



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 07:02 AM GMT

PDB ID : 2O7S
Title : Crystal Structure of the A. thaliana DHQ-dehydroshikimate-SDH-shikimate-NADP(H)
Authors : Christendat, D.; Singh, S.A.
Deposited on : 2006-12-11
Resolution : 1.78 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

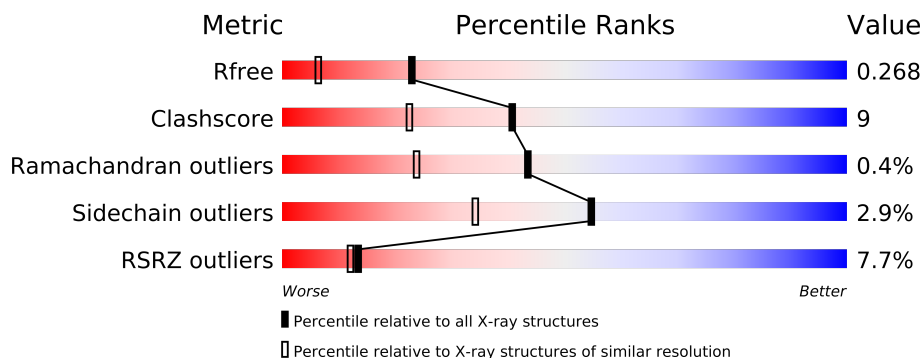
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.78 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}	66092	4987 (1.80-1.76)
Clashscore	79885	6152 (1.80-1.76)
Ramachandran outliers	78287	6074 (1.80-1.76)
Sidechain outliers	78261	6073 (1.80-1.76)
RSRZ outliers	66119	4990 (1.80-1.76)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	523	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	A	1403	-	X
3	DHK	A	9241[A]	-	X
4	TLA	A	1241[B]	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4150 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Bifunctional 3-dehydroquinase dehydratase/shikimate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	1	0
			3859	2452	645	745	17			

There are 11 discrepancies between the modelled and reference sequences:

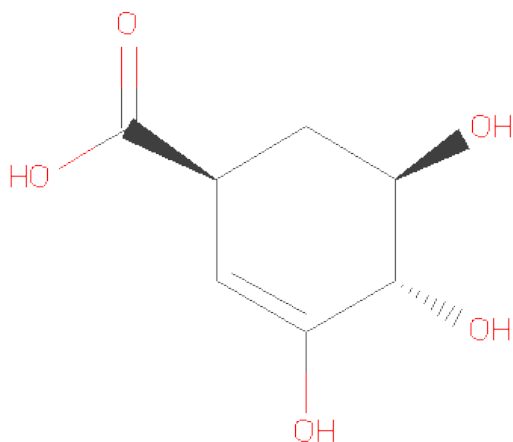
Chain	Residue	Modelled	Actual	Comment	Reference
A	391	CSO	CYS	MODIFIED RESIDUE	UNP Q9SQT8
A	424	CSO	CYS	MODIFIED RESIDUE	UNP Q9SQT8
A	604	GLY	-	EXPRESSION TAG	UNP Q9SQT8
A	605	SER	-	EXPRESSION TAG	UNP Q9SQT8
A	606	ARG	-	EXPRESSION TAG	UNP Q9SQT8
A	607	GLU	-	EXPRESSION TAG	UNP Q9SQT8
A	608	ASN	-	EXPRESSION TAG	UNP Q9SQT8
A	609	LEU	-	EXPRESSION TAG	UNP Q9SQT8
A	610	TYR	-	EXPRESSION TAG	UNP Q9SQT8
A	611	PHE	-	EXPRESSION TAG	UNP Q9SQT8
A	612	GLN	-	EXPRESSION TAG	UNP Q9SQT8

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



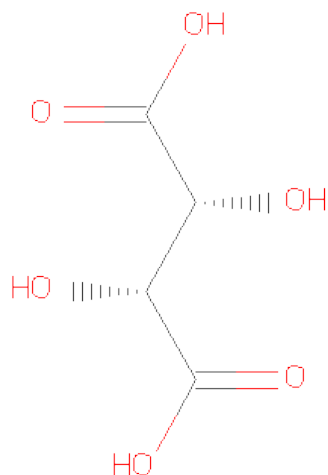
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 3-DEHYDROSHIKIMATE (three-letter code: DHK) (formula: C₇H₁₀O₅).



