



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 04:40 am GMT

PDB ID : 3FLP
Title : Crystal structure of native heptameric SAP-like pentraxin from *Limulus polyphemus*
Authors : Shrive, A.K.; Greenhough, T.J.; Armstrong, P.B.
Deposited on : 2008-12-19
Resolution : 2.30 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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

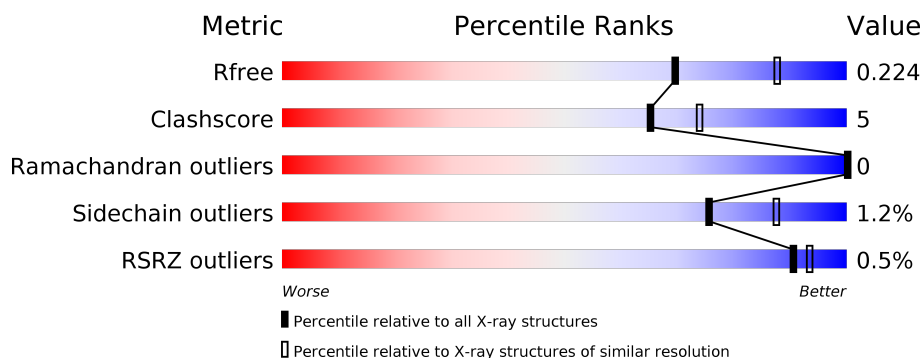
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION







The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	217	 89% 11%
1	B	217	 91% 9%
1	C	217	 89% 11%
1	D	217	 86% 14%
1	E	217	 89% 11%
1	F	217	 87% 12%

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Mol	Chain	Length	Quality of chain
1	G	217	 90%10%
1	H	217	 85%15%
1	I	217	 85%15%
1	J	217	 85%15%
1	K	217	 85%15%
1	L	217	 82%18%
1	M	217	 89%11%
1	N	217	 82%18%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 24261 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 SAP-like pentraxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	B	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	C	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	D	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	E	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	F	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	G	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	H	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	I	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	J	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	K	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	L	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	M	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			
1	N	217	Total	C	N	O	S	0	0	0
			1668	1041	292	322	13			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	Total 2 Ca 2	0	0
2	J	2	Total 2 Ca 2	0	0
2	D	2	Total 2 Ca 2	0	0
2	K	2	Total 2 Ca 2	0	0
2	E	2	Total 2 Ca 2	0	0
2	H	2	Total 2 Ca 2	0	0
2	B	2	Total 2 Ca 2	0	0
2	I	2	Total 2 Ca 2	0	0
2	C	2	Total 2 Ca 2	0	0
2	A	2	Total 2 Ca 2	0	0
2	N	2	Total 2 Ca 2	0	0
2	L	2	Total 2 Ca 2	0	0
2	F	2	Total 2 Ca 2	0	0
2	M	2	Total 2 Ca 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	74	Total 74 O 74	0	0
3	B	62	Total 62 O 62	0	0
3	C	71	Total 71 O 71	0	0
3	D	74	Total 74 O 74	0	0
3	E	68	Total 68 O 68	0	0
3	F	65	Total 65 O 65	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	62	Total 62	O 62	0	0
3	H	56	Total 56	O 56	0	0
3	I	54	Total 54	O 54	0	0
3	J	60	Total 60	O 60	0	0
3	K	52	Total 52	O 52	0	0
3	L	59	Total 59	O 59	0	0
3	M	67	Total 67	O 67	0	0
3	N	57	Total 57	O 57	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.

