



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2023 – 12:59 AM EDT

PDB ID : 1EUH
Title : APO FORM OF A NADP DEPENDENT ALDEHYDE DEHYDROGENASE
FROM STREPTOCOCCUS MUTANS
Authors : Cobessi, D.; Tete-Favier, F.; Marchal, S.; Branlant, G.; Aubry, A.
Deposited on : 1998-11-05
Resolution : 1.82 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

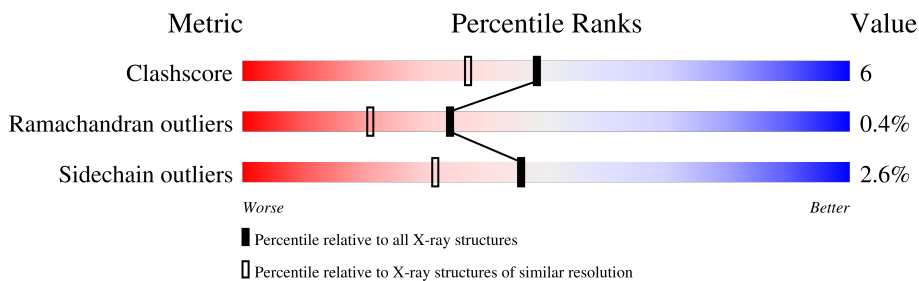
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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))
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	475	
1	B	475	
1	C	475	
1	D	475	

2 Entry composition [i](#)

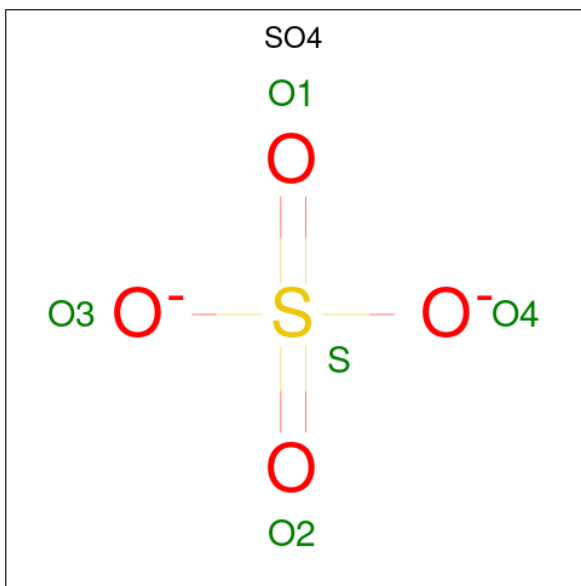
There are 3 unique types of molecules in this entry. The entry contains 15976 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NADP DEPENDENT NON PHOSPHORYLATING GLYCE RALDEHYDE-3-PHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	474	Total 3596	C 2286	N 600	O 699	S 11	0	0	0
1	B	474	Total 3596	C 2286	N 600	O 699	S 11	0	0	0
1	C	474	Total 3596	C 2286	N 600	O 699	S 11	0	0	0
1	D	474	Total 3596	C 2286	N 600	O 699	S 11	0	0	0

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



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

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

- Molecule 3 is water.


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	389	Total O 389 389	0	0
3	B	332	Total O 332 332	0	0
3	C	428	Total O 428 428	0	0
3	D	393	Total O 393 393	0	0

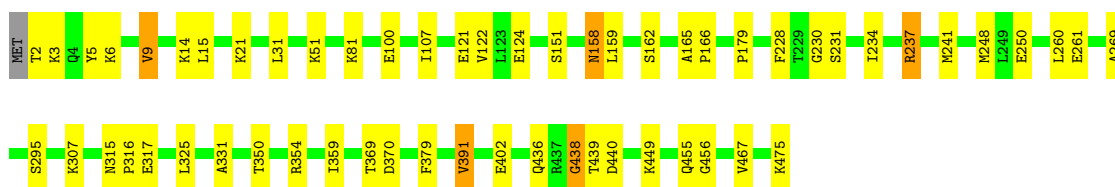
3 Residue-property plots [i](#)

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. 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. 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.


Note EDS was not executed.

