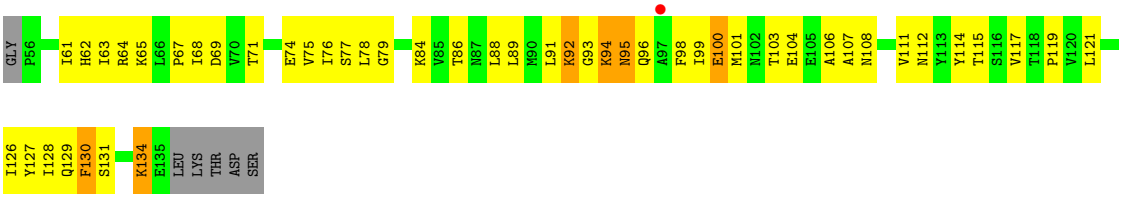
Chain E:



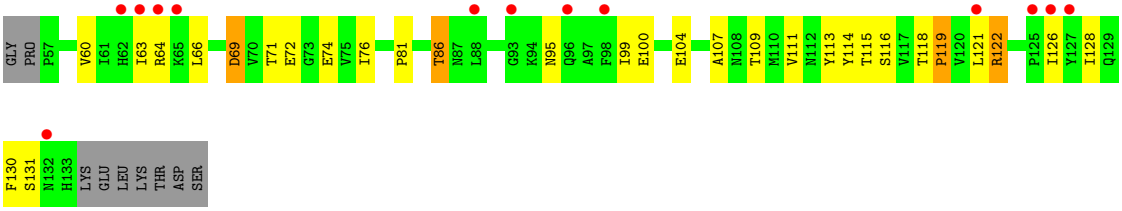
• Molecule 1: Polypyrimidine tract-binding protein 1



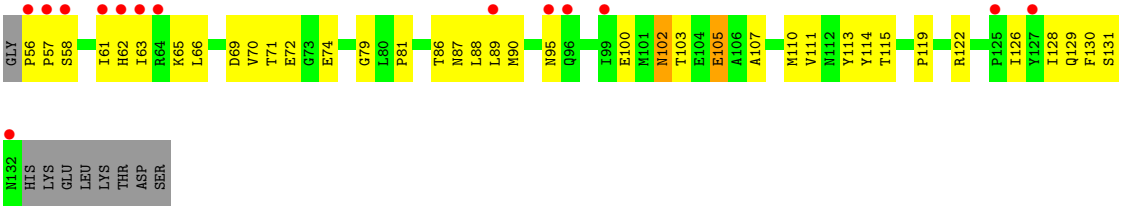
• Molecule 1: Polypyrimidine tract-binding protein 1



• Molecule 1: Polypyrimidine tract-binding protein 1

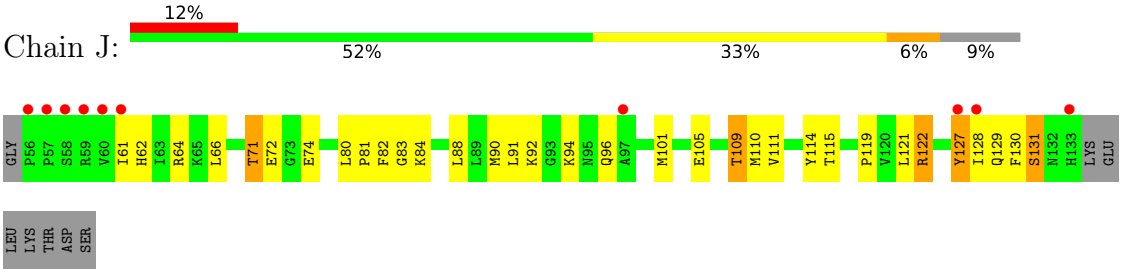


• Molecule 1: Polypyrimidine tract-binding protein 1



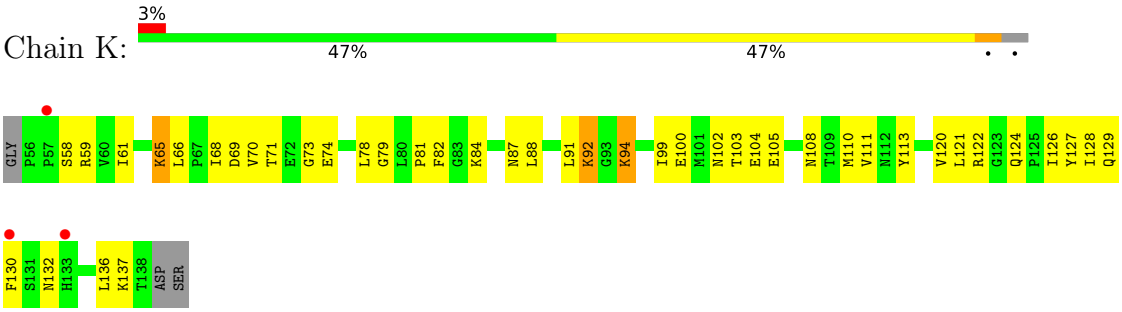
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain J:



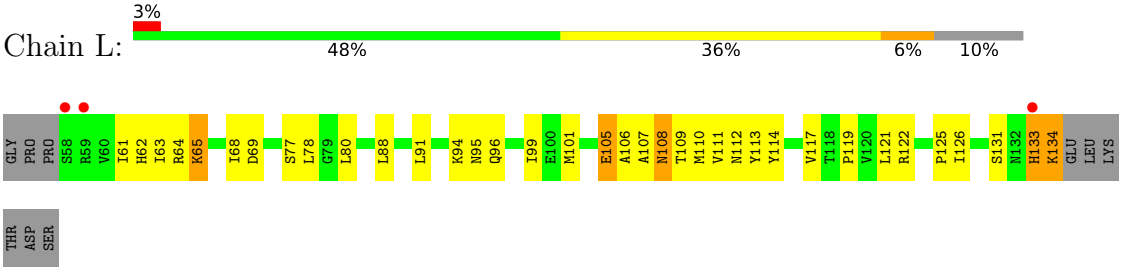
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain K:



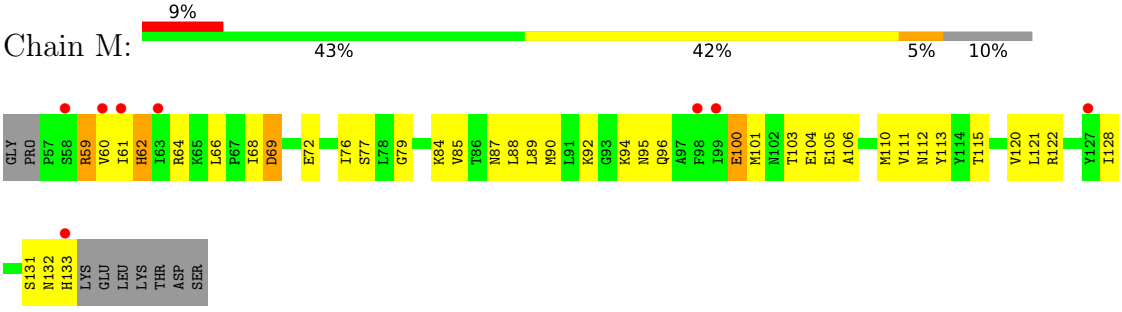
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain L:



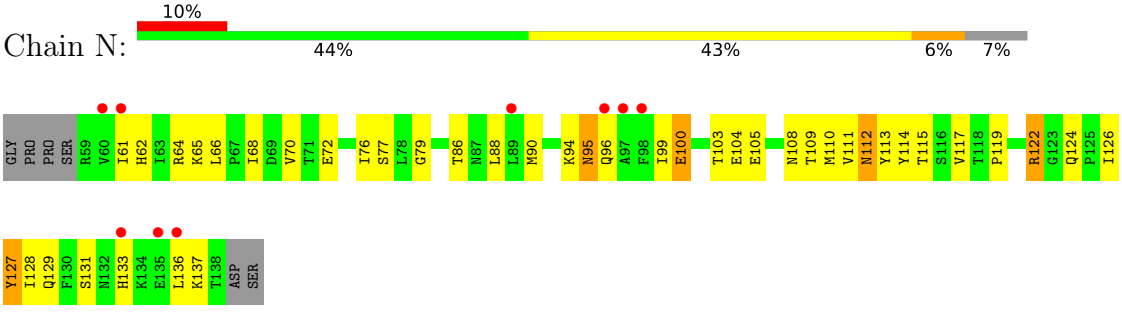
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain M:



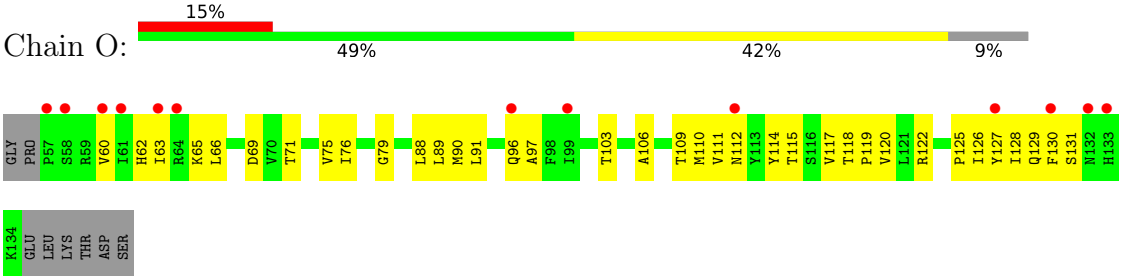
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain N:



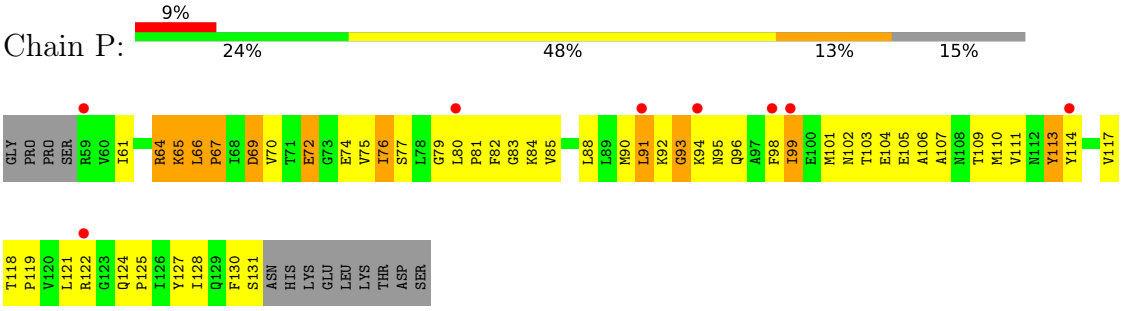
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain O:



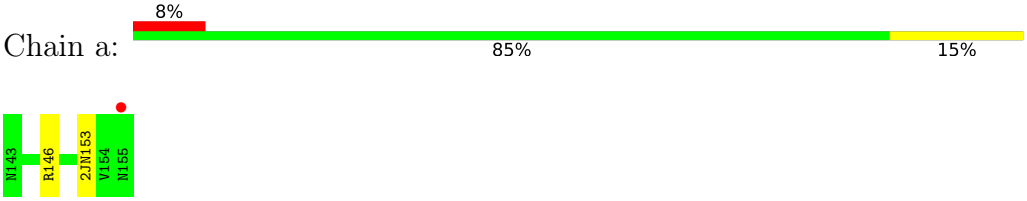
• Molecule 1: Polypyrimidine tract-binding protein 1

Chain P:



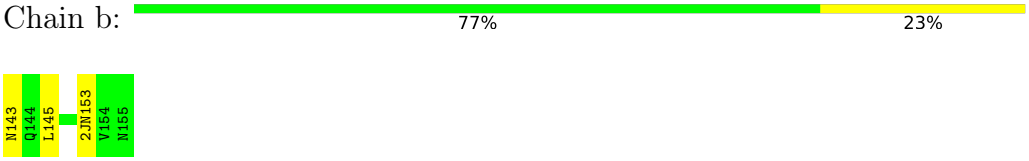
• Molecule 2: Ligand

Chain a:



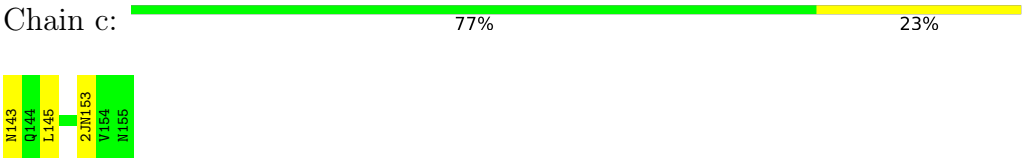
• Molecule 2: Ligand

Chain b:



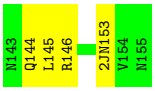
• Molecule 2: Ligand

Chain c:



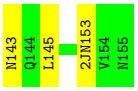
• Molecule 2: Ligand

Chain d:



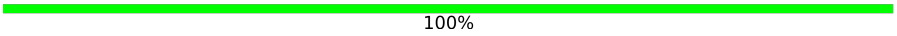
• Molecule 2: Ligand

Chain e:



• Molecule 2: Ligand

Chain f:



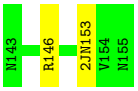
There are no outlier residues recorded for this chain.

• Molecule 2: Ligand

Chain g:

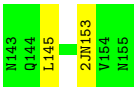
• Molecule 2: Ligand

Chain h:



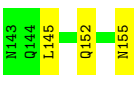
• Molecule 2: Ligand

Chain i:



• Molecule 2: Ligand

Chain j:

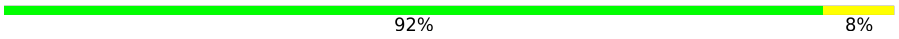


• Molecule 2: Ligand

Chain k:

• Molecule 2: Ligand

Chain l:

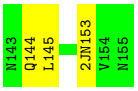


• Molecule 2: Ligand

Chain m:

• Molecule 2: Ligand

Chain n:



• Molecule 2: Ligand

Chain o:

• Molecule 2: Ligand

Chain p:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	244.20Å 76.63Å 94.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.21 – 2.90 46.21 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.21-2.90) 99.4 (46.21-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.45 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.243 , 0.340 0.245 , 0.338	Depositor DCC
R_{free} test set	1992 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	97.1	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 86.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11682	wwPDB-VP
Average B, all atoms (Å^2)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2JN, MK8, GOL, SO4, S9X, NH2

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	0.57	0/627	0.72	0/851
1	B	0.59	0/616	0.77	0/836
1	C	0.52	0/631	0.68	0/857
1	D	0.49	0/620	0.69	0/839
1	E	0.50	0/600	0.69	0/813
1	F	0.70	1/631 (0.2%)	0.90	2/857 (0.2%)
1	G	0.51	0/645	0.74	0/874
1	H	0.65	1/619 (0.2%)	0.77	1/839 (0.1%)
1	I	0.53	0/620	0.70	0/841
1	J	0.47	0/623	0.68	0/844
1	K	0.58	0/669	0.81	0/906
1	L	0.57	0/620	0.75	0/839
1	M	0.54	0/615	0.75	0/833
1	N	0.52	0/647	0.71	0/875
1	O	0.48	0/628	0.70	0/850
1	P	0.48	0/586	0.75	1/794 (0.1%)
2	a	0.66	0/75	0.80	0/95
2	b	0.68	0/75	0.72	0/95
2	c	0.56	0/75	0.88	0/95
2	d	0.53	0/75	0.68	0/95
2	e	0.52	0/75	0.88	0/95
2	f	0.72	0/75	0.76	0/95
2	g	0.71	0/75	0.70	0/95
2	h	0.56	0/75	0.89	0/95
2	i	0.50	0/75	0.63	0/95
2	j	0.58	0/75	0.71	0/95
2	k	0.55	0/75	0.64	0/95
2	l	0.61	0/75	0.87	0/95
2	m	0.70	0/75	0.67	0/95
2	n	0.65	0/75	0.86	0/95
2	o	0.70	0/75	0.82	0/95
2	p	0.53	0/75	0.83	0/95

