



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 02:52 AM GMT

PDB ID : 2GPT
Title : Crystal structure of Arabidopsis Dehydroquinate dehydratase-shikimate dehydrogenase in complex with tartrate and shikimate
Authors : Singh, S.A.; Christendat, D.
Deposited on : 2006-04-18
Resolution : 1.95 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>

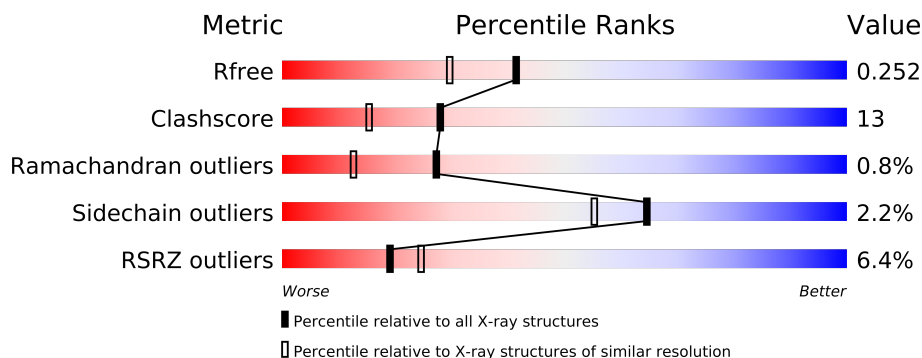
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.95 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	1321 (1.96-1.96)
Clashscore	79885	1488 (1.96-1.96)
Ramachandran outliers	78287	1475 (1.96-1.96)
Sidechain outliers	78261	1475 (1.96-1.96)
RSRZ outliers	66119	1321 (1.96-1.96)

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	1402	-	X
2	SO4	A	1403	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4143 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.

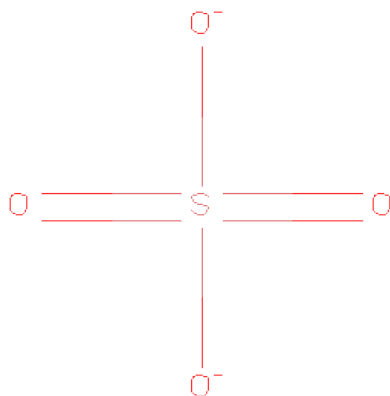
- Molecule 1 is a protein called 3-dehydroquinate dehydratase/ shikimate 5-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	498	3840	2441	642	740	17	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

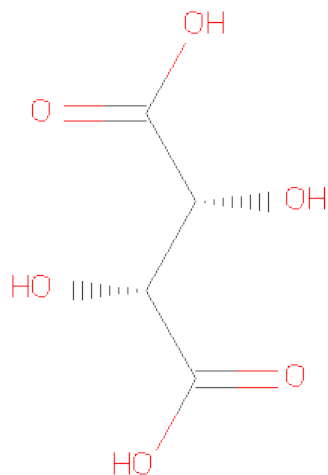
Chain	Residue	Modelled	Actual	Comment	Reference
A	604	GLY	-	CLONING ARTIFACT	UNP Q9SQT8
A	605	SER	-	CLONING ARTIFACT	UNP Q9SQT8
A	606	ARG	-	CLONING ARTIFACT	UNP Q9SQT8
A	607	GLU	-	CLONING ARTIFACT	UNP Q9SQT8
A	608	ASN	-	CLONING ARTIFACT	UNP Q9SQT8
A	609	LEU	-	CLONING ARTIFACT	UNP Q9SQT8
A	610	TYR	-	CLONING ARTIFACT	UNP Q9SQT8
A	611	PHE	-	CLONING ARTIFACT	UNP Q9SQT8
A	612	GLN	-	CLONING ARTIFACT	UNP Q9SQT8

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



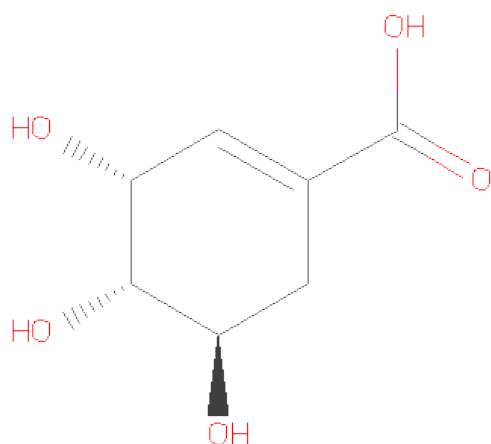
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: $C_4H_6O_6$).



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

- Molecule 4 is (3R,4S,5R)-3,4,5-TRIHYDROXYCYCLOHEX-1-ENE-1-CARBOXYLIC ACID (three-letter code: SKM) (formula: $C_7H_{10}O_5$).



