wwPDB X-ray Structure Validation Summary Report (i)

Nov 4, 2024 – 04:19 PM EST

PDB ID	:	8SRW
Title	:	Crystal structure of O-acetyl-L-serine sulfhydrylase A (CysK) from Staphylococcus aureus NCTC 8325 complexed with a modified peptide inhibitor
Authors	:	Pederick, J.L.; Vandborg, B.C.; Bruning, J.B.
Deposited on	:	2023-05-07
Resolution	:	2.15 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 (i)) were used in the production of this report:

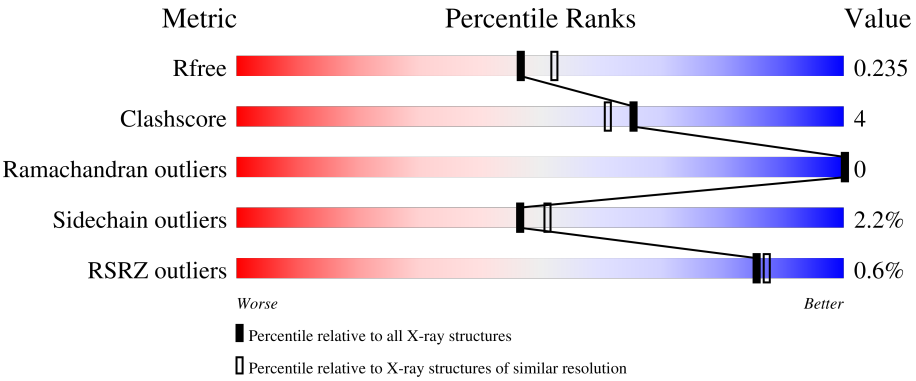
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.15 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	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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	318	86% 10%
1	B	318	87% 9%
1	C	318	% 86% 10%
1	D	318	87% 9%
2	E	5	20% 60% 40%

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Mol	Chain	Length	Quality of chain
2	F	5	40% 20% 40%
2	G	5	60% 40%
2	H	5	20% 60% 40%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9909 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 Cysteine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	P	S	0	0	0
			2289	1447	384	449	1	8			
1	D	307	Total	C	N	O	P	S	0	0	0
			2290	1449	385	447	1	8			
1	B	307	Total	C	N	O	P	S	0	0	0
			2287	1445	382	451	1	8			
1	C	307	Total	C	N	O	P	S	0	0	0
			2280	1443	383	445	1	8			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q2G0Q8
A	-6	GLY	-	expression tag	UNP Q2G0Q8
A	-5	HIS	-	expression tag	UNP Q2G0Q8
A	-4	HIS	-	expression tag	UNP Q2G0Q8
A	-3	HIS	-	expression tag	UNP Q2G0Q8
A	-2	HIS	-	expression tag	UNP Q2G0Q8
A	-1	HIS	-	expression tag	UNP Q2G0Q8
A	0	HIS	-	expression tag	UNP Q2G0Q8
D	-7	MET	-	expression tag	UNP Q2G0Q8
D	-6	GLY	-	expression tag	UNP Q2G0Q8
D	-5	HIS	-	expression tag	UNP Q2G0Q8
D	-4	HIS	-	expression tag	UNP Q2G0Q8
D	-3	HIS	-	expression tag	UNP Q2G0Q8
D	-2	HIS	-	expression tag	UNP Q2G0Q8
D	-1	HIS	-	expression tag	UNP Q2G0Q8
D	0	HIS	-	expression tag	UNP Q2G0Q8
B	-7	MET	-	expression tag	UNP Q2G0Q8
B	-6	GLY	-	expression tag	UNP Q2G0Q8
B	-5	HIS	-	expression tag	UNP Q2G0Q8
B	-4	HIS	-	expression tag	UNP Q2G0Q8
B	-3	HIS	-	expression tag	UNP Q2G0Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP Q2G0Q8
B	-1	HIS	-	expression tag	UNP Q2G0Q8
B	0	HIS	-	expression tag	UNP Q2G0Q8
C	-7	MET	-	expression tag	UNP Q2G0Q8
C	-6	GLY	-	expression tag	UNP Q2G0Q8
C	-5	HIS	-	expression tag	UNP Q2G0Q8
C	-4	HIS	-	expression tag	UNP Q2G0Q8
C	-3	HIS	-	expression tag	UNP Q2G0Q8
C	-2	HIS	-	expression tag	UNP Q2G0Q8
C	-1	HIS	-	expression tag	UNP Q2G0Q8
C	0	HIS	-	expression tag	UNP Q2G0Q8

- Molecule 2 is a protein called TYR-MET-NAL-TYR-ILE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	5	Total	C	N	O	S	0	0	0
			49	36	5	7	1			
2	F	5	Total	C	N	O	S	0	0	0
			56	42	5	8	1			
2	G	5	Total	C	N	O	S	0	0	0
			49	36	5	7	1			
2	H	5	Total	C	N	O	S	0	0	0
			49	36	5	7	1			

- Molecule 3 is water.