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	0.56	2/11197 (0.0%)	0.74	4/15068 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	119	PRO	N-CD	-5.66	1.40	1.47
1	F	119	PRO	CB-CG	-5.29	1.23	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	119	PRO	N-CD-CG	-10.51	87.44	103.20
1	H	119	PRO	N-CD-CG	-7.61	91.78	103.20
1	P	66	LEU	CA-CB-CG	5.93	128.93	115.30
1	F	119	PRO	CA-N-CD	-5.20	104.22	111.50

There are no chirality outliers.

There are no planarity outliers.

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	614	0	631	24	0
1	B	604	0	624	24	0
1	C	618	0	633	25	0
1	D	609	0	629	27	0
1	E	590	0	609	38	0
1	F	618	0	633	36	0
1	G	632	0	650	42	1
1	H	607	0	624	22	0
1	I	608	0	626	31	0
1	J	611	0	624	24	0
1	K	656	0	681	41	0
1	L	609	0	629	29	0
1	M	604	0	617	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	636	0	661	35	0
1	O	616	0	637	35	0
1	P	576	0	598	47	0
2	a	109	0	93	0	0
2	b	109	0	93	0	0
2	c	109	0	93	0	0
2	d	109	0	92	0	0
2	e	109	0	94	0	0
2	f	109	0	95	0	0
2	g	109	0	94	0	0
2	h	109	0	94	0	0
2	i	109	0	93	0	0
2	j	109	0	93	0	0
2	k	109	0	93	0	0
2	l	109	0	94	0	0
2	m	109	0	93	0	0
2	n	109	0	95	0	0
2	o	109	0	94	0	0
2	p	109	0	93	0	0
3	A	25	0	0	0	1
3	C	5	0	0	1	0
3	D	10	0	0	0	0
3	F	10	0	0	0	0
3	G	10	0	0	1	0
3	H	5	0	0	0	0
3	K	10	0	0	2	0
3	L	5	0	0	0	0
3	O	5	0	0	0	0
3	g	5	0	0	0	0
4	a	1	0	0	0	0
4	b	1	0	0	0	0
4	c	1	0	0	0	0
4	d	1	0	0	0	0
4	e	1	0	0	0	0
4	f	1	0	0	0	0
4	g	1	0	0	0	0
4	h	1	0	0	0	0
4	i	1	0	0	0	0
4	j	1	0	0	0	0
4	k	1	0	0	0	0
4	l	1	0	0	0	0
4	m	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	n	1	0	0	0	0
4	o	1	0	0	0	0
4	p	1	0	0	0	0
5	C	6	0	8	0	0
5	F	6	0	8	0	0
5	I	6	0	8	0	0
5	i	6	0	8	0	0
All	All	11682	0	11634	480	1

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 24.

The worst 5 of 480 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:E:67:PRO:HD3	1:E:124:GLN:HG2	1.43	0.99
1:H:74:GLU:HG2	1:H:121:LEU:HD11	1.48	0.94
1:F:76:ILE:HD11	1:F:88:LEU:HD12	1.49	0.93
1:K:71:THR:HB	1:K:74:GLU:HG3	1.51	0.92
1:M:62:HIS:HD2	1:M:132:ASN:HB2	1.36	0.90

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:134:LYS:NZ	3:A:202:SO4:O3[3_455]	2.11	0.09

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	76/86 (88%)	67 (88%)	9 (12%)	0	100	100
1	B	75/86 (87%)	71 (95%)	4 (5%)	0	100	100
1	C	77/86 (90%)	72 (94%)	5 (6%)	0	100	100
1	D	75/86 (87%)	71 (95%)	4 (5%)	0	100	100
1	E	73/86 (85%)	69 (94%)	4 (6%)	0	100	100
1	F	77/86 (90%)	69 (90%)	6 (8%)	2 (3%)	5	20
1	G	78/86 (91%)	71 (91%)	6 (8%)	1 (1%)	12	37
1	H	75/86 (87%)	72 (96%)	3 (4%)	0	100	100
1	I	76/86 (88%)	70 (92%)	6 (8%)	0	100	100
1	J	76/86 (88%)	71 (93%)	5 (7%)	0	100	100
1	K	81/86 (94%)	77 (95%)	4 (5%)	0	100	100
1	L	75/86 (87%)	68 (91%)	5 (7%)	2 (3%)	5	19
1	M	75/86 (87%)	63 (84%)	12 (16%)	0	100	100
1	N	78/86 (91%)	71 (91%)	7 (9%)	0	100	100
1	O	76/86 (88%)	68 (90%)	7 (9%)	1 (1%)	12	37
1	P	71/86 (83%)	56 (79%)	11 (16%)	4 (6%)	2	5
2	a	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	b	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	c	8/13 (62%)	8 (100%)	0	0	100	100
2	d	8/13 (62%)	8 (100%)	0	0	100	100
2	e	8/13 (62%)	8 (100%)	0	0	100	100
2	f	8/13 (62%)	8 (100%)	0	0	100	100
2	g	8/13 (62%)	8 (100%)	0	0	100	100
2	h	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	i	8/13 (62%)	8 (100%)	0	0	100	100
2	j	8/13 (62%)	8 (100%)	0	0	100	100
2	k	8/13 (62%)	8 (100%)	0	0	100	100
2	l	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	m	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	n	8/13 (62%)	8 (100%)	0	0	100	100
2	o	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
2	p	8/13 (62%)	7 (88%)	1 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1342/1584 (85%)	1227 (91%)	105 (8%)	10 (1%)	22 54