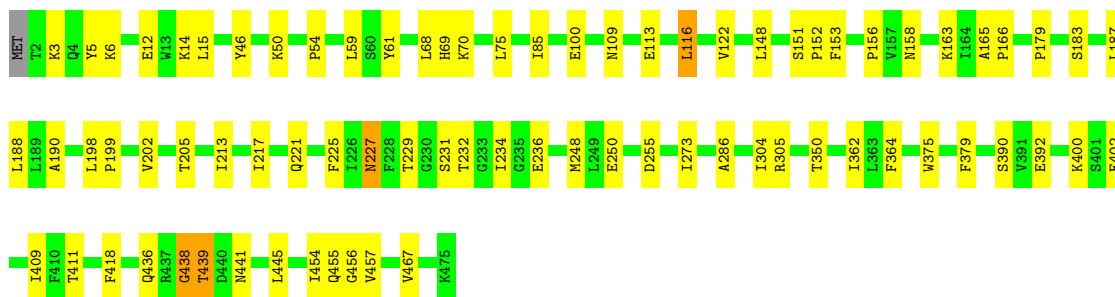
- Molecule 1: NADP DEPENDENT NON PHOSPHORYLATING GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain A: 




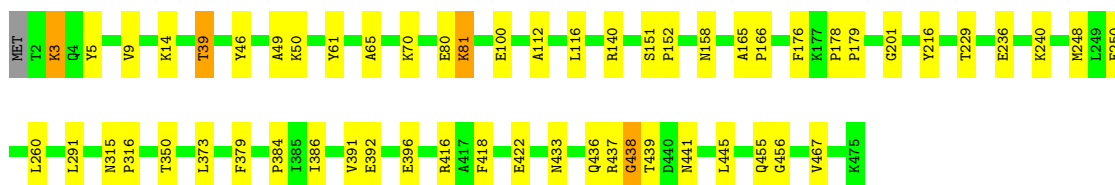
- Molecule 1: NADP DEPENDENT NON PHOSPHORYLATING GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain B: 




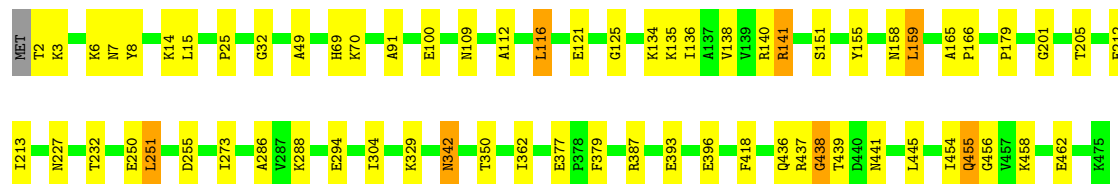
- Molecule 1: NADP DEPENDENT NON PHOSPHORYLATING GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain C: 



● Molecule 1: NADP DEPENDENT NON PHOSPHORYLATING GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain D:  86% 13%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	144.40Å 154.70Å 114.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.82	Depositor
% Data completeness (in resolution range)	94.0 (8.00-1.82)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.221 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	15976	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.34	0/3654	0.61	1/4942 (0.0%)
1	B	0.34	0/3654	0.61	1/4942 (0.0%)
1	C	0.35	0/3654	0.62	1/4942 (0.0%)
1	D	0.35	0/3654	0.61	1/4942 (0.0%)
All	All	0.35	0/14616	0.61	4/19768 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	GLY	N-CA-C	-6.17	97.68	113.10
1	B	456	GLY	N-CA-C	-5.93	98.27	113.10
1	C	456	GLY	N-CA-C	-5.77	98.68	113.10
1	D	456	GLY	N-CA-C	-5.36	99.70	113.10

There are no chirality outliers.

There are no planarity outliers.

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	3596	0	3649	41	0
1	B	3596	0	3649	47	0
1	C	3596	0	3649	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3596	0	3649	46	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	15	0	0	0	0
3	A	389	0	0	4	0
3	B	332	0	0	4	0
3	C	428	0	0	4	0
3	D	393	0	0	4	0
All	All	15976	0	14596	175	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 6.