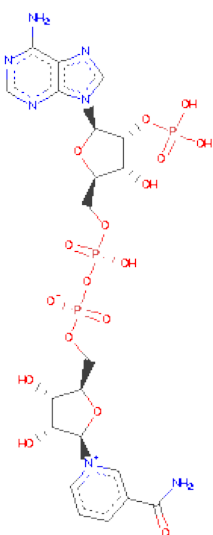
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			11	7	4		
3	A	1	Total	C	O	0	0
			12	7	5		

- Molecule 4 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	1
			10	4	6		

- Molecule 5 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O P	0	0
			48	21	7	17 3		

- Molecule 6 is water.

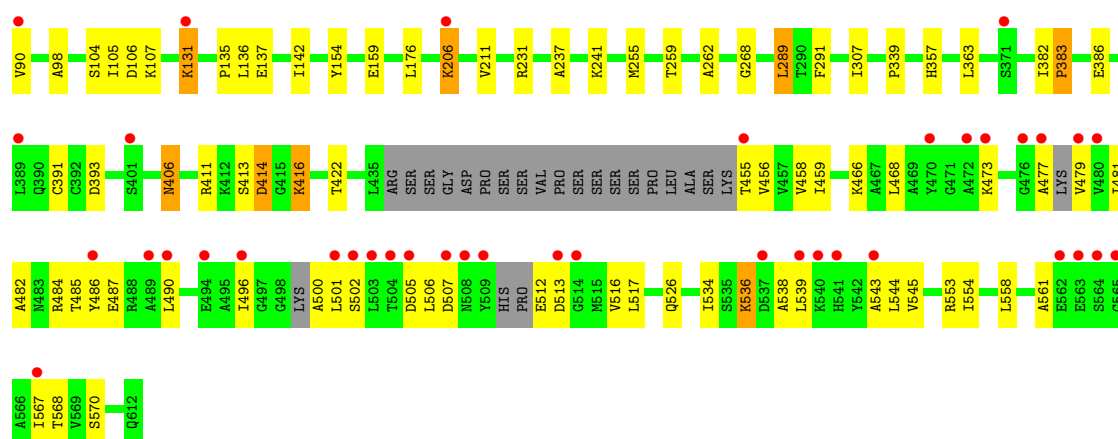
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	205	Total 205	O 205	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.45Å 97.45Å 116.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.78 44.95 – 1.78	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.78) 91.9 (44.95-1.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 1.78Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.269 , 0.233 0.234 , 0.268	Depositor DCC
R_{free} test set	2894 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.4	EDS
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 61461 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4150	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TLA, CSO, DHK, NAP, 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	0.32	0/3910	0.60	1/5282 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	289	LEU	CA-CB-CG	5.15	127.14	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3859	0	3877	73	0
2	A	5	0	0	0	0
3	A	23	0	15	1	0
4	A	10	0	4	1	0
5	A	48	0	25	1	0
6	A	205	0	0	6	0
All	All	4150	0	3921	73	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (73) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:MET:HE1	1:A:268:GLY:HA3	1.50	0.93
1:A:545:VAL:HG11	1:A:561:ALA:HB1	1.53	0.90
1:A:411:ARG:NH2	1:A:416:LYS:HD2	1.95	0.82
1:A:105:ILE:HD11	1:A:142:ILE:HG13	1.65	0.79
1:A:411:ARG:HH21	1:A:416:LYS:HD2	1.49	0.77
1:A:545:VAL:HG11	1:A:561:ALA:CB	2.14	0.77
1:A:241[B]:LYS:NZ	4:A:1241[B]:TLA:O1	2.23	0.70
1:A:544:LEU:HD23	1:A:545:VAL:N	2.11	0.65
1:A:255:MET:O	1:A:255:MET:HE3	1.96	0.64
1:A:206:LYS:H	1:A:206:LYS:HD3	1.61	0.64
1:A:416:LYS:HB3	1:A:416:LYS:NZ	2.15	0.62
1:A:414:ASP:OD1	1:A:416:LYS:HG2	2.00	0.61
1:A:455:THR:HG21	1:A:512:GLU:OE2	2.02	0.60
1:A:459:ILE:HD11	1:A:517:LEU:HD11	1.84	0.59
1:A:406:ASN:HD21	1:A:422:THR:H	1.49	0.59
1:A:553:ARG:HD2	6:A:9337:HOH:O	2.02	0.59
1:A:255:MET:CE	1:A:268:GLY:HA3	2.30	0.58
1:A:231:ARG:HD3	6:A:9347:HOH:O	2.03	0.57
1:A:543:ALA:O	1:A:567:ILE:HG22	2.04	0.56
1:A:502:SER:HB3	1:A:505:ASP:OD1	2.07	0.55