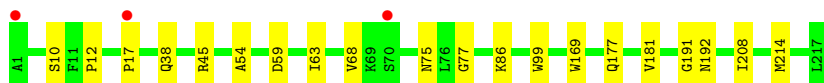
- Molecule 1: SAP-like pentraxin

Chain A: 



- Molecule 1: SAP-like pentraxin

Chain B: 




- Molecule 1: SAP-like pentraxin

Chain C: 



- Molecule 1: SAP-like pentraxin

Chain D: 

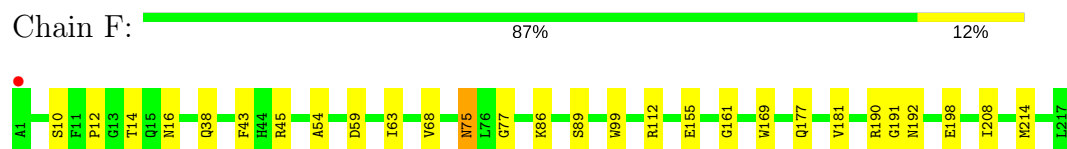


- Molecule 1: SAP-like pentraxin

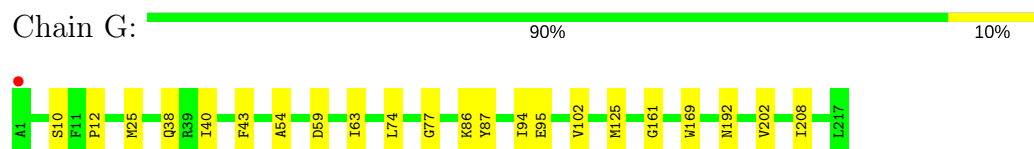
Chain E: 