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

- Molecule 5 is water.

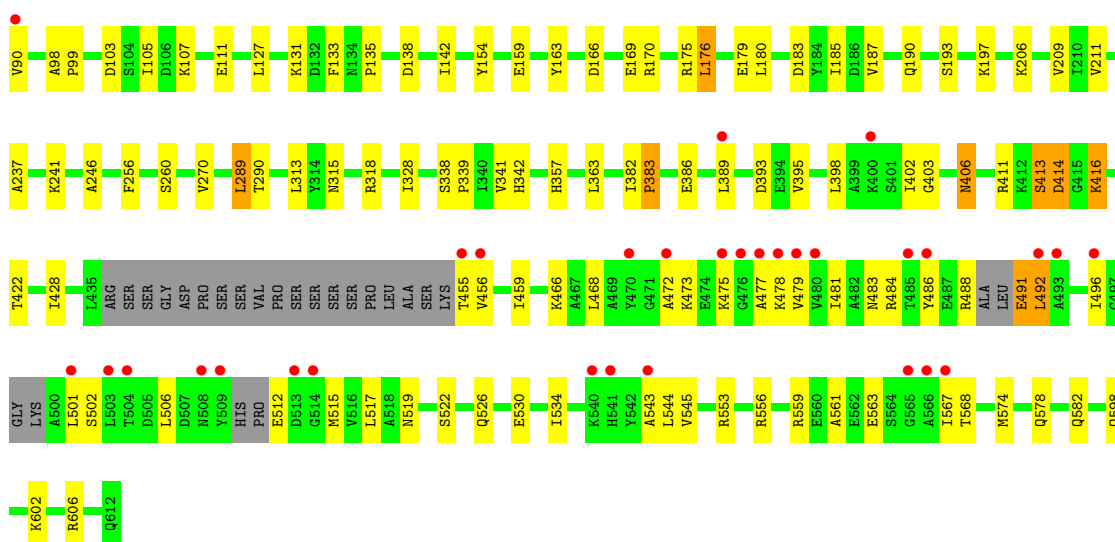
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	271	Total	O	0	0
			271	271		

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: 3-dehydroquinate dehydratase/ shikimate 5-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	96.93Å 96.93Å 116.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.46 – 1.95 39.48 – 1.95	Depositor EDS
% Data completeness (in resolution range)	94.4 (28.46-1.95) 66.9 (39.48-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 1.95Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.256 0.219 , 0.252	Depositor DCC
R_{free} test set	936 reflections (3.01%)	DCC
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.6	EDS
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 32328 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4143	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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: SKM, TLA, 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	0.33	0/3907	0.60	0/5281

There are no bond length outliers.

There are no bond angle outliers.

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	3840	0	3861	98	0
2	A	10	0	0	1	0
3	A	10	0	4	0	0
4	A	12	0	9	1	0
5	A	271	0	0	10	0
All	All	4143	0	3874	98	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 13.