1:A:482:ALA:HA	1:A:501:LEU:O	2.06	0.55
1:A:501:LEU:HD23	1:A:502:SER:N	2.21	0.54
1:A:104:SER:OG	1:A:107:LYS:HD3	2.08	0.54
1:A:485:THR:HG22	1:A:487:GLU:HG3	1.89	0.54
1:A:363:LEU:HD12	1:A:391:CSO:SG	2.48	0.54
1:A:131:LYS:HA	1:A:131:LYS:HE3	1.90	0.54
1:A:255:MET:HE1	1:A:259:THR:HG23	1.90	0.53
1:A:131:LYS:HE3	1:A:131:LYS:O	2.08	0.53
1:A:490:LEU:HA	1:A:500:ALA:HB2	1.89	0.53
1:A:484:ARG:HD2	5:A:1411:NAP:O2X	2.09	0.53
1:A:416:LYS:HB3	1:A:416:LYS:HZ3	1.74	0.53
1:A:90:VAL:HB	6:A:9282:HOH:O	2.08	0.53
1:A:291:PHE:CE1	3:A:9241[A]:DHK:H6C1	2.45	0.52
1:A:231:ARG:HG3	6:A:9396:HOH:O	2.11	0.51
1:A:255:MET:CE	1:A:259:THR:HG23	2.41	0.51
1:A:486:TYR:HA	6:A:9378:HOH:O	2.09	0.51
1:A:456:VAL:HA	1:A:516:VAL:HG13	1.93	0.50
1:A:137:GLU:N	1:A:137:GLU:OE1	2.41	0.49
1:A:516:VAL:HG23	1:A:544:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:544:LEU:C	1:A:544:LEU:HD23	2.33	0.49
1:A:473:LYS:HD2	1:A:496:ILE:O	2.13	0.49
1:A:526:GLN:NE2	6:A:9414:HOH:O	2.46	0.49
1:A:131:LYS:HE3	1:A:131:LYS:CA	2.43	0.48
1:A:98:ALA:HB2	1:A:307:ILE:HD11	1.95	0.48
1:A:206:LYS:HD3	1:A:206:LYS:N	2.27	0.48
1:A:456:VAL:HG22	1:A:516:VAL:HG11	1.96	0.48
1:A:458:VAL:HB	1:A:481:ILE:HD13	1.96	0.47
1:A:406:ASN:ND2	1:A:422:THR:H	2.12	0.47
1:A:539:LEU:HD13	1:A:561:ALA:HA	1.95	0.47
1:A:544:LEU:HG	1:A:567:ILE:HG23	1.96	0.47
1:A:553:ARG:NH1	1:A:554:ILE:HD11	2.30	0.46
1:A:105:ILE:HG23	1:A:106:ASP:N	2.30	0.46
1:A:473:LYS:HD2	1:A:496:ILE:HB	1.97	0.46
1:A:105:ILE:HD11	1:A:142:ILE:CG1	2.40	0.46
1:A:159:GLU:HG3	1:A:159:GLU:O	2.16	0.46
1:A:363:LEU:C	1:A:363:LEU:HD13	2.36	0.46
1:A:468:LEU:O	1:A:468:LEU:HD23	2.16	0.45
1:A:339:PRO:HG2	1:A:357:HIS:CE1	2.51	0.45
1:A:393:ASP:OD2	1:A:416:LYS:HB2	2.16	0.45
1:A:411:ARG:HH21	1:A:416:LYS:CD	2.25	0.45
1:A:211:VAL:CG2	1:A:237:ALA:HB2	2.46	0.45
1:A:506:LEU:HG	1:A:534:ILE:HD12	1.98	0.45
1:A:386:GLU:OE2	1:A:466:LYS:HE2	2.17	0.44
1:A:558:LEU:HD11	1:A:570:SER:HA	2.00	0.43
1:A:545:VAL:HG13	1:A:568:THR:HG22	2.01	0.43
1:A:477:ALA:O	1:A:479:VAL:HG13	2.19	0.42
1:A:507:ASP:O	1:A:538:ALA:HB2	2.20	0.42
1:A:477:ALA:C	1:A:479:VAL:HG13	2.40	0.41
1:A:536:LYS:HA	1:A:539:LEU:HG	2.03	0.41
1:A:406:ASN:H	1:A:406:ASN:HD22	1.68	0.41
1:A:90:VAL:HG21	1:A:262:ALA:O	2.20	0.41
1:A:255:MET:HE1	1:A:259:THR:CG2	2.51	0.40
1:A:382:ILE:HA	1:A:383:PRO:HA	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	489/523 (94%)	471 (96%)	16 (3%)	2 (0%)	43 24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	413	SER
1	A	135	PRO