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	94	LYS
1	L	109	THR
1	P	92	LYS
1	P	93	GLY
1	G	94	LYS

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	70/77 (91%)	66 (94%)	4 (6%)	20 51
1	B	69/77 (90%)	66 (96%)	3 (4%)	29 62
1	C	70/77 (91%)	63 (90%)	7 (10%)	7 23
1	D	69/77 (90%)	59 (86%)	10 (14%)	3 9
1	E	67/77 (87%)	60 (90%)	7 (10%)	7 21
1	F	70/77 (91%)	66 (94%)	4 (6%)	20 51
1	G	72/77 (94%)	65 (90%)	7 (10%)	8 25
1	H	69/77 (90%)	62 (90%)	7 (10%)	7 23
1	I	69/77 (90%)	64 (93%)	5 (7%)	14 39
1	J	69/77 (90%)	63 (91%)	6 (9%)	10 30
1	K	75/77 (97%)	68 (91%)	7 (9%)	9 27
1	L	69/77 (90%)	61 (88%)	8 (12%)	5 16
1	M	68/77 (88%)	60 (88%)	8 (12%)	5 16
1	N	72/77 (94%)	65 (90%)	7 (10%)	8 25
1	O	70/77 (91%)	68 (97%)	2 (3%)	42 76
1	P	65/77 (84%)	53 (82%)	12 (18%)	1 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	a	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	b	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	c	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	d	8/8 (100%)	6 (75%)	2 (25%)	0 2
2	e	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	f	8/8 (100%)	8 (100%)	0	100 100
2	g	8/8 (100%)	8 (100%)	0	100 100
2	h	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	i	8/8 (100%)	8 (100%)	0	100 100
2	j	8/8 (100%)	6 (75%)	2 (25%)	0 2
2	k	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	l	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	m	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	n	8/8 (100%)	7 (88%)	1 (12%)	4 14
2	o	8/8 (100%)	8 (100%)	0	100 100
2	p	8/8 (100%)	8 (100%)	0	100 100
All	All	1241/1360 (91%)	1124 (91%)	117 (9%)	8 26

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	87	ASN
1	P	91	LEU
1	K	92	LYS
1	P	76	ILE
1	N	114	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	m	148	GLN
2	n	148	GLN
2	o	155	ASN
1	N	112	ASN
2	j	148	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)

