



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:30 pm BST

PDB ID : 4HSN
Title : Crystal structure of DAH7PS from *Neisseria meningitidis*
Authors : Cross, P.J.; Pietersma, A.L.; Allison, T.M.; Wilson-Coutts, S.M.; Cochrane, F.C.; Parker, E.J.
Deposited on : 2012-10-30
Resolution : 2.00 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

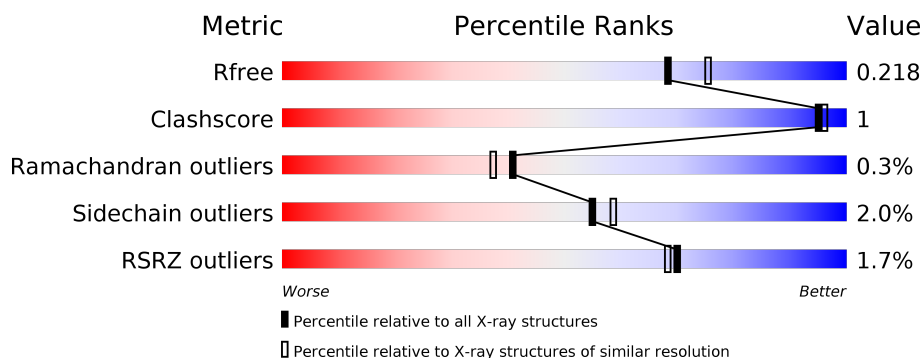
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	351	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>•</div> </div> </div>
1	B	351	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div>•</div> </div> </div>
1	C	351	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div>•</div> </div> </div>
1	D	351	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>•</div> <div>•</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11063 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 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2614	1637	470	493	14			
1	B	341	Total	C	N	O	S	0	1	0
			2608	1635	469	490	14			
1	C	341	Total	C	N	O	S	0	0	0
			2610	1635	471	490	14			
1	D	341	Total	C	N	O	S	0	0	0
			2606	1634	465	493	14			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

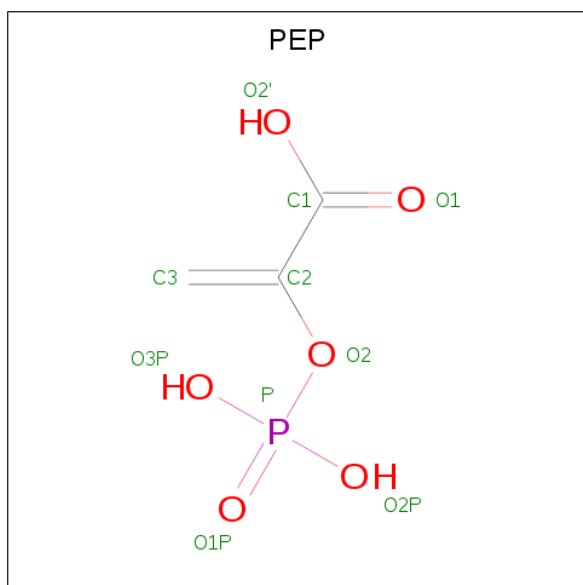
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is PHOSPHOENOLPYRUVATE (three-letter code: PEP) (formula: $C_3H_5O_6P$).

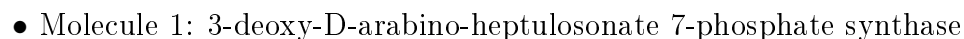
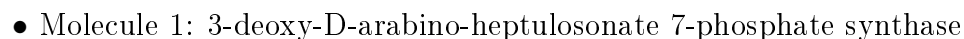
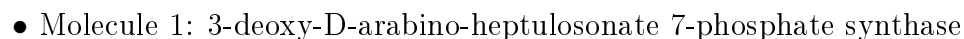


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			10	3	6	1		
4	B	1	Total	C	O	P	0	0
			10	3	6	1		
4	C	1	Total	C	O	P	0	0
			10	3	6	1		
4	D	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	179	Total	O	0	0
			179	179		
5	B	150	Total	O	0	0
			150	150		
5	C	125	Total	O	0	0
			125	125		
5	D	107	Total	O	0	0
			107	107		

- Molecule 1: 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.46 Å 137.28 Å 76.36 Å 90.00° 96.42° 90.00°	Depositor
Resolution (Å)	19.79 – 2.00 19.65 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.79-2.00) 99.3 (19.65-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.01 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.175 , 0.208 0.181 , 0.218	Depositor DCC
R_{free} test set	6233 reflections (6.20%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11063	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, PEP, SO4

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	1.01	0/2662	0.94	8/3601 (0.2%)
1	B	0.95	0/2659	0.90	3/3597 (0.1%)
1	C	0.93	1/2658 (0.0%)	0.91	3/3596 (0.1%)
1	D	0.90	1/2654 (0.0%)	0.87	1/3591 (0.0%)
All	All	0.95	2/10633 (0.0%)	0.90	15/14385 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	76	GLU	CD-OE2	5.68	1.31	1.25
1	C	27	GLU	CD-OE2	-5.50	1.19	1.25