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	417/437 (95%)	405 (97%)	12 (3%)	55 34

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	136	LEU
1	A	154	TYR
1	A	176	LEU
1	A	206	LYS
1	A	289	LEU
1	A	383	PRO
1	A	406	ASN
1	A	414	ASP
1	A	416	LYS
1	A	513	ASP
1	A	536	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	A	190	GLN
1	A	234	GLN
1	A	263	GLN
1	A	315	ASN
1	A	368	GLN
1	A	406	ASN
1	A	526	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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	$\# Z > 2$
1	CSO	A	391	1	6,6,7	7.17	3 (50%)	3,6,8	1.04	0
1	CSO	A	424	1	6,6,7	7.51	2 (33%)	3,6,8	0.94	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
1	CSO	A	391	1	-	0/2/5/7	0/0/0/0
1	CSO	A	424	1	-	0/2/5/7	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	424	CSO	O-C	18.15	1.23	1.11
1	A	391	CSO	O-C	17.21	1.23	1.11
1	A	391	CSO	CA-C	2.66	1.53	1.48
1	A	391	CSO	OD-SG	-2.22	1.53	1.62
1	A	424	CSO	CA-C	2.13	1.52	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

5 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	TLA	A	1241[B]	-	9,9,9	0.80	0	12,12,12	1.16	1 (8%)
2	SO4	A	1403	-	4,4,4	0.27	0	6,6,6	0.06	0
5	NAP	A	1411	-	52,52,52	2.02	12 (23%)	80,80,80	2.44	25 (31%)
3	DHK	A	4733	-	12,12,12	3.85	5 (41%)	17,17,17	3.20	6 (35%)
3	DHK	A	9241[A]	1	11,11,12	4.17	6 (54%)	11,15,17	4.26	6 (54%)