32 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	2JN	b	153	2	5,8,9	0.68	0	4,10,12	1.61	1 (25%)
2	MK8	l	145	2	5,8,9	0.74	0	4,10,12	1.13	0
2	MK8	p	145	2	5,8,9	0.79	0	4,10,12	1.19	0
2	2JN	n	153	2	5,8,9	0.77	0	4,10,12	1.34	1 (25%)
2	2JN	g	153	2	5,8,9	0.81	0	4,10,12	1.26	1 (25%)
2	MK8	a	145	2	5,8,9	0.59	0	4,10,12	1.01	0
2	2JN	d	153	2	5,8,9	0.65	0	4,10,12	1.34	1 (25%)
2	2JN	h	153	2	5,8,9	0.79	0	4,10,12	1.14	1 (25%)
2	2JN	e	153	2	5,8,9	0.72	0	4,10,12	1.69	1 (25%)
2	MK8	o	145	2	5,8,9	0.82	0	4,10,12	1.23	1 (25%)
2	MK8	c	145	2	5,8,9	0.88	0	4,10,12	1.23	1 (25%)
2	MK8	i	145	2	5,8,9	0.71	0	4,10,12	1.33	1 (25%)
2	2JN	p	153	2	5,8,9	1.10	1 (20%)	4,10,12	1.90	1 (25%)
2	2JN	l	153	2	5,8,9	0.66	0	4,10,12	1.01	0
2	2JN	k	153	2	5,8,9	0.97	1 (20%)	4,10,12	1.00	0
2	MK8	h	145	2	5,8,9	0.84	0	4,10,12	1.08	0
2	MK8	e	145	2	5,8,9	0.84	0	4,10,12	1.71	1 (25%)
2	2JN	m	153	2	5,8,9	0.85	0	4,10,12	0.95	0
2	MK8	g	145	2	5,8,9	0.76	0	4,10,12	0.97	0
2	2JN	c	153	2	5,8,9	0.96	1 (20%)	4,10,12	1.86	1 (25%)
2	MK8	d	145	2	5,8,9	0.75	0	4,10,12	1.21	1 (25%)
2	2JN	j	153	2	5,8,9	0.68	0	4,10,12	1.13	0
2	MK8	k	145	2	5,8,9	0.67	0	4,10,12	1.38	1 (25%)
2	2JN	f	153	2	5,8,9	0.83	0	4,10,12	1.01	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	2JN	o	153	2	5,8,9	0.87	0	4,10,12	1.00	0
2	MK8	n	145	2	5,8,9	0.71	0	4,10,12	1.33	1 (25%)
2	MK8	j	145	2	5,8,9	0.74	0	4,10,12	1.79	1 (25%)
2	MK8	m	145	2	5,8,9	0.89	0	4,10,12	1.18	0
2	MK8	f	145	2	5,8,9	0.94	0	4,10,12	0.86	0
2	MK8	b	145	2	5,8,9	0.69	0	4,10,12	2.02	2 (50%)
2	2JN	a	153	2	5,8,9	0.95	1 (20%)	4,10,12	0.84	0
2	2JN	i	153	2	5,8,9	0.92	1 (20%)	4,10,12	1.29	1 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2JN	b	153	2	-	1/6/8/11	-
2	MK8	l	145	2	-	4/6/8/11	-
2	MK8	p	145	2	-	4/6/8/11	-
2	2JN	n	153	2	-	1/6/8/11	-
2	2JN	g	153	2	-	4/6/8/11	-
2	MK8	a	145	2	-	1/6/8/11	-
2	2JN	d	153	2	-	0/6/8/11	-
2	2JN	h	153	2	-	0/6/8/11	-
2	2JN	e	153	2	-	0/6/8/11	-
2	MK8	o	145	2	-	1/6/8/11	-
2	MK8	c	145	2	-	1/6/8/11	-
2	MK8	i	145	2	-	1/6/8/11	-
2	2JN	p	153	2	-	0/6/8/11	-
2	2JN	l	153	2	-	4/6/8/11	-
2	2JN	k	153	2	-	4/6/8/11	-
2	MK8	h	145	2	-	4/6/8/11	-
2	MK8	e	145	2	-	1/6/8/11	-
2	2JN	m	153	2	-	4/6/8/11	-
2	MK8	g	145	2	-	4/6/8/11	-
2	2JN	c	153	2	-	4/6/8/11	-
2	MK8	d	145	2	-	4/6/8/11	-
2	2JN	j	153	2	-	4/6/8/11	-
2	MK8	k	145	2	-	1/6/8/11	-
2	2JN	f	153	2	-	4/6/8/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2JN	o	153	2	-	4/6/8/11	-
2	MK8	n	145	2	-	1/6/8/11	-
2	MK8	j	145	2	-	5/6/8/11	-
2	MK8	m	145	2	-	1/6/8/11	-
2	MK8	f	145	2	-	1/6/8/11	-
2	MK8	b	145	2	-	5/6/8/11	-
2	2JN	a	153	2	-	1/6/8/11	-
2	2JN	i	153	2	-	0/6/8/11	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	p	153	2JN	O-C	2.40	1.27	1.19
2	c	153	2JN	O-C	2.13	1.26	1.19
2	k	153	2JN	O-C	2.12	1.26	1.19
2	a	153	2JN	O-C	2.10	1.26	1.19
2	i	153	2JN	O-C	2.03	1.26	1.19

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	p	153	2JN	CAA-CA-CAO	-3.68	104.53	111.00
2	j	145	MK8	CB1-CA-CB	-3.50	104.83	111.00
2	c	153	2JN	CAA-CA-CAO	-3.43	104.95	111.00
2	b	153	2JN	CAA-CA-CAO	-3.21	105.34	111.00
2	b	145	MK8	CB1-CA-CB	-3.15	105.45	111.00

There are no chirality outliers.

5 of 74 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	b	145	MK8	C-CA-CB-CG
2	b	145	MK8	N-CA-CB-CG
2	b	145	MK8	CB1-CA-CB-CG
2	d	145	MK8	N-CA-CB-CG
2	g	145	MK8	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 38 ligands modelled in this entry, 16 are modelled with single atom - leaving 22 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	g	202	-	4,4,4	0.16	0	6,6,6	0.19	0
5	GOL	I	201	-	5,5,5	1.42	1 (20%)	5,5,5	0.98	0
3	SO4	K	202	-	4,4,4	0.13	0	6,6,6	0.26	0
3	SO4	A	203	-	4,4,4	0.18	0	6,6,6	0.34	0
3	SO4	G	202	-	4,4,4	0.22	0	6,6,6	0.18	0
3	SO4	F	202	-	4,4,4	0.21	0	6,6,6	0.23	0
3	SO4	G	201	-	4,4,4	0.13	0	6,6,6	0.14	0
3	SO4	A	204	-	4,4,4	0.31	0	6,6,6	0.55	0
3	SO4	D	201	-	4,4,4	0.17	0	6,6,6	0.16	0
3	SO4	L	201	-	4,4,4	0.18	0	6,6,6	0.32	0
3	SO4	K	201	-	4,4,4	0.22	0	6,6,6	0.37	0
5	GOL	C	202	-	5,5,5	1.24	0	5,5,5	0.83	0
3	SO4	H	201	-	4,4,4	0.16	0	6,6,6	0.17	0
3	SO4	O	201	-	4,4,4	0.15	0	6,6,6	0.12	0
3	SO4	F	201	-	4,4,4	0.13	0	6,6,6	0.36	0
3	SO4	D	202	-	4,4,4	0.11	0	6,6,6	0.23	0
5	GOL	i	202	-	5,5,5	1.15	1 (20%)	5,5,5	1.00	0
3	SO4	A	201	-	4,4,4	0.16	0	6,6,6	0.84	0
3	SO4	C	201	-	4,4,4	0.14	0	6,6,6	0.57	0
3	SO4	A	202	-	4,4,4	0.16	0	6,6,6	0.20	0
3	SO4	A	205	-	4,4,4	0.18	0	6,6,6	0.40	0
5	GOL	F	203	-	5,5,5	1.33	1 (20%)	5,5,5	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	I	201	-	-	0/4/4/4	-
5	GOL	C	202	-	-	0/4/4/4	-
5	GOL	i	202	-	-	2/4/4/4	-
5	GOL	F	203	-	-	3/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	201	GOL	C3-C2	2.44	1.61	1.51
5	F	203	GOL	C3-C2	2.14	1.60	1.51
5	i	202	GOL	C3-C2	2.10	1.60	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	203	GOL	O1-C1-C2-C3
5	F	203	GOL	C1-C2-C3-O3
5	i	202	GOL	C1-C2-C3-O3
5	F	203	GOL	O1-C1-C2-O2
5	i	202	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	202	SO4	1	0
3	K	201	SO4	2	0
3	C	201	SO4	1	0
3	A	202	SO4	0	1