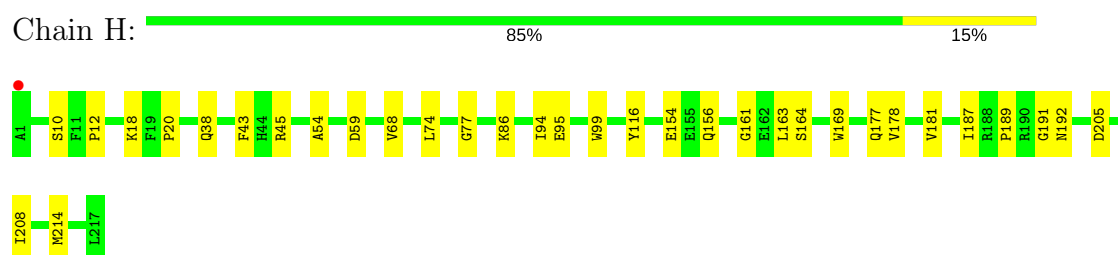
- Molecule 1: SAP-like pentraxin



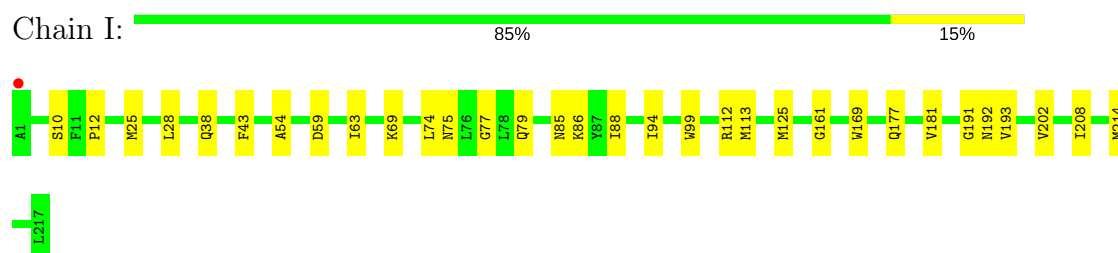
- Molecule 1: SAP-like pentraxin



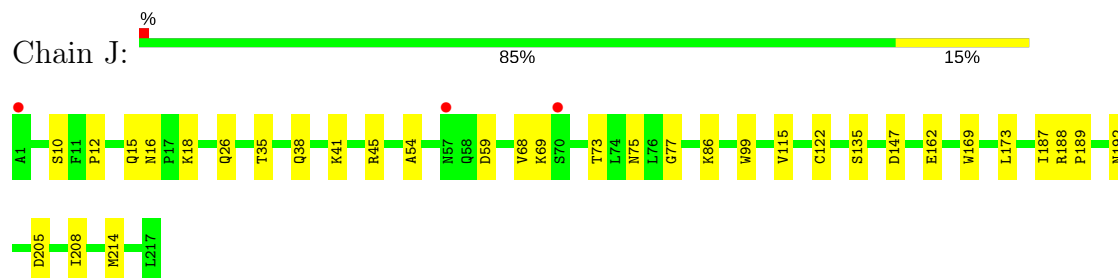
- Molecule 1: SAP-like pentraxin



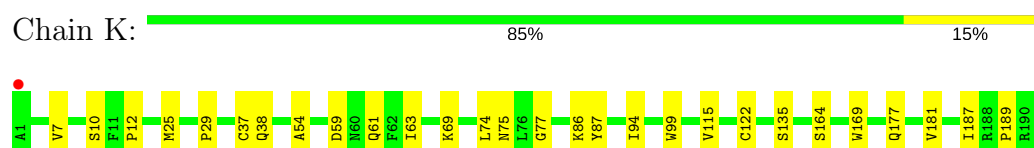
- Molecule 1: SAP-like pentraxin



- Molecule 1: SAP-like pentraxin



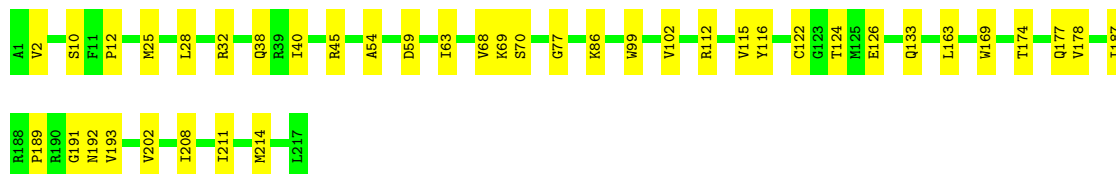
- Molecule 1: SAP-like pentraxin





- Molecule 1: SAP-like pentraxin

Chain L: 82% 18%



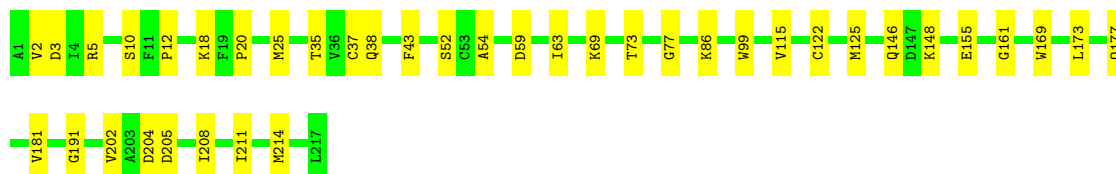
- Molecule 1: SAP-like pentraxin

Chain M: 89% 11%



- Molecule 1: SAP-like pentraxin

Chain N: 82% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.32Å 167.56Å 140.87Å 90.00° 92.50° 90.00°	Depositor
Resolution (Å)	45.27 – 2.30 45.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.4 (45.27-2.30) 89.3 (45.27-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.92 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.201 , 0.223 0.201 , 0.224	Depositor DCC
R_{free} test set	9112 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 32.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	24261	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.23 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5722e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.36	0/1705	0.63	1/2312 (0.0%)
1	B	0.35	0/1705	0.63	0/2312
1	C	0.35	0/1705	0.63	0/2312
1	D	0.35	0/1705	0.63	0/2312
1	E	0.35	0/1705	0.63	0/2312
1	F	0.35	0/1705	0.63	0/2312
1	G	0.35	0/1705	0.63	0/2312
1	H	0.34	0/1705	0.62	0/2312
1	I	0.34	0/1705	0.62	0/2312
1	J	0.35	0/1705	0.62	0/2312
1	K	0.34	0/1705	0.62	1/2312 (0.0%)
1	L	0.34	0/1705	0.62	0/2312
1	M	0.36	0/1705	0.63	1/2312 (0.0%)
1	N	0.35	0/1705	0.62	1/2312 (0.0%)
All	All	0.35	0/23870	0.63	4/32368 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	37	CYS	CA-CB-SG	5.66	124.20	114.00
1	N	37	CYS	CA-CB-SG	5.58	124.05	114.00
1	A	37	CYS	CA-CB-SG	5.56	124.01	114.00
1	M	37	CYS	CA-CB-SG	5.22	123.40	114.00