All (175) 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:C:3:LYS:HE2	1:C:3:LYS:HA	1.41	0.98
1:B:69:HIS:HD2	1:B:109:ASN:HD22	1.06	0.94
1:C:248:MET:CE	1:C:455:GLN:HE21	1.81	0.93
1:D:8:TYR:H	1:D:205:THR:HG22	1.42	0.84
1:B:69:HIS:HD2	1:B:109:ASN:ND2	1.78	0.80
1:B:225:PHE:HZ	1:B:248:MET:HG3	1.48	0.79
1:B:69:HIS:CD2	1:B:109:ASN:HD22	1.96	0.76
1:D:100:GLU:HG3	1:D:158:ASN:HB2	1.68	0.74
1:B:225:PHE:CZ	1:B:248:MET:HG3	2.22	0.74
1:D:232:THR:HA	1:D:251:LEU:HG	1.70	0.74
1:B:231:SER:HB2	1:B:234:ILE:HD13	1.69	0.74
1:D:134:LYS:HA	1:D:134:LYS:HE2	1.70	0.73
1:D:437:ARG:NH2	1:D:455:GLN:HG2	2.05	0.71
1:A:100:GLU:HG3	1:A:158:ASN:HB2	1.70	0.71
1:C:248:MET:CE	1:C:455:GLN:NE2	2.52	0.70
1:A:248:MET:HG2	1:A:455:GLN:HE21	1.56	0.69
1:C:248:MET:HE3	1:C:455:GLN:HE21	1.58	0.69
1:A:248:MET:HG2	1:A:455:GLN:NE2	2.08	0.68
1:D:232:THR:HG22	1:D:251:LEU:HB3	1.75	0.68
1:A:436:GLN:NE2	1:A:438:GLY:HA3	2.08	0.67
1:D:2:THR:HG22	1:D:3:LYS:H	1.59	0.67
1:B:6:LYS:HG2	1:B:15:LEU:HD13	1.76	0.67
1:D:2:THR:HB	1:D:32:GLY:HA2	1.76	0.67
1:B:100:GLU:HG3	1:B:158:ASN:HB2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ILE:HD12	1:B:188:LEU:HD21	1.76	0.66
1:B:198:LEU:HB3	1:B:202:VAL:HG21	1.79	0.65
1:C:81:LYS:HE3	3:C:706:HOH:O	1.96	0.64
3:B:707:HOH:O	1:D:116:LEU:HD12	1.96	0.64
1:C:39:THR:HG22	3:C:823:HOH:O	1.99	0.63
1:D:8:TYR:H	1:D:205:THR:CG2	2.10	0.63
1:D:112:ALA:O	1:D:116:LEU:HD23	1.98	0.62
1:C:248:MET:HG2	1:C:455:GLN:NE2	2.14	0.61
1:A:3:LYS:HE2	1:A:31:LEU:O	2.01	0.61
1:B:213:ILE:HD12	1:B:217:ILE:HD11	1.83	0.61
1:B:305:ARG:HH11	1:B:305:ARG:HB3	1.66	0.60
1:D:7:ASN:OD1	1:D:205:THR:HG23	2.01	0.60
1:B:148:LEU:HD21	1:B:217:ILE:HG22	1.83	0.60
1:D:6:LYS:HG2	1:D:15:LEU:HG	1.84	0.60
1:C:81:LYS:HE2	1:C:81:LYS:H	1.67	0.59
1:C:3:LYS:HA	1:C:3:LYS:CE	2.20	0.59
1:B:199:PRO:O	1:B:202:VAL:HG22	2.03	0.58
1:B:69:HIS:HE1	1:B:113:GLU:OE1	1.86	0.58
1:B:436:GLN:NE2	1:B:438:GLY:HA3	2.21	0.56
1:D:165:ALA:HB3	1:D:166:PRO:HD3	1.87	0.56
1:B:12:GLU:HB3	1:B:14:LYS:HE2	1.88	0.56
1:C:152:PRO:HD3	1:C:229:THR:HB	1.87	0.56
1:A:124:GLU:OE1	1:D:140:ARG:HD2	2.05	0.56
1:B:255:ASP:HB2	1:B:286:ALA:O	2.06	0.56
3:B:725:HOH:O	1:C:116:LEU:HB3	2.05	0.56
1:A:315:ASN:HB3	1:A:317:GLU:OE2	2.06	0.55
1:C:439:THR:HG23	1:C:441:ASN:OD1	2.07	0.55
1:A:107:ILE:HD11	1:A:440:ASP:CG	2.27	0.55
1:A:248:MET:CG	1:A:455:GLN:HE21	2.19	0.55
1:A:436:GLN:HE21	1:A:438:GLY:HA3	1.70	0.55
1:A:3:LYS:HE3	1:A:5:TYR:CE1	2.42	0.54
1:A:475:LYS:HD3	1:C:416:ARG:NH2	2.22	0.54
1:C:39:THR:HG23	1:C:216:TYR:CZ	2.43	0.54
1:A:248:MET:HG3	3:A:675:HOH:O	2.08	0.53
1:A:369:THR:HB	3:A:830:HOH:O	2.09	0.53
1:A:228:PHE:CZ	1:A:230:GLY:HA3	2.44	0.53