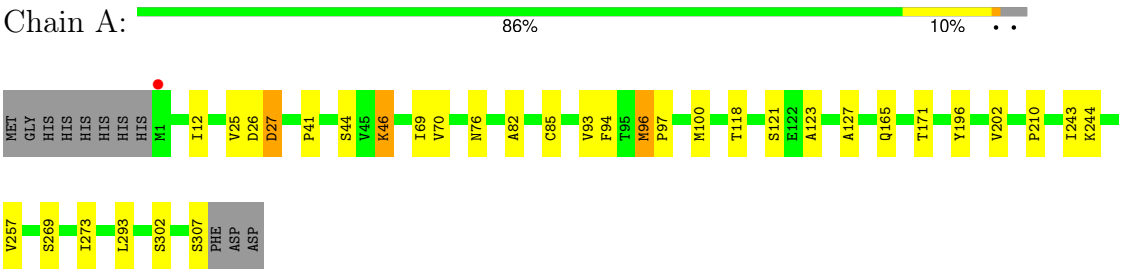
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	159	Total	O	0	0
			159	159		
3	D	140	Total	O	0	0
			140	140		
3	B	143	Total	O	0	0
			143	143		
3	C	105	Total	O	0	0
			105	105		
3	E	4	Total	O	0	0
			4	4		
3	F	5	Total	O	0	0
			5	5		
3	G	1	Total	O	0	0
			1	1		
3	H	3	Total	O	0	0
			3	3		

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.

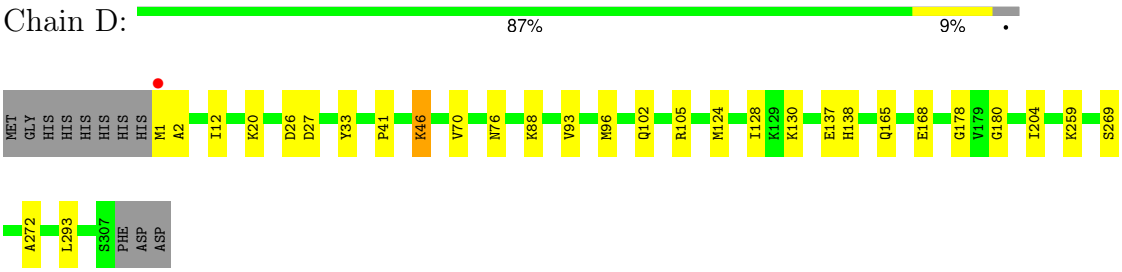
- Molecule 1: Cysteine synthase

Chain A:



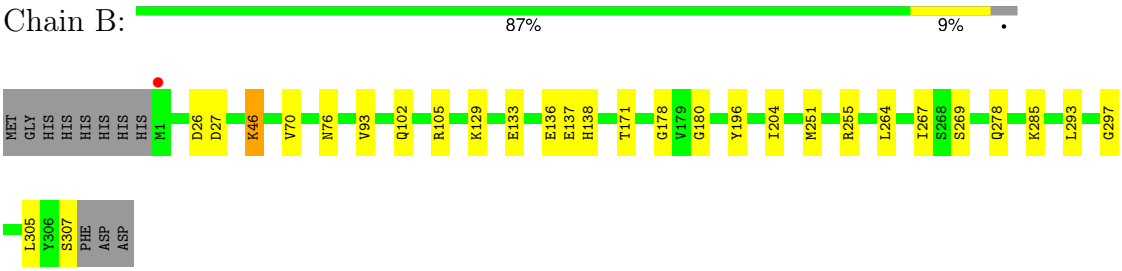
- Molecule 1: Cysteine synthase

Chain D:



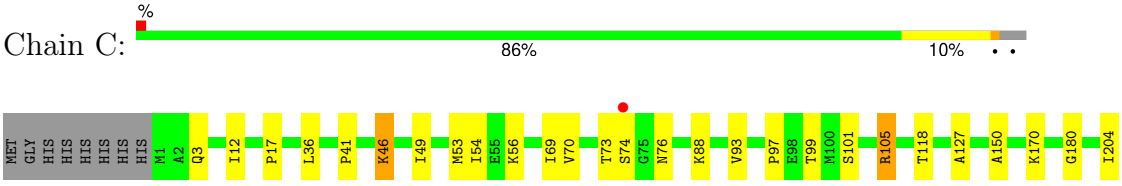
- Molecule 1: Cysteine synthase

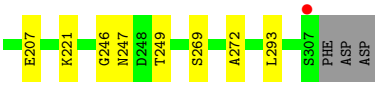
Chain B:



- Molecule 1: Cysteine synthase

Chain C:



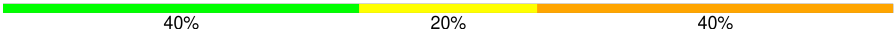


• Molecule 2: TYR-MET-NAL-TYR-ILE

Chain E:

• Molecule 2: TYR-MET-NAL-TYR-ILE

Chain F:



• Molecule 2: TYR-MET-NAL-TYR-ILE

Chain G:

• Molecule 2: TYR-MET-NAL-TYR-ILE

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	65.93Å 119.71Å 84.66Å 90.00° 98.71° 90.00°	Depositor
Resolution (Å)	39.50 – 2.15 39.50 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.50-2.15) 88.5 (39.50-2.15)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.00 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.194 , 0.235 0.194 , 0.235	Depositor DCC
R_{free} test set	3535 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	27.6	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 43.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9909	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% 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: LLP, NAL

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	0/2302	0.46	0/3115
1	B	0.25	0/2300	0.46	0/3114
1	C	0.25	0/2293	0.46	0/3104
1	D	0.26	0/2303	0.47	0/3115
2	E	0.20	0/33	0.32	0/40
2	F	0.23	0/41	0.25	0/51
2	G	0.20	0/33	0.32	0/40
2	H	0.20	0/33	0.28	0/40
All	All	0.25	0/9338	0.46	0/12619

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	2
2	F	0	2
2	G	0	2
2	H	0	2
All	All	0	8

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	2	MET	Peptide

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Mol	Chain	Res	Type	Group
2	E	3	NAL	Mainchain
2	F	2	MET	Mainchain
2	F	3	NAL	Mainchain
2	G	2	MET	Peptide

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	2289	0	2314	18	0
1	B	2287	0	2300	14	0
1	C	2280	0	2301	19	0
1	D	2290	0	2323	20	0
2	E	49	0	43	0	0
2	F	56	0	51	3	0
2	G	49	0	44	0	0
2	H	49	0	43	0	0
3	A	159	0	0	0	0
3	B	143	0	0	1	0
3	C	105	0	0	2	0
3	D	140	0	0	3	0
3	E	4	0	0	0	0
3	F	5	0	0	1	0
3	G	1	0	0	0	0
3	H	3	0	0	0	0
All	All	9909	0	9419	70	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 70 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:B:102:GLN:HA	1:B:105:ARG:HD2	1.63	0.80
1:B:267:ILE:HG13	1:B:305:LEU:HD22	1.63	0.79
1:C:207:GLU:HG2	1:C:246:GLY:HA2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1:TYR:N	3:F:101:HOH:O	2.29	0.65
1:C:221:LYS:HE2	1:C:247:ASN:HB3	1.80	0.62

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	304/318 (96%)	299 (98%)	5 (2%)	0	100	100
1	B	304/318 (96%)	299 (98%)	5 (2%)	0	100	100
1	C	304/318 (96%)	299 (98%)	5 (2%)	0	100	100
1	D	304/318 (96%)	298 (98%)	6 (2%)	0	100	100
2	E	2/5 (40%)	1 (50%)	1 (50%)	0	100	100
2	F	2/5 (40%)	2 (100%)	0	0	100	100
2	G	2/5 (40%)	1 (50%)	1 (50%)	0	100	100
2	H	2/5 (40%)	2 (100%)	0	0	100	100
All	All	1224/1292 (95%)	1201 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	237/251 (94%)	230 (97%)	7 (3%)	36 37
1	B	236/251 (94%)	231 (98%)	5 (2%)	48 53
1	C	234/251 (93%)	229 (98%)	5 (2%)	48 53
1	D	237/251 (94%)	234 (99%)	3 (1%)	65 71
2	E	3/4 (75%)	3 (100%)	0	100 100
2	F	4/4 (100%)	3 (75%)	1 (25%)	0 0
2	G	3/4 (75%)	3 (100%)	0	100 100
2	H	3/4 (75%)	3 (100%)	0	100 100
All	All	957/1020 (94%)	936 (98%)	21 (2%)	47 51

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	307	SER
1	C	105	ARG
2	F	2	MET
1	C	170	LYS
1	C	74	SER