All (98) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:103:ASP:HB2	1:A:131:LYS:HG2	1.47	0.96
1:A:481:ILE:HG13	1:A:492:LEU:HD12	1.53	0.90
1:A:411:ARG:HH21	1:A:416:LYS:HD2	1.38	0.89
1:A:411:ARG:NH2	1:A:416:LYS:HD2	1.88	0.88
1:A:545:VAL:HG11	1:A:561:ALA:HB1	1.59	0.84
1:A:456:VAL:HB	1:A:479:VAL:HG12	1.63	0.80
1:A:428:ILE:HG21	1:A:475:LYS:HD2	1.63	0.80
1:A:105:ILE:HD11	1:A:142:ILE:HG13	1.69	0.75
1:A:473:LYS:HD2	1:A:496:ILE:HB	1.70	0.73
1:A:545:VAL:HG11	1:A:561:ALA:CB	2.19	0.71
1:A:416:LYS:HB3	1:A:416:LYS:NZ	2.07	0.69
1:A:105:ILE:HG22	5:A:5247:HOH:O	1.93	0.68
1:A:543:ALA:O	1:A:567:ILE:HG22	1.92	0.68
1:A:393:ASP:OD2	1:A:416:LYS:HB2	1.95	0.67
1:A:556:ARG:HG3	1:A:559:ARG:NH2	2.10	0.67
1:A:206:LYS:HG3	5:A:5199:HOH:O	1.94	0.66
1:A:456:VAL:HB	1:A:479:VAL:CG1	2.27	0.64
1:A:175:ARG:O	1:A:179:GLU:HG2	1.98	0.64
1:A:166:ASP:OD2	1:A:169:GLU:HG3	1.98	0.63
1:A:501:LEU:HD23	1:A:502:SER:N	2.14	0.62
1:A:544:LEU:HD23	1:A:545:VAL:N	2.14	0.62
1:A:105:ILE:HD11	1:A:142:ILE:CG1	2.31	0.60
1:A:459:ILE:HD11	1:A:517:LEU:HD11	1.83	0.60
1:A:473:LYS:HG3	1:A:478:LYS:NZ	2.16	0.60
1:A:559:ARG:O	1:A:563:GLU:HG3	2.02	0.60
1:A:386:GLU:HG3	1:A:466:LYS:HZ2	1.69	0.58
1:A:506:LEU:HG	1:A:534:ILE:HD12	1.87	0.57
1:A:190:GLN:HA	1:A:190:GLN:HE21	1.69	0.57
1:A:414:ASP:OD1	1:A:416:LYS:HG2	2.06	0.56
1:A:406:ASN:HD21	1:A:422:THR:H	1.54	0.56
1:A:414:ASP:OD2	1:A:416:LYS:HE2	2.05	0.56
1:A:416:LYS:HB3	1:A:416:LYS:HZ3	1.70	0.55
1:A:598:GLN:NE2	5:A:5139:HOH:O	2.39	0.54
1:A:185:ILE:HD11	1:A:209:VAL:HG13	1.91	0.52
1:A:159:GLU:HG3	1:A:159:GLU:O	2.10	0.52
1:A:211:VAL:CG2	1:A:237:ALA:HB2	2.39	0.52
1:A:246:ALA:HB2	1:A:270:VAL:CG1	2.39	0.52
1:A:183:ASP:HA	5:A:5199:HOH:O	2.09	0.52
1:A:526:GLN:NE2	5:A:5056:HOH:O	2.43	0.51
1:A:289:LEU:HD23	1:A:290:THR:N	2.26	0.51
1:A:468:LEU:O	1:A:468:LEU:HD23	2.11	0.50
1:A:406:ASN:ND2	1:A:422:THR:H	2.10	0.50
1:A:339:PRO:HG2	1:A:357:HIS:CE1	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:363:LEU:C	1:A:363:LEU:HD13	2.33	0.49
1:A:389:LEU:HD22	1:A:403:GLY:C	2.33	0.49
1:A:241:LYS:HE3	5:A:5019:HOH:O	2.12	0.49
1:A:578:GLN:O	1:A:582:GLN:HG3	2.12	0.48
1:A:606:ARG:HH11	1:A:606:ARG:HG3	1.78	0.48
1:A:398:LEU:O	1:A:402:ILE:HG13	2.14	0.48
1:A:105:ILE:HD13	1:A:138:ASP:HB3	1.96	0.48
1:A:484:ARG:HB3	1:A:484:ARG:NH1	2.29	0.48
1:A:328:ILE:HD13	4:A:4733:SKM:H51	1.95	0.48
1:A:606:ARG:NH1	1:A:606:ARG:HG3	2.29	0.47
1:A:315:ASN:HB3	1:A:318:ARG:HD3	1.97	0.47
1:A:491:GLU:OE1	1:A:491:GLU:N	2.48	0.47
1:A:313:LEU:O	1:A:313:LEU:HD23	2.15	0.47
1:A:90:VAL:HB	5:A:5009:HOH:O	2.14	0.47
1:A:246:ALA:HB2	1:A:270:VAL:HG12	1.97	0.46
1:A:163:TYR:CD2	1:A:170:ARG:HD3	2.50	0.46
1:A:383:PRO:HA	2:A:1402:SO4:O2	2.16	0.46
1:A:544:LEU:C	1:A:544:LEU:HD23	2.36	0.46
1:A:473:LYS:HG3	1:A:478:LYS:HZ2	1.80	0.46
1:A:382:ILE:HD12	1:A:522:SER:OG	2.15	0.46
1:A:185:ILE:C	1:A:185:ILE:HD12	2.37	0.45
1:A:567:ILE:HG12	1:A:568:THR:N	2.31	0.45
1:A:553:ARG:HD2	5:A:5251:HOH:O	2.17	0.45
1:A:483:ASN:HD22	1:A:488:ARG:HB2	1.82	0.45
1:A:411:ARG:HH21	1:A:416:LYS:CD	2.17	0.44
1:A:574:MET:SD	1:A:574:MET:C	2.96	0.44
1:A:459:ILE:HB	1:A:519:ASN:HA	2.00	0.43
1:A:544:LEU:HG	1:A:567:ILE:HG23	2.00	0.43
1:A:211:VAL:HG21	1:A:237:ALA:HB2	2.00	0.43
1:A:341:VAL:HG23	1:A:342:HIS:N	2.34	0.43
1:A:598:GLN:HE21	1:A:602:LYS:HE3	1.84	0.42
1:A:455:THR:HG23	1:A:455:THR:O	2.19	0.42
1:A:501:LEU:HD23	1:A:502:SER:O	2.19	0.42
1:A:98:ALA:HA	1:A:99:PRO:HD3	1.83	0.42
1:A:406:ASN:C	1:A:406:ASN:ND2	2.72	0.42
1:A:512:GLU:HB2	1:A:515:MET:CG	2.50	0.42
1:A:107:LYS:O	1:A:111:GLU:HG3	2.20	0.42
1:A:472:ALA:CB	1:A:479:VAL:HG11	2.50	0.42
1:A:289:LEU:HD23	1:A:289:LEU:C	2.40	0.41
1:A:338:SER:N	1:A:339:PRO:CD	2.83	0.41
1:A:256:PHE:O	1:A:260:SER:HB3	2.20	0.41
1:A:193:SER:O	1:A:197:LYS:HG3	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:176:LEU:HD22	1:A:180:LEU:CD1	2.51	0.41
1:A:530:GLU:OE2	1:A:530:GLU:HA	2.20	0.41
1:A:187:VAL:O	1:A:211:VAL:HA	2.20	0.41
1:A:338:SER:HB2	1:A:339:PRO:HD3	2.02	0.41
1:A:131:LYS:HE2	5:A:5154:HOH:O	2.20	0.41
1:A:473:LYS:HG3	1:A:478:LYS:HZ3	1.83	0.41
1:A:483:ASN:ND2	1:A:488:ARG:HB2	2.35	0.41
1:A:598:GLN:NE2	1:A:602:LYS:NZ	2.68	0.41
1:A:389:LEU:HD11	1:A:395:VAL:HG11	2.02	0.40
1:A:501:LEU:C	1:A:501:LEU:HD23	2.41	0.40
1:A:411:ARG:HG2	1:A:413:SER:HB2	2.03	0.40
1:A:512:GLU:N	5:A:5257:HOH:O	2.54	0.40
1:A:127:LEU:HD22	1:A:133:PHE:CZ	2.56	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	488/523 (93%)	465 (95%)	19 (4%)	4 (1%)	27	12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	413	SER
1	A	477	ALA
1	A	135	PRO
1	A	486	TYR