1:C:248:MET:HE3	1:C:455:GLN:NE2	2.20	0.53
1:A:402:GLU:HB2	1:A:449:LYS:HE3	1.90	0.53
1:C:165:ALA:HB3	1:C:166:PRO:HD3	1.92	0.52
1:B:402:GLU:H	1:B:402:GLU:CD	2.13	0.52
1:C:100:GLU:HG3	1:C:158:ASN:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:LYS:H	1:C:81:LYS:CE	2.23	0.52
1:B:409:ILE:HG22	1:B:411:THR:HG22	1.92	0.52
1:C:436:GLN:NE2	1:C:438:GLY:HA3	2.25	0.52
1:B:234:ILE:N	1:B:234:ILE:HD12	2.26	0.51
1:B:198:LEU:HB3	1:B:202:VAL:CG2	2.40	0.51
1:C:112:ALA:O	1:C:116:LEU:HG	2.10	0.51
1:A:317:GLU:H	1:A:317:GLU:CD	2.14	0.50
1:C:100:GLU:CG	1:C:158:ASN:HB2	2.41	0.50
1:D:294:GLU:OE2	1:D:387:ARG:HD3	2.12	0.50
1:A:121:GLU:HA	1:D:121:GLU:HA	1.93	0.50
1:D:212:GLU:HG2	1:D:213:ILE:HG23	1.94	0.50
1:A:165:ALA:HB3	1:A:166:PRO:HD3	1.94	0.50
1:D:436:GLN:NE2	1:D:438:GLY:HA3	2.27	0.49
1:C:433:ASN:HB3	3:C:848:HOH:O	2.12	0.49
1:B:250:GLU:OE2	1:B:455:GLN:HG3	2.13	0.49
1:C:373:LEU:HG	1:C:384:PRO:HB3	1.94	0.49
1:A:402:GLU:O	1:A:449:LYS:HE2	2.13	0.49
1:A:354:ARG:HB2	1:A:359:ILE:HD13	1.94	0.49
1:B:445:LEU:HD13	1:B:454:ILE:HG12	1.94	0.49
1:C:439:THR:HG21	1:D:125:GLY:HA2	1.94	0.49
1:D:288:LYS:HE2	1:D:377:GLU:HG3	1.93	0.49
1:B:350:THR:OG1	1:B:362:ILE:HA	2.13	0.49
1:D:2:THR:HG22	1:D:3:LYS:N	2.25	0.49
1:D:250:GLU:HG3	3:D:659:HOH:O	2.11	0.49
1:B:163:LYS:HE3	1:B:227:ASN:ND2	2.27	0.48
1:A:6:LYS:HG2	1:A:15:LEU:HG	1.95	0.48
1:D:8:TYR:N	1:D:205:THR:HG22	2.21	0.48
1:C:9:VAL:HB	1:C:14:LYS:HD2	1.96	0.47
1:C:418:PHE:O	1:C:422:GLU:HG3	2.14	0.47
1:B:250:GLU:HG3	3:B:549:HOH:O	2.13	0.47
1:B:153:PHE:O	1:B:156:PRO:HD3	2.14	0.47
1:C:3:LYS:HD3	1:C:5:TYR:CE2	2.50	0.47
1:C:46:TYR:O	1:C:50:LYS:HG2	2.15	0.47
1:C:80:GLU:H	1:C:81:LYS:HZ3	1.62	0.47
1:C:236:GLU:O	1:C:240:LYS:HG2	2.15	0.46
1:D:439:THR:CG2	1:D:441:ASN:OD1	2.63	0.46
1:B:46:TYR:OH	1:B:217:ILE:HG23	2.16	0.46
1:C:291:LEU:HD23	1:C:386:ILE:HB	1.97	0.46
1:A:261:GLU:HG2	1:A:295:SER:HG	1.81	0.46
1:B:390:SER:HB2	1:B:392:GLU:OE2	2.15	0.46
1:C:248:MET:CG	1:C:455:GLN:NE2	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:255:ASP:HB2	1:D:286:ALA:O	2.15	0.45
1:D:439:THR:HG23	1:D:441:ASN:OD1	2.16	0.45
1:A:269:ALA:HB3	1:A:307:LYS:HZ2	1.80	0.45
1:D:141:ARG:NH1	1:D:462:GLU:HB2	2.31	0.45
1:A:316:PRO:HB2	3:A:704:HOH:O	2.16	0.45
1:A:9:VAL:HG13	1:A:14:LYS:HD3	1.98	0.45
1:B:221:GLN:H	1:B:221:GLN:CD	2.21	0.45
1:D:141:ARG:HH11	1:D:462:GLU:HB2	1.82	0.45
1:B:375:TRP:CH2	1:B:400:LYS:HD3	2.52	0.45
1:C:151:SER:O	1:C:179:PRO:HD3	2.17	0.45
1:D:273:ILE:HD11	1:D:304:ILE:HG23	1.97	0.45
1:C:439:THR:CG2	1:C:441:ASN:OD1	2.65	0.44
1:B:183:SER:O	1:B:187:LEU:HG	2.17	0.44
1:D:151:SER:O	1:D:179:PRO:HD3	2.17	0.44
1:A:2:THR:HG21	1:A:21:LYS:NZ	2.33	0.44