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	1668	0	1600	13	0
1	B	1668	0	1600	9	0
1	C	1668	0	1600	12	0
1	D	1668	0	1600	16	0
1	E	1668	0	1600	13	0
1	F	1668	0	1600	17	0
1	G	1668	0	1600	13	0
1	H	1668	0	1600	19	0
1	I	1668	0	1600	19	0
1	J	1668	0	1600	18	0
1	K	1668	0	1600	17	0
1	L	1668	0	1600	23	0
1	M	1668	0	1600	11	0
1	N	1668	0	1600	20	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
3	A	74	0	0	1	0
3	B	62	0	0	0	0
3	C	71	0	0	0	0
3	D	74	0	0	0	0
3	E	68	0	0	1	0
3	F	65	0	0	0	0
3	G	62	0	0	0	0
3	H	56	0	0	0	0
3	I	54	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	60	0	0	0	0
3	K	52	0	0	0	0
3	L	59	0	0	0	0
3	M	67	0	0	0	0
3	N	57	0	0	1	0
All	All	24261	0	22400	216	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 5.

The worst 5 of 216 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:D:69:LYS:HE3	1:D:75:ASN:OD1	1.77	0.83
1:H:18:LYS:HD3	1:H:20:PRO:HD3	1.73	0.69
1:I:69:LYS:HE3	1:I:75:ASN:OD1	1.95	0.66
1:D:32:ARG:HG2	1:D:133:GLN:HG2	1.76	0.66
1:A:155:GLU:HG2	3:A:330:HOH:O	1.94	0.65

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	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	B	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	C	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	D	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	E	215/217 (99%)	210 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	G	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	H	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	I	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	J	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	K	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	L	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	M	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
1	N	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
All	All	3010/3038 (99%)	2940 (98%)	70 (2%)	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	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	B	185/185 (100%)	181 (98%)	4 (2%)	57	74
1	C	185/185 (100%)	182 (98%)	3 (2%)	68	82
1	D	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	E	185/185 (100%)	184 (100%)	1 (0%)	91	96
1	F	185/185 (100%)	182 (98%)	3 (2%)	68	82
1	G	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	H	185/185 (100%)	184 (100%)	1 (0%)	91	96
1	I	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	J	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	K	185/185 (100%)	183 (99%)	2 (1%)	78	89
1	L	185/185 (100%)	183 (99%)	2 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	185/185 (100%)	182 (98%)	3 (2%)	68	82
1	N	185/185 (100%)	183 (99%)	2 (1%)	78	89
All	All	2590/2590 (100%)	2559 (99%)	31 (1%)	75	87

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	75	ASN
1	H	38	GLN
1	M	75	ASN
1	G	38	GLN
1	I	38	GLN