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	78/86 (90%)	0.07	0 100 100	70, 80, 100, 113	0
1	B	77/86 (89%)	0.20	3 (3%) 39 35	69, 83, 105, 112	0
1	C	79/86 (91%)	0.20	1 (1%) 77 77	76, 94, 114, 123	0
1	D	77/86 (89%)	0.35	5 (6%) 18 14	84, 106, 125, 134	0
1	E	75/86 (87%)	0.52	6 (8%) 12 9	84, 106, 125, 135	0
1	F	79/86 (91%)	0.08	1 (1%) 77 77	81, 92, 107, 114	0
1	G	80/86 (93%)	0.16	1 (1%) 77 77	82, 104, 131, 138	0
1	H	77/86 (89%)	0.72	13 (16%) 1 1	82, 109, 131, 139	0
1	I	77/86 (89%)	0.83	14 (18%) 1 1	97, 113, 135, 160	0
1	J	78/86 (90%)	0.75	10 (12%) 3 2	86, 113, 134, 145	0
1	K	83/86 (96%)	0.34	3 (3%) 42 37	79, 98, 114, 125	0
1	L	77/86 (89%)	0.37	3 (3%) 39 35	70, 92, 113, 130	0
1	M	77/86 (89%)	0.58	8 (10%) 6 5	89, 113, 129, 138	0
1	N	80/86 (93%)	0.70	9 (11%) 5 4	91, 117, 135, 148	0
1	O	78/86 (90%)	0.82	13 (16%) 1 1	93, 120, 136, 149	0
1	P	73/86 (84%)	0.82	8 (10%) 5 4	104, 129, 144, 145	0
2	a	10/13 (76%)	0.86	1 (10%) 7 5	69, 80, 94, 99	0
2	b	10/13 (76%)	0.14	0 100 100	73, 79, 100, 103	0
2	c	10/13 (76%)	0.26	0 100 100	83, 90, 99, 117	0
2	d	10/13 (76%)	0.25	0 100 100	83, 93, 110, 120	0
2	e	10/13 (76%)	0.67	0 100 100	89, 91, 112, 121	0
2	f	10/13 (76%)	0.17	0 100 100	80, 85, 100, 111	0
2	g	10/13 (76%)	0.33	0 100 100	84, 90, 98, 101	0
2	h	10/13 (76%)	0.73	0 100 100	88, 95, 111, 115	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
2	i	10/13 (76%)	0.68	0	100	100	90, 99, 109, 117	0
2	j	10/13 (76%)	0.07	0	100	100	91, 98, 107, 114	0
2	k	10/13 (76%)	0.57	0	100	100	75, 81, 92, 110	0
2	l	10/13 (76%)	0.41	0	100	100	77, 86, 99, 106	0
2	m	10/13 (76%)	0.71	0	100	100	82, 88, 106, 119	0
2	n	10/13 (76%)	0.24	0	100	100	93, 98, 108, 113	0
2	o	10/13 (76%)	0.45	0	100	100	86, 89, 104, 108	0
2	p	10/13 (76%)	0.48	0	100	100	93, 104, 117, 121	0
All	All	1405/1584 (88%)	0.46	99 (7%)	16	12	69, 103, 131, 160	0

The worst 5 of 99 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	57	PRO	7.5
1	N	98	PHE	6.2
1	P	98	PHE	6.0
1	J	61	ILE	5.6
1	O	130	PHE	5.3