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

Mol	Chain	Res	Type
1	A	165	GLN
1	B	102	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)

8 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	NAL	G	3	2	15,16,17	0.98	0	16,21,23	0.63	0
2	NAL	H	3	2	15,16,17	0.98	0	16,21,23	0.74	0
1	LLP	A	46	1	23,24,25	2.47	6 (26%)	25,32,34	1.31	3 (12%)
2	NAL	F	3	2	15,16,17	0.97	0	16,21,23	0.70	0
2	NAL	E	3	2	15,16,17	0.98	0	16,21,23	0.67	0
1	LLP	C	46	1	23,24,25	2.46	6 (26%)	25,32,34	1.29	3 (12%)
1	LLP	B	46	1	23,24,25	2.47	6 (26%)	25,32,34	1.24	3 (12%)
1	LLP	D	46	1	23,24,25	2.46	6 (26%)	25,32,34	1.30	4 (16%)

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	NAL	G	3	2	-	0/5/6/8	0/2/2/2
2	NAL	H	3	2	-	1/5/6/8	0/2/2/2
1	LLP	A	46	1	-	2/16/17/19	0/1/1/1
2	NAL	F	3	2	-	0/5/6/8	0/2/2/2
2	NAL	E	3	2	-	0/5/6/8	0/2/2/2
1	LLP	C	46	1	-	3/16/17/19	0/1/1/1
1	LLP	B	46	1	-	3/16/17/19	0/1/1/1
1	LLP	D	46	1	-	0/16/17/19	0/1/1/1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	46	LLP	C4-C4'	7.27	1.62	1.46
1	B	46	LLP	C4-C4'	7.24	1.62	1.46
1	A	46	LLP	C4-C4'	7.21	1.62	1.46
1	C	46	LLP	C4-C4'	7.19	1.61	1.46
1	D	46	LLP	C4'-NZ	4.91	1.43	1.27

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	46	LLP	CE-NZ-C4'	-3.35	107.99	118.72
1	C	46	LLP	CE-NZ-C4'	-3.16	108.59	118.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	46	LLP	CE-NZ-C4'	-3.04	108.98	118.72
1	B	46	LLP	C4-C4'-NZ	-3.03	110.05	124.04
1	B	46	LLP	CE-NZ-C4'	-2.99	109.15	118.72

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	3	NAL	O-C-CA-C9
1	B	46	LLP	CA-CB-CG-CD
1	C	46	LLP	C3-C4-C4'-NZ
1	A	46	LLP	CG-CD-CE-NZ
1	C	46	LLP	CG-CD-CE-NZ

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	46	LLP	2	0
2	F	3	NAL	2	0
1	C	46	LLP	2	0
1	B	46	LLP	3	0
1	D	46	LLP	4	0

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

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	306/318 (96%)	-0.10	1 (0%) 90 92	22, 31, 46, 70	0
1	B	306/318 (96%)	-0.08	1 (0%) 90 92	22, 32, 46, 70	0
1	C	306/318 (96%)	0.21	2 (0%) 84 86	27, 38, 51, 64	0
1	D	306/318 (96%)	0.04	1 (0%) 90 92	25, 35, 48, 66	0
2	E	4/5 (80%)	0.72	1 (25%) 2 3	32, 33, 37, 48	0
2	F	4/5 (80%)	0.54	0 100 100	34, 36, 38, 38	1 (25%)
2	G	4/5 (80%)	0.88	0 100 100	29, 32, 44, 51	1 (25%)
2	H	4/5 (80%)	1.59	1 (25%) 2 3	41, 41, 45, 55	0
All	All	1240/1292 (95%)	0.03	7 (0%) 85 87	22, 34, 49, 70	2 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	1	TYR	4.9
1	A	1	MET	2.9
2	E	1	TYR	2.7
1	D	1	MET	2.6
1	C	307	SER	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

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
2	NAL	E	3	15/16	0.84	0.12	28,33,36,36	15

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAL	G	3	15/16	0.84	0.12	30,35,38,39	0
2	NAL	F	3	15/16	0.89	0.11	30,34,38,39	0
2	NAL	H	3	15/16	0.89	0.11	39,42,46,47	0
1	LLP	D	46	24/25	0.94	0.08	25,30,34,36	0
1	LLP	B	46	24/25	0.96	0.07	21,26,29,31	0
1	LLP	C	46	24/25	0.96	0.07	29,31,34,35	0
1	LLP	A	46	24/25	0.96	0.07	22,26,29,30	0

6.3 Carbohydrates (i)

There are no monosaccharides 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.