Full wwPDB X-ray Structure Validation Report (i)

Mar 10, 2025 – 06:17 PM EDT

PDB ID	:	8UHN
Title	:	anti-Phosphohistidine Fab hSC44.ck.20.N32F with 3pHis peptide
Authors	:	Kalagiri, R.; Stanfield, R.L.; Hunter, T.; Wilson, I.A.
Deposited on	:	2023-10-09
Resolution	:	2.09 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 (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:

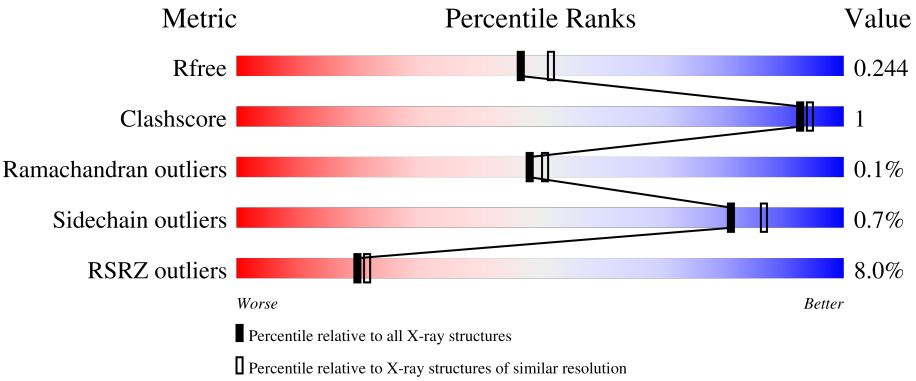
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

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 2.09 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}	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	225	16% 92% • 5%
1	H	225	4% 94% • •
2	B	218	6% 94% 5% •
2	L	218	3% 97% •
3	C	9	33% 56% 11% 33%

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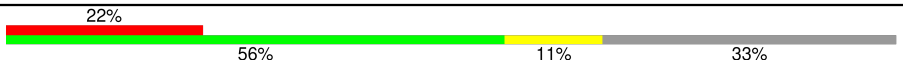
Mol	Chain	Length	Quality of chain
3	D	9	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 13371 atoms, of which 6439 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 hSC44.ck.20.N32F Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	218	Total	C	H	N	O	S	0	0	0
			3198	1010	1593	275	315	5			
1	A	213	Total	C	H	N	O	S	0	0	0
			3121	989	1553	269	305	5			

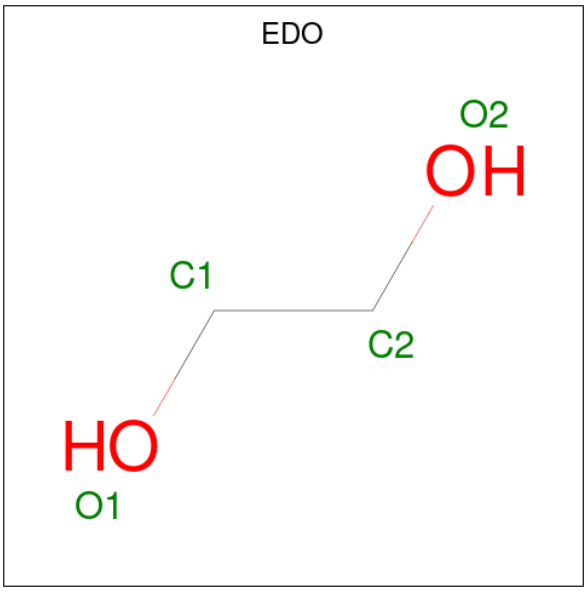
- Molecule 2 is a protein called hSC44.ck.20.N32F Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	218	Total	C	H	N	O	S	0	0	0
			3300	1055	1618	281	340	6			
2	B	217	Total	C	H	N	O	S	0	0	0
			3285	1051	1611	280	337	6			

- Molecule 3 is a protein called 3pHis peptide.