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

Mol	Chain	Res	Type
1	F	75	ASN
1	G	75	ASN
1	J	98	GLN
1	K	61	GLN

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 ⓘ

Of 28 ligands modelled in this entry, 28 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	217/217 (100%)	-0.54	1 (0%) 90 93	5, 11, 26, 35	0
1	B	217/217 (100%)	-0.43	3 (1%) 75 80	5, 13, 26, 36	0
1	C	217/217 (100%)	-0.56	1 (0%) 90 93	3, 11, 24, 36	0
1	D	217/217 (100%)	-0.47	1 (0%) 90 93	4, 12, 26, 36	0
1	E	217/217 (100%)	-0.50	1 (0%) 90 93	4, 11, 25, 37	0
1	F	217/217 (100%)	-0.48	1 (0%) 90 93	5, 12, 25, 35	0
1	G	217/217 (100%)	-0.42	1 (0%) 90 93	5, 13, 27, 37	0
1	H	217/217 (100%)	-0.35	1 (0%) 90 93	6, 14, 28, 36	0
1	I	217/217 (100%)	-0.31	1 (0%) 90 93	6, 14, 27, 36	0
1	J	217/217 (100%)	-0.40	3 (1%) 75 80	7, 13, 27, 37	0
1	K	217/217 (100%)	-0.41	1 (0%) 90 93	5, 13, 28, 35	0
1	L	217/217 (100%)	-0.41	0 100 100	7, 14, 28, 35	0
1	M	217/217 (100%)	-0.54	0 100 100	4, 13, 25, 33	0
1	N	217/217 (100%)	-0.50	0 100 100	5, 13, 28, 35	0
All	All	3038/3038 (100%)	-0.45	15 (0%) 90 93	3, 13, 27, 37	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	1	ALA	6.0
1	E	1	ALA	5.6
1	H	1	ALA	5.3
1	A	1	ALA	5.0
1	D	1	ALA	4.9

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	CA	H	302	1/1	0.98	0.06	-2.15	16,16,16,16	0
2	CA	E	302	1/1	0.98	0.05	-2.96	18,18,18,18	0
2	CA	K	302	1/1	0.97	0.06	-3.03	22,22,22,22	0
2	CA	J	302	1/1	0.98	0.06	-3.08	13,13,13,13	0
2	CA	N	302	1/1	0.96	0.04	-3.12	31,31,31,31	0
2	CA	C	302	1/1	0.99	0.03	-3.40	12,12,12,12	0
2	CA	A	302	1/1	0.99	0.05	-3.53	15,15,15,15	0
2	CA	F	302	1/1	0.98	0.04	-3.54	13,13,13,13	0
2	CA	G	302	1/1	0.98	0.05	-3.65	16,16,16,16	0
2	CA	B	302	1/1	0.98	0.04	-4.48	17,17,17,17	0
2	CA	D	302	1/1	0.99	0.02	-4.60	13,13,13,13	0
2	CA	L	302	1/1	0.98	0.03	-5.80	23,23,23,23	0
2	CA	M	302	1/1	0.98	0.04	-7.90	17,17,17,17	0
2	CA	I	302	1/1	0.98	0.03	-10.41	20,20,20,20	0
2	CA	E	301	1/1	0.99	0.05	-	10,10,10,10	0
2	CA	L	301	1/1	0.98	0.04	-	21,21,21,21	0
2	CA	F	301	1/1	0.98	0.05	-	13,13,13,13	0
2	CA	H	301	1/1	0.96	0.05	-	16,16,16,16	0
2	CA	N	301	1/1	0.98	0.06	-	23,23,23,23	0
2	CA	C	301	1/1	0.99	0.03	-	12,12,12,12	0
2	CA	I	301	1/1	0.93	0.05	-	17,17,17,17	0
2	CA	M	301	1/1	0.97	0.04	-	16,16,16,16	0
2	CA	G	301	1/1	0.98	0.04	-	14,14,14,14	0
2	CA	A	301	1/1	0.99	0.04	-	11,11,11,11	0
2	CA	K	301	1/1	0.99	0.04	-	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CA	D	301	1/1	0.99	0.04	-	14,14,14,14	0
2	CA	J	301	1/1	0.98	0.03	-	12,12,12,12	0
2	CA	B	301	1/1	0.99	0.03	-	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.