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	304	GLU	OE1-CD-OE2	-8.14	113.53	123.30
1	B	40	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	A	33	GLU	OE1-CD-OE2	-5.87	116.26	123.30
1	A	262	ASP	CB-CG-OD1	5.67	123.41	118.30
1	A	279	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	C	236	ARG	NE-CZ-NH2	5.55	123.07	120.30
1	A	236	ARG	NE-CZ-NH2	5.37	122.99	120.30
1	A	346	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	304	GLU	CG-CD-OE2	5.33	128.96	118.30
1	C	346	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	167	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	C	262	ASP	CB-CG-OD1	5.05	122.85	118.30
1	D	12	ILE	CG1-CB-CG2	-5.04	100.30	111.40
1	A	94	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	A	44	GLU	OE1-CD-OE2	-5.00	117.30	123.30

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	2614	0	2601	8	0
1	B	2608	0	2594	11	0
1	C	2610	0	2599	6	0
1	D	2606	0	2590	4	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	10	0	2	0	0
4	B	10	0	2	0	0
4	C	10	0	2	2	0
4	D	10	0	2	1	0
5	A	179	0	0	0	0
5	B	150	0	0	2	0
5	C	125	0	0	3	0
5	D	107	0	0	1	0
All	All	11063	0	10392	26	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 (26) 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:276:ASP:OD2	1:B:278:THR:OG1	2.00	0.79
1:B:80:LYS:HD3	5:B:562:HOH:O	1.86	0.74
1:C:11:LYS:HD2	1:D:181:LEU:O	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:403:PEP:O1	5:D:557:HOH:O	2.17	0.59
1:A:181:LEU:O	1:B:11:LYS:HD2	2.02	0.58
4:C:403:PEP:O1	5:C:585:HOH:O	2.17	0.57
4:C:403:PEP:C2	5:C:625:HOH:O	2.57	0.51
1:A:228:ASN:HA	1:B:11:LYS:HE2	1.93	0.51
1:C:317:VAL:CG1	1:C:320:LYS:CB	2.89	0.51
1:C:317:VAL:HG13	1:C:320:LYS:CB	2.42	0.49
1:D:14:GLU:CD	1:D:16:LYS:HE3	2.34	0.48
1:B:80:LYS:NZ	1:B:333:GLU:OE2	2.48	0.46
1:A:12:ILE:HD12	1:B:225:THR:HG22	1.98	0.46
1:C:167:ARG:HG2	1:D:170:GLU:HG2	1.98	0.45
1:A:25:LEU:HD23	1:A:129:ARG:CZ	2.48	0.44
1:C:25:LEU:HD23	1:C:129:ARG:CZ	2.48	0.43
1:A:312:GLN:O	1:A:322:ILE:HA	2.19	0.42
1:B:11:LYS:NZ	5:B:605:HOH:O	2.39	0.42
1:B:264:LEU:HD12	1:B:264:LEU:C	2.40	0.42
1:A:185:VAL:O	1:A:231:CYS:HA	2.19	0.42
1:B:349:ARG:O	1:B:350:ALA:C	2.57	0.42
1:C:153:GLN:HG3	5:C:587:HOH:O	2.20	0.42
1:A:222:ILE:HB	1:B:16:LYS:HB2	2.01	0.41
1:D:151:THR:N	1:D:152:PRO:CD	2.84	0.41
1:B:185:VAL:O	1:B:231:CYS:HA	2.21	0.40
1:A:151:THR:N	1:A:152:PRO:CD	2.85	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	339/351 (97%)	333 (98%)	5 (2%)	1 (0%)	41 37
1	B	340/351 (97%)	332 (98%)	7 (2%)	1 (0%)	41 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	339/351 (97%)	330 (97%)	8 (2%)	1 (0%)	41	37
1	D	339/351 (97%)	329 (97%)	9 (3%)	1 (0%)	41	37
All	All	1357/1404 (97%)	1324 (98%)	29 (2%)	4 (0%)	41	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	ASP
1	C	294	ASP
1	D	294	ASP
1	B	294	ASP

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	275/289 (95%)	270 (98%)	5 (2%)	59	63
1	B	273/289 (94%)	266 (97%)	7 (3%)	46	48
1	C	274/289 (95%)	267 (97%)	7 (3%)	46	48
1	D	274/289 (95%)	270 (98%)	4 (2%)	65	69
All	All	1096/1156 (95%)	1073 (98%)	23 (2%)	55	57

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LYS
1	A	189	ASN
1	A	233	VAL
1	A	236	ARG
1	A	306	HIS
1	B	17[A]	GLU
1	B	17[B]	GLU
1	B	43	GLN