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	TLA	A	1241[B]	-	-	0/12/12/12	0/0/0/0
2	SO4	A	1403	-	-	0/0/0/0	0/0/0/0
5	NAP	A	1411	-	1/1/12/12	0/35/67/67	0/3/5/5
3	DHK	A	4733	-	1/1/5/6	0/4/20/20	0/1/1/1
3	DHK	A	9241[A]	1	3/3/4/6	0/4/17/20	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	9241[A]	DHK	C2-C3	10.40	1.55	1.32
3	A	4733	DHK	C2-C3	8.49	1.51	1.32
3	A	4733	DHK	C1-C2	-7.80	1.33	1.50
3	A	9241[A]	DHK	C5-C6	-6.79	1.30	1.51
5	A	1411	NAP	C2N-N1N	5.41	1.42	1.35
5	A	1411	NAP	C5A-C4A	-5.30	1.28	1.40
5	A	1411	NAP	C2A-N3A	4.71	1.41	1.32
5	A	1411	NAP	C2A-N1A	4.33	1.42	1.33
5	A	1411	NAP	PN-O3	4.32	1.69	1.60
3	A	4733	DHK	C4-C3	3.89	1.56	1.50
3	A	9241[A]	DHK	O1-C	3.75	1.35	1.22
3	A	4733	DHK	O1-C	3.52	1.34	1.22
5	A	1411	NAP	C2N-C3N	3.26	1.43	1.38
5	A	1411	NAP	C4A-N3A	3.20	1.40	1.35
5	A	1411	NAP	C8A-N9A	3.19	1.41	1.36
5	A	1411	NAP	O4D-C1D	2.93	1.45	1.41
5	A	1411	NAP	C4N-C3N	2.84	1.44	1.39
3	A	9241[A]	DHK	O3-C3	2.77	1.44	1.32
5	A	1411	NAP	C6N-N1N	2.74	1.43	1.35
3	A	4733	DHK	O3-C3	2.64	1.43	1.32
3	A	9241[A]	DHK	O2-C	-2.54	1.21	1.30
5	A	1411	NAP	P2B-O2X	-2.51	1.45	1.54
3	A	9241[A]	DHK	C4-C3	2.06	1.55	1.50