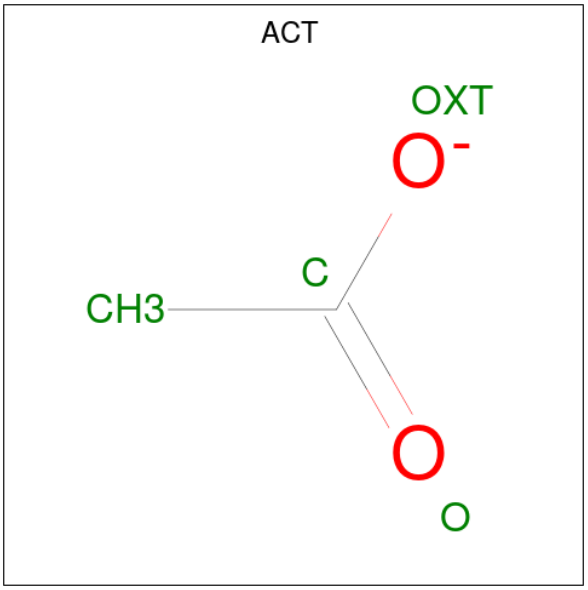
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	6	Total	C	H	N	O	P	0	0	0
			59	18	23	8	9	1			
3	D	6	Total	C	H	N	O	P	0	0	0
			59	18	23	8	9	1			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	L	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	H	O	0	0
			7	2	3	2		
5	B	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 6 is water.

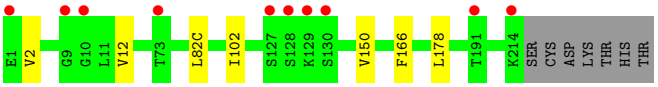
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	117	Total O 117 117	0	0
6	L	75	Total O 75 75	0	0
6	A	40	Total O 40 40	0	0
6	B	81	Total O 81 81	0	0
6	D	2	Total O 2 2	0	0

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.

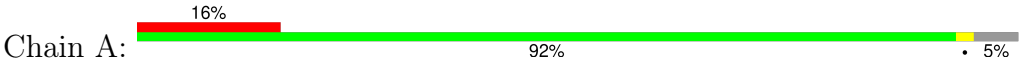
• Molecule 1: hSC44.ck.20.N32F Fab heavy chain

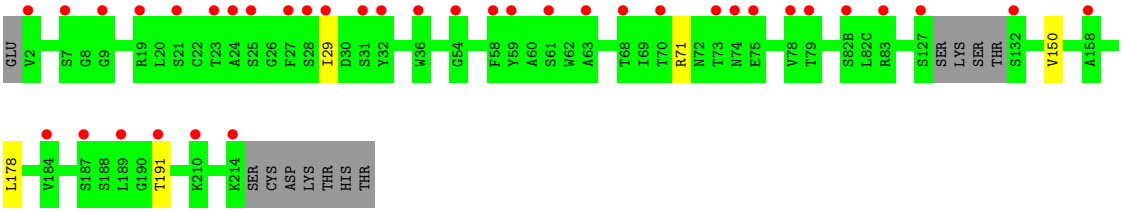
Chain H:



• Molecule 1: hSC44.ck.20.N32F Fab heavy chain

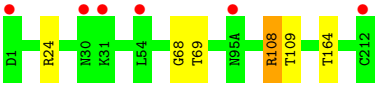
Chain A:





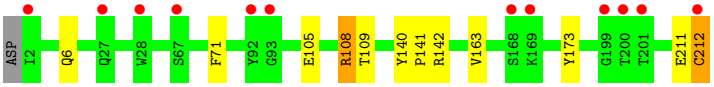
• Molecule 2: hSC44.ck.20.N32F Fab light chain

Chain L:



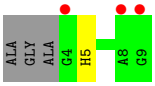
• Molecule 2: hSC44.ck.20.N32F Fab light chain

Chain B:



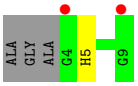
• Molecule 3: 3pHis peptide

Chain C:



• Molecule 3: 3pHis peptide

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.28Å 74.03Å 239.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.19 – 2.09 47.19 – 2.09	Depositor EDS
% Data completeness (in resolution range)	94.7 (47.19-2.09) 94.7 (47.19-2.09)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.217 , 0.245 0.218 , 0.244	Depositor DCC
R_{free} test set	3703 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	35.0	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 32.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.033 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13371	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, EDO, NEP

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	0.25	0/1603	0.50	0/2181
1	H	0.26	0/1641	0.50	0/2233
2	B	0.26	0/1712	0.49	0/2324
2	L	0.26	0/1720	0.48	0/2335
3	C	0.23	0/20	0.37	0/23
3	D	0.24	0/20	0.41	0/23
All	All	0.25	0/6716	0.49	0/9119

There are no bond length outliers.

There are no bond angle outliers.