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Mol	Chain	Res	Type
1	B	189	ASN
1	B	233	VAL
1	B	236	ARG
1	B	306	HIS
1	C	17	GLU
1	C	189	ASN
1	C	233	VAL
1	C	236	ARG
1	C	240	GLU
1	C	274	ARG
1	C	306	HIS
1	D	17	GLU
1	D	189	ASN
1	D	233	VAL
1	D	236	ARG

Some 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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	A	402	-	4,4,4	0.52	0	6,6,6	0.23	0
3	SO4	B	402	-	4,4,4	0.51	0	6,6,6	0.47	0
3	SO4	D	402	-	4,4,4	0.41	0	6,6,6	0.69	0
4	PEP	D	403	2	6,9,9	1.18	1 (16%)	8,13,13	1.34	1 (12%)
4	PEP	C	403	2	6,9,9	2.18	2 (33%)	8,13,13	1.68	3 (37%)
4	PEP	B	403	-	6,9,9	1.73	2 (33%)	8,13,13	2.18	2 (25%)
4	PEP	A	403	-	6,9,9	1.15	1 (16%)	8,13,13	2.29	3 (37%)
3	SO4	C	402	-	4,4,4	0.36	0	6,6,6	0.35	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	PEP	B	403	-	-	0/5/9/9	-
4	PEP	A	403	-	-	0/5/9/9	-
4	PEP	D	403	2	-	0/5/9/9	-
4	PEP	C	403	2	-	0/5/9/9	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	403	PEP	P-O2	3.93	1.65	1.59
4	C	403	PEP	O2-C2	3.28	1.48	1.39
4	B	403	PEP	O2-C2	2.93	1.47	1.39
4	A	403	PEP	O2-C2	2.40	1.45	1.39
4	B	403	PEP	P-O2	2.26	1.62	1.59
4	D	403	PEP	O2-C2	2.14	1.45	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	403	PEP	O2P-P-O1P	3.95	126.15	110.68
4	A	403	PEP	O2-P-O1P	-3.93	95.34	109.32
4	B	403	PEP	O2-P-O1P	-3.55	96.69	109.32
4	A	403	PEP	O2P-P-O1P	3.35	123.80	110.68
4	C	403	PEP	O2P-P-O1P	2.58	120.77	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	403	PEP	O2-P-O1P	-2.56	100.23	109.32
4	A	403	PEP	O3P-P-O1P	2.41	120.10	110.68
4	D	403	PEP	O3P-P-O2P	2.26	116.28	107.64
4	C	403	PEP	O3P-P-O1P	2.22	119.37	110.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	403	PEP	1	0
4	C	403	PEP	2	0

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	341/351 (97%)	-0.37	4 (1%) 79 78	21, 30, 47, 85	0
1	B	341/351 (97%)	-0.17	8 (2%) 60 59	23, 35, 52, 100	0
1	C	341/351 (97%)	-0.23	8 (2%) 60 59	23, 36, 55, 103	0
1	D	341/351 (97%)	-0.13	3 (0%) 84 83	28, 39, 55, 87	0
All	All	1364/1404 (97%)	-0.22	23 (1%) 70 68	21, 35, 53, 103	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	ILE	11.9
1	A	10	ILE	8.7
1	C	350	ALA	8.3
1	C	10	ILE	8.1
1	D	350	ALA	7.1
1	A	350	ALA	6.7
1	B	12	ILE	5.7
1	D	10	ILE	5.0
1	B	350	ALA	4.1
1	C	12	ILE	4.0
1	C	11	LYS	3.2
1	C	257	ALA	3.0
1	B	348	ALA	2.8
1	C	13	LYS	2.7
1	A	348	ALA	2.5
1	B	316	GLU	2.5
1	D	316	GLU	2.4
1	C	293	GLN	2.3
1	B	14	GLU	2.3
1	B	13	LYS	2.2
1	C	15	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	246	GLU	2.0
1	B	11	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no 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. 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(\AA^2)	Q<0.9
3	SO4	B	402	5/5	0.65	0.29	72,76,105,106	0
3	SO4	A	402	5/5	0.85	0.28	66,92,99,102	0
4	PEP	B	403	10/10	0.86	0.19	30,41,46,56	10
4	PEP	C	403	10/10	0.89	0.17	33,45,54,56	10
3	SO4	C	402	5/5	0.91	0.28	83,86,96,97	0
4	PEP	A	403	10/10	0.96	0.11	23,37,46,47	10
3	SO4	D	402	5/5	0.96	0.26	65,71,74,75	0
4	PEP	D	403	10/10	0.96	0.09	25,32,39,39	10
2	MN	C	401	1/1	0.97	0.05	41,41,41,41	0
2	MN	D	401	1/1	0.98	0.04	37,37,37,37	0
2	MN	A	401	1/1	0.99	0.06	26,26,26,26	0
2	MN	B	401	1/1	1.00	0.03	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.