1:A:51:LYS:HE3	1:A:51:LYS:HB2	1.84	0.44
1:A:107:ILE:HG21	1:A:162:SER:HA	1.99	0.44
1:B:165:ALA:HB3	1:B:166:PRO:HD3	1.99	0.44
1:C:260:LEU:HD22	1:C:391:VAL:HG22	2.00	0.43
1:D:6:LYS:HE2	1:D:15:LEU:HG	2.00	0.43
1:A:9:VAL:CG1	1:A:14:LYS:HD3	2.48	0.43
1:C:396:GLU:HG3	3:C:651:HOH:O	2.19	0.43
1:C:65:ALA:HB2	1:C:116:LEU:HD21	2.00	0.43
1:C:61:TYR:HB3	1:C:116:LEU:HD23	2.00	0.43
1:A:151:SER:O	1:A:179:PRO:HD3	2.18	0.43
1:C:250:GLU:CD	1:C:437:ARG:HH22	2.22	0.43
1:D:458:LYS:HG2	3:D:497:HOH:O	2.18	0.43
1:B:61:TYR:HB3	1:B:116:LEU:HD23	2.01	0.43
1:B:305:ARG:HB3	1:B:305:ARG:NH1	2.33	0.42
1:D:69:HIS:ND1	1:D:109:ASN:ND2	2.67	0.42
1:A:402:GLU:HB2	1:A:449:LYS:CE	2.50	0.42
1:C:176:PHE:CZ	1:C:178:PRO:HB3	2.55	0.42
1:C:418:PHE:HE1	3:D:778:HOH:O	2.03	0.42
1:B:3:LYS:HD2	1:B:5:TYR:CE2	2.55	0.42
1:D:49:ALA:HA	1:D:201:GLY:O	2.20	0.42
1:A:237:ARG:O	1:A:241:MET:HG3	2.20	0.42
1:B:273:ILE:HD11	1:B:304:ILE:HG23	2.02	0.42
1:A:269:ALA:HB3	1:A:307:LYS:NZ	2.35	0.41
1:D:393:GLU:HA	1:D:396:GLU:HG2	2.02	0.41
1:A:260:LEU:HD22	1:A:391:VAL:HG12	2.02	0.41
1:C:70:LYS:HA	1:C:70:LYS:HD2	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:LYS:HE3	3:D:626:HOH:O	2.19	0.41
1:B:152:PRO:HD3	1:B:229:THR:HB	2.03	0.41
1:B:436:GLN:HE21	1:B:438:GLY:HA3	1.84	0.41
1:C:250:GLU:OE2	1:C:455:GLN:HG3	2.20	0.41
1:C:315:ASN:HA	1:C:316:PRO:HD3	1.93	0.41
1:D:155:TYR:HB2	1:D:159:LEU:HD22	2.03	0.41
1:A:122:VAL:HG21	1:D:138:VAL:HG13	2.02	0.41
1:A:231:SER:OG	1:A:234:ILE:HG12	2.21	0.41
1:D:25:PRO:HB2	1:D:91:ALA:HB2	2.02	0.41
1:D:70:LYS:HD2	1:D:70:LYS:HA	1.86	0.41
1:B:439:THR:HB	1:B:441:ASN:OD1	2.21	0.41
1:D:342:ASN:HD22	1:D:342:ASN:HA	1.61	0.41
1:B:122:VAL:HG11	1:C:140:ARG:HD3	2.02	0.41
1:A:261:GLU:HG2	1:A:295:SER:OG	2.21	0.41
1:B:54:PRO:HG2	3:B:728:HOH:O	2.19	0.41
1:B:190:ALA:HB2	1:B:205:THR:HG21	2.03	0.41
1:C:260:LEU:CD2	1:C:391:VAL:HG22	2.51	0.41
1:D:350:THR:OG1	1:D:362:ILE:HA	2.21	0.41
1:A:250:GLU:HG3	3:A:661:HOH:O	2.19	0.40
1:B:232:THR:O	1:B:236:GLU:HG2	2.21	0.40
1:A:325:LEU:HD12	1:A:331:ALA:HA	2.04	0.40
1:B:151:SER:O	1:B:179:PRO:HD3	2.22	0.40
1:D:2:THR:CG2	1:D:3:LYS:H	2.26	0.40
1:C:49:ALA:HA	1:C:201:GLY:O	2.21	0.40
1:D:135:LYS:C	1:D:136:ILE:HD12	2.41	0.40
1:D:445:LEU:HD13	1:D:454:ILE:HG12	2.03	0.40
1:A:2:THR:HG21	1:A:21:LYS:HZ2	1.85	0.40
1:B:148:LEU:CD2	1:B:217:ILE:HG22	2.51	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	472/475 (99%)	456 (97%)	14 (3%)	2 (0%)	34	21
1	B	472/475 (99%)	452 (96%)	17 (4%)	3 (1%)	25	12
1	C	472/475 (99%)	458 (97%)	13 (3%)	1 (0%)	47	33
1	D	472/475 (99%)	459 (97%)	12 (2%)	1 (0%)	47	33
All	All	1888/1900 (99%)	1825 (97%)	56 (3%)	7 (0%)	34	21