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	1568	1553	1553	4	0
1	H	1605	1593	1593	6	0
2	B	1674	1611	1611	6	0
2	L	1682	1618	1618	4	0
3	C	36	23	23	0	0
3	D	36	23	23	0	0
4	B	4	6	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	4	6	6	0	0
5	B	4	3	3	0	0
5	L	4	3	3	0	0
6	A	40	0	0	0	0
6	B	81	0	0	0	0
6	D	2	0	0	0	0
6	H	117	0	0	0	0
6	L	75	0	0	0	0
All	All	6932	6439	6439	18	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 1.

All (18) 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:29:ILE:HD12	1:A:71:ARG:HB2	1.80	0.63
1:H:2:VAL:HG12	1:H:102:ILE:HD12	1.85	0.59
1:H:12:VAL:HG11	1:H:82(C):LEU:HD12	1.89	0.54
1:A:150:VAL:CG2	1:A:178:LEU:HD21	2.40	0.52
2:B:211:GLU:O	2:B:212:CYS:HB3	2.10	0.52
2:B:142:ARG:CZ	2:B:163:VAL:HG21	2.41	0.50
1:H:2:VAL:CG1	1:H:102:ILE:HD12	2.43	0.48
1:H:178:LEU:C	1:H:178:LEU:HD12	2.34	0.48
1:A:178:LEU:C	1:A:178:LEU:HD12	2.36	0.46
2:B:140:TYR:CG	2:B:141:PRO:HA	2.51	0.46
2:L:108:ARG:HD3	2:L:109:THR:O	2.18	0.43
2:L:24:ARG:HA	2:L:69:THR:O	2.20	0.42
1:H:166:PHE:CD1	2:L:164:THR:HG23	2.55	0.41
2:B:105:GLU:HG3	2:B:173:TYR:OH	2.21	0.41
1:A:150:VAL:HG23	1:A:178:LEU:HD21	2.03	0.41
2:B:108:ARG:HD3	2:B:109:THR:O	2.21	0.40
2:L:24:ARG:HD3	2:B:6:GLN:O	2.21	0.40
1:H:150:VAL:CG2	1:H:178:LEU:HD21	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	209/225 (93%)	204 (98%)	5 (2%)	0	100	100
1	H	216/225 (96%)	213 (99%)	3 (1%)	0	100	100
2	B	215/218 (99%)	207 (96%)	8 (4%)	0	100	100
2	L	216/218 (99%)	209 (97%)	6 (3%)	1 (0%)	25	23
3	C	3/9 (33%)	3 (100%)	0	0	100	100
3	D	3/9 (33%)	3 (100%)	0	0	100	100
All	All	862/904 (95%)	839 (97%)	22 (3%)	1 (0%)	48	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	68	GLY

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	173/185 (94%)	172 (99%)	1 (1%)	84	89
1	H	178/185 (96%)	178 (100%)	0	100	100
2	B	187/188 (100%)	184 (98%)	3 (2%)	58	65
2	L	188/188 (100%)	187 (100%)	1 (0%)	86	91
All	All	726/746 (97%)	721 (99%)	5 (1%)	81	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	108	ARG
1	A	191	THR
2	B	71	PHE
2	B	108	ARG
2	B	212	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	$\#\|Z\| > 2$
3	NEP	D	5	3	11,14,15	2.01	4 (36%)	4,20,22	2.18	2 (50%)
3	NEP	C	5	3	11,14,15	1.99	4 (36%)	4,20,22	2.18	2 (50%)

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
3	NEP	D	5	3	-	0/5/12/14	0/1/1/1
3	NEP	C	5	3	-	0/5/12/14	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	5	NEP	P-NE2	-3.34	1.59	1.76
3	D	5	NEP	P-NE2	-3.26	1.59	1.76
3	D	5	NEP	P-O1P	3.10	1.61	1.54
3	C	5	NEP	P-O1P	3.09	1.61	1.54
3	D	5	NEP	CD2-CG	3.05	1.40	1.36
3	C	5	NEP	CD2-CG	2.84	1.40	1.36
3	C	5	NEP	P-O2P	2.83	1.60	1.54
3	D	5	NEP	P-O2P	2.82	1.60	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	5	NEP	O1P-P-O2P	-3.15	94.17	106.57
3	D	5	NEP	O1P-P-O2P	-3.13	94.26	106.57
3	D	5	NEP	O1P-P-O3P	-2.55	108.41	113.76
3	C	5	NEP	O1P-P-O3P	-2.37	108.78	113.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands 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	$\#\|Z\| > 2$
4	EDO	B	301	-	3,3,3	0.44	0	2,2,2	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	EDO	L	301	-	3,3,3	0.44	0	2,2,2	0.32	0
5	ACT	L	302	-	3,3,3	1.31	0	3,3,3	1.38	0
5	ACT	B	302	-	3,3,3	1.40	1 (33%)	3,3,3	1.35	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
4	EDO	B	301	-	-	1/1/1/1	-
4	EDO	L	301	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	302	ACT	CH3-C	2.04	1.57	1.49