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	418/439 (95%)	409 (98%)	9 (2%)	64	55

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	TYR
1	A	176	LEU
1	A	289	LEU
1	A	383	PRO
1	A	406	ASN
1	A	414	ASP
1	A	416	LYS
1	A	491	GLU
1	A	492	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	190	GLN
1	A	263	GLN
1	A	315	ASN
1	A	344	GLN
1	A	368	GLN
1	A	406	ASN
1	A	483	ASN
1	A	526	GLN
1	A	598	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	$\# Z > 2$
2	SO4	A	1402	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	A	1403	-	4,4,4	0.26	0	6,6,6	0.08	0
4	SKM	A	4733	-	12,12,12	1.13	2 (16%)	17,17,17	0.65	0
3	TLA	A	4988	-	9,9,9	0.88	0	12,12,12	1.13	1 (8%)

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	SO4	A	1402	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1403	-	-	0/0/0/0	0/0/0/0
4	SKM	A	4733	-	-	0/4/20/20	0/1/1/1
3	TLA	A	4988	-	-	0/12/12/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4733	SKM	C6-C8	2.55	1.56	1.52
4	A	4733	SKM	C8-C9	2.01	1.57	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4988	TLA	O11-C1-C2	2.02	119.77	113.89

There are no chirality outliers.

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	498/523 (95%)	0.20	31 (6%) 20 25	19, 33, 73, 93	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	540	LYS	6.0
1	A	90	VAL	5.4
1	A	478	LYS	4.9
1	A	479	VAL	4.9
1	A	514	GLY	4.6
1	A	477	ALA	4.5
1	A	567	ILE	4.0
1	A	513	ASP	4.0
1	A	496	ILE	3.8
1	A	389	LEU	3.6
1	A	504	THR	3.3
1	A	541	HIS	3.0
1	A	492	LEU	3.0
1	A	565	GLY	2.9
1	A	508	ASN	2.9
1	A	503	LEU	2.6
1	A	480	VAL	2.6
1	A	470	TYR	2.6
1	A	472	ALA	2.5
1	A	543	ALA	2.5
1	A	455	THR	2.5
1	A	400	LYS	2.5
1	A	509	TYR	2.5
1	A	486	TYR	2.4
1	A	476	GLY	2.4
1	A	475	LYS	2.3
1	A	501	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	485	THR	2.3
1	A	456	VAL	2.2
1	A	493	ALA	2.1
1	A	566	ALA	2.1

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

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

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	0.37	11.79	53,53,55,55	5
2	SO4	A	1402	5/5	0.16	2.17	23,24,27,28	5
4	SKM	A	4733	12/12	0.12	0.98	25,27,33,36	0
3	TLA	A	4988	10/10	0.10	-0.26	33,39,45,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.