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MK8	c	145	9/10	0.93	0.27	82,90,102,106	0
2	2JN	a	153	9/10	0.93	0.33	69,81,83,85	0
2	2JN	f	153	9/10	0.93	0.29	77,89,97,99	0
2	2JN	i	153	9/10	0.94	0.30	75,82,87,89	0
2	MK8	o	145	9/10	0.95	0.23	76,81,86,88	0
2	MK8	p	145	9/10	0.95	0.27	95,105,107,111	0
2	MK8	e	145	9/10	0.95	0.23	92,100,102,103	0
2	MK8	f	145	9/10	0.95	0.21	77,85,90,93	0
2	MK8	j	145	9/10	0.95	0.27	84,92,97,103	0
2	MK8	m	145	9/10	0.96	0.33	81,88,94,94	0
2	MK8	n	145	9/10	0.96	0.18	86,90,94,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MK8	b	145	9/10	0.96	0.26	68,79,84,84	0
2	MK8	a	145	9/10	0.96	0.29	65,68,73,74	0
2	MK8	h	145	9/10	0.96	0.25	76,83,96,102	0
2	2JN	c	153	9/10	0.96	0.23	72,76,81,88	0
2	2JN	d	153	9/10	0.96	0.28	68,79,83,87	0
2	2JN	e	153	9/10	0.96	0.30	73,78,91,91	0
2	MK8	i	145	9/10	0.96	0.28	89,98,103,104	0
2	2JN	g	153	9/10	0.96	0.25	79,87,93,94	0
2	MK8	d	145	9/10	0.96	0.21	87,96,100,100	0
2	2JN	n	153	9/10	0.96	0.24	81,87,94,99	0
2	2JN	o	153	9/10	0.96	0.32	77,87,89,91	0
2	2JN	b	153	9/10	0.97	0.29	72,79,86,89	0
2	2JN	k	153	9/10	0.97	0.28	68,77,85,86	0
2	MK8	l	145	9/10	0.97	0.23	76,79,84,85	0
2	2JN	h	153	9/10	0.97	0.31	83,86,92,95	0
2	2JN	p	153	9/10	0.97	0.21	82,93,97,99	0
2	2JN	l	153	9/10	0.98	0.28	70,78,84,85	0
2	2JN	m	153	9/10	0.98	0.30	74,83,89,90	0
2	MK8	k	145	9/10	0.98	0.16	71,76,83,89	0
2	2JN	j	153	9/10	0.98	0.27	83,92,93,97	0
2	MK8	g	145	9/10	0.98	0.23	71,80,81,84	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	GOL	I	201	6/6	0.56	0.26	103,114,125,133	0
4	NH2	f	201	1/1	0.60	0.54	100,100,100,100	0
3	SO4	A	202	5/5	0.61	0.71	100,103,110,117	5
3	SO4	g	202	5/5	0.63	0.41	109,115,120,124	5
5	GOL	i	202	6/6	0.65	0.25	101,102,112,113	0
3	SO4	A	203	5/5	0.73	0.30	117,119,122,127	5
3	SO4	G	202	5/5	0.73	0.29	107,109,115,122	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	GOL	C	202	6/6	0.74	0.41	97,103,111,114	0
3	SO4	H	201	5/5	0.75	0.23	118,125,131,137	5
3	SO4	O	201	5/5	0.75	0.26	118,123,132,136	5
3	SO4	D	201	5/5	0.76	0.21	115,116,120,126	5
3	SO4	G	201	5/5	0.77	0.29	127,134,138,140	5
3	SO4	K	202	5/5	0.78	0.20	115,117,124,126	5
3	SO4	F	202	5/5	0.79	0.21	88,99,107,117	5
5	GOL	F	203	6/6	0.80	0.16	92,100,112,121	0
3	SO4	D	202	5/5	0.81	0.35	109,113,122,123	5
4	NH2	n	201	1/1	0.82	0.30	80,80,80,80	0
3	SO4	L	201	5/5	0.84	0.17	106,106,121,122	5
3	SO4	K	201	5/5	0.85	0.14	115,121,131,136	5
3	SO4	F	201	5/5	0.85	0.46	85,89,98,104	5
4	NH2	d	201	1/1	0.85	0.43	90,90,90,90	0
4	NH2	p	201	1/1	0.86	0.23	101,101,101,101	0
3	SO4	A	205	5/5	0.87	0.21	93,94,99,113	5
3	SO4	A	204	5/5	0.90	0.17	79,86,92,93	5
3	SO4	C	201	5/5	0.93	0.18	88,89,97,98	5
4	NH2	g	201	1/1	0.93	0.23	107,107,107,107	0
4	NH2	h	201	1/1	0.94	0.19	93,93,93,93	0
4	NH2	i	201	1/1	0.94	0.31	90,90,90,90	0
4	NH2	m	201	1/1	0.94	0.12	87,87,87,87	0
4	NH2	e	201	1/1	0.94	0.33	86,86,86,86	0
4	NH2	o	201	1/1	0.94	0.26	95,95,95,95	0
4	NH2	b	201	1/1	0.95	0.60	92,92,92,92	0
4	NH2	k	201	1/1	0.95	0.23	83,83,83,83	0
4	NH2	j	201	1/1	0.96	0.17	105,105,105,105	0
3	SO4	A	201	5/5	0.96	0.14	78,79,88,88	0
4	NH2	l	201	1/1	0.97	0.16	94,94,94,94	0
4	NH2	a	201	1/1	0.97	0.35	86,86,86,86	0
4	NH2	c	201	1/1	0.97	0.25	84,84,84,84	0

6.5 Other polymers (i)

There are no such residues in this entry.