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	301	EDO	O1-C1-C2-O2

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, 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	213/225 (94%)	1.02	37 (17%) 5 5	31, 57, 84, 99	0
1	H	218/225 (96%)	0.10	10 (4%) 38 40	29, 41, 58, 76	0
2	B	217/218 (99%)	0.42	12 (5%) 32 34	32, 45, 70, 221	0
2	L	218/218 (100%)	0.26	6 (2%) 55 57	29, 44, 64, 89	0
3	C	5/9 (55%)	2.74	3 (60%) 0 0	68, 74, 101, 104	0
3	D	5/9 (55%)	1.39	2 (40%) 1 1	54, 55, 56, 70	0
All	All	876/904 (96%)	0.47	70 (7%) 20 21	29, 44, 77, 221	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	212	CYS	9.2
1	A	29	ILE	5.8
1	A	132	SER	4.6
2	B	2	ILE	4.5
3	C	8	ALA	4.3
2	B	92	TYR	3.9
1	A	63	ALA	3.3
1	A	54	GLY	3.3
3	C	4	GLY	3.2
2	B	199	GLY	3.2
3	C	9	GLY	3.2
2	L	212	CYS	3.1
1	H	130	SER	3.1
2	B	168	SER	3.1
2	B	200	THR	3.0
1	A	7	SER	2.9
2	B	67	SER	2.9
1	A	73	THR	2.9
2	L	1	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	23	THR	2.9
1	H	128	SER	2.9
1	H	129	LYS	2.8
3	D	9	GLY	2.8
2	L	54	LEU	2.8
1	H	73	THR	2.7
1	A	191	THR	2.7
1	A	187	SER	2.6
1	A	9	GLY	2.6
1	A	58	PHE	2.6
1	A	189	LEU	2.6
1	H	9	GLY	2.6
1	H	214	LYS	2.6
1	A	2	VAL	2.5
1	A	25	SER	2.5
1	A	127	SER	2.5
2	B	201	THR	2.5
1	A	31	SER	2.5
3	D	4	GLY	2.5
1	A	70	THR	2.5
1	A	59	TYR	2.4
1	H	127	SER	2.4
1	A	79	THR	2.4
2	L	31	LYS	2.4
1	A	32	TYR	2.4
1	A	74	ASN	2.3
2	B	93	GLY	2.3
1	A	75	GLU	2.3
1	A	27	PHE	2.3
1	A	28	SER	2.3
1	A	214	LYS	2.2
2	B	27	GLN	2.2
1	A	78	VAL	2.2
1	A	83	ARG	2.2
1	A	158	ALA	2.2
1	H	191	THR	2.2
1	A	68	THR	2.2
1	A	82(B)	SER	2.1
2	B	169	LYS	2.1
1	H	10	GLY	2.1
2	L	30	ASN	2.1
2	L	95(A)	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	24	ALA	2.1
1	A	36	TRP	2.1
1	A	184	VAL	2.1
1	A	19	ARG	2.1
1	A	21	SER	2.1
1	H	1	GLU	2.0
1	A	210	LYS	2.0
1	A	61	SER	2.0
2	B	28	TRP	2.0

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, 95^{th} 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
3	NEP	C	5	14/15	0.95	0.10	49,59,76,78	0
3	NEP	D	5	14/15	0.96	0.09	30,43,52,57	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, 95^{th} 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	ACT	B	302	4/4	0.77	0.18	43,52,54,59	0
5	ACT	L	302	4/4	0.80	0.22	45,48,57,57	0
4	EDO	L	301	4/4	0.85	0.15	39,48,52,52	0
4	EDO	B	301	4/4	0.91	0.14	32,39,49,49	0

6.5 Other polymers (i)

There are no such residues in this entry.