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	9241[A]	DHK	C4-C3-C2	-12.57	110.87	123.47
5	A	1411	NAP	N3A-C2A-N1A	-10.30	120.09	128.71
3	A	4733	DHK	C4-C3-C2	-9.73	113.72	123.47
5	A	1411	NAP	O3B-C3B-C2B	6.50	130.34	111.20
5	A	1411	NAP	P2B-O2B-C2B	-5.71	109.92	121.96
5	A	1411	NAP	O4D-C1D-N1N	5.46	113.54	107.95
3	A	4733	DHK	C6-C1-C2	5.26	123.22	107.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1411	NAP	C8A-N9A-C4A	-4.27	103.64	106.90
5	A	1411	NAP	O3-PA-O1A	-4.24	80.84	111.28
5	A	1411	NAP	O3-PA-O5B	-4.10	85.08	103.41
3	A	4733	DHK	O3-C3-C2	-3.89	108.54	121.97
5	A	1411	NAP	C4A-C5A-N7A	3.77	112.75	109.52
3	A	4733	DHK	C2-C1-C	3.62	118.47	110.94
3	A	9241[A]	DHK	O3-C3-C2	-3.53	109.80	121.97
5	A	1411	NAP	C5B-C4B-C3B	3.51	129.29	115.21
5	A	1411	NAP	O2A-PA-O3	-3.47	88.68	105.14
5	A	1411	NAP	C3N-C2N-N1N	-3.39	114.64	120.36
5	A	1411	NAP	PN-O3-PA	-3.34	118.59	132.95
5	A	1411	NAP	C2N-C3N-C4N	3.31	122.06	118.31
3	A	9241[A]	DHK	O4-C4-C3	-3.19	108.90	113.79
5	A	1411	NAP	O2N-PN-O1N	-3.10	109.36	118.72
3	A	4733	DHK	C6-C1-C	2.99	118.31	111.39
5	A	1411	NAP	C4B-O4B-C1B	-2.95	106.54	109.75
3	A	9241[A]	DHK	O3-C3-C4	-2.66	109.21	113.23
5	A	1411	NAP	C3D-C2D-C1D	2.63	105.03	100.91
5	A	1411	NAP	PN-O5D-C5D	-2.58	111.33	120.24
5	A	1411	NAP	C2B-C1B-N9A	2.52	123.29	113.74
5	A	1411	NAP	O4B-C1B-N9A	2.52	110.78	108.44
5	A	1411	NAP	O5B-PA-O1A	2.48	119.07	109.37
5	A	1411	NAP	O7N-C7N-N7N	-2.42	119.09	122.59
5	A	1411	NAP	C1B-N9A-C4A	2.40	130.79	126.64
3	A	4733	DHK	O3-C3-C4	-2.39	109.61	113.23
5	A	1411	NAP	C6N-N1N-C2N	2.31	124.64	122.04
3	A	9241[A]	DHK	C1-C2-C3	-2.25	109.10	121.19
5	A	1411	NAP	C3N-C7N-N7N	2.15	120.21	117.77
4	A	1241[B]	TLA	O11-C1-C2	2.08	119.95	113.89
5	A	1411	NAP	O3-PN-O5D	2.07	109.68	101.36
3	A	9241[A]	DHK	O2-C-O1	-2.06	119.42	124.07

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	9241[A]	DHK	C5
3	A	9241[A]	DHK	C1
3	A	9241[A]	DHK	C4
3	A	4733	DHK	C1
5	A	1411	NAP	C1B

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	500/523 (95%)	0.39	39 (7%) 13 12	17, 29, 56, 76	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	VAL	7.0
1	A	490	LEU	6.9
1	A	540	LYS	5.7
1	A	508	ASN	5.0
1	A	496	ILE	4.7
1	A	480	VAL	4.7
1	A	489	ALA	4.5
1	A	504	THR	3.9
1	A	514	GLY	3.9
1	A	567	ILE	3.7
1	A	455	THR	3.7
1	A	206	LYS	3.6
1	A	502	SER	3.4
1	A	513	ASP	3.4
1	A	505	ASP	3.2
1	A	494	GLU	3.0
1	A	131	LYS	2.8
1	A	389	LEU	2.8
1	A	476	GLY	2.8
1	A	539	LEU	2.8
1	A	537	ASP	2.8
1	A	541	HIS	2.7
1	A	565	GLY	2.7
1	A	479	VAL	2.7
1	A	401	SER	2.6
1	A	562	GLU	2.5
1	A	503	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	564	SER	2.4
1	A	501	LEU	2.4
1	A	543	ALA	2.3
1	A	473	LYS	2.3
1	A	507	ASP	2.2
1	A	371	SER	2.1
1	A	472	ALA	2.1
1	A	563	GLU	2.1
1	A	470	TYR	2.1
1	A	486	TYR	2.1
1	A	477	ALA	2.0
1	A	509	TYR	2.0

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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	CSO	A	391	7/8	0.11	-0.54	40,41,44,46	0
1	CSO	A	424	7/8	0.08	-0.80	26,28,32,36	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	A	1403	5/5	0.27	9.51	45,45,49,50	5

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	TLA	A	1241[B]	10/10	0.17	2.96	19,24,27,28	10
3	DHK	A	9241[A]	11/12	0.16	2.70	16,23,25,25	11
5	NAP	A	1411	48/48	0.13	0.54	27,39,52,53	0
3	DHK	A	4733	12/12	0.10	0.52	20,25,30,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.