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	438	GLY
1	B	438	GLY
1	A	439	THR
1	B	439	THR
1	C	438	GLY
1	D	438	GLY
1	B	457	VAL

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	378/379 (100%)	368 (97%)	10 (3%)	46	32
1	B	378/379 (100%)	367 (97%)	11 (3%)	42	28
1	C	378/379 (100%)	370 (98%)	8 (2%)	53	41
1	D	378/379 (100%)	368 (97%)	10 (3%)	46	32
All	All	1512/1516 (100%)	1473 (97%)	39 (3%)	46	32

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	81	LYS
1	A	158	ASN
1	A	159	LEU

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Mol	Chain	Res	Type
1	A	237	ARG
1	A	350	THR
1	A	370	ASP
1	A	379	PHE
1	A	391	VAL
1	A	467	VAL
1	B	50	LYS
1	B	59	LEU
1	B	68	LEU
1	B	70	LYS
1	B	75	LEU
1	B	116	LEU
1	B	227	ASN
1	B	364	PHE
1	B	379	PHE
1	B	418	PHE
1	B	467	VAL
1	C	3	LYS
1	C	39	THR
1	C	81	LYS
1	C	350	THR
1	C	379	PHE
1	C	392	GLU
1	C	445	LEU
1	C	467	VAL
1	D	116	LEU
1	D	141	ARG
1	D	159	LEU
1	D	227	ASN
1	D	251	LEU
1	D	329	LYS
1	D	342	ASN
1	D	379	PHE
1	D	418	PHE
1	D	455	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	ASN
1	A	436	GLN
1	A	455	GLN

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Mol	Chain	Res	Type
1	B	10	ASN
1	B	69	HIS
1	B	158	ASN
1	B	227	ASN
1	B	436	GLN
1	C	339	ASN
1	C	436	GLN
1	C	455	GLN
1	D	109	ASN
1	D	158	ASN
1	D	227	ASN
1	D	342	ASN
1	D	436	GLN
1	D	455	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](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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	B	477	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	C	477	-	4,4,4	0.31	0	6,6,6	0.07	0
2	SO4	C	476	-	4,4,4	0.27	0	6,6,6	0.16	0
2	SO4	B	476	-	4,4,4	0.29	0	6,6,6	0.14	0
2	SO4	A	476	-	4,4,4	0.29	0	6,6,6	0.10	0
2	SO4	D	477	-	4,4,4	0.21	0	6,6,6	0.10	0
2	SO4	D	476	-	4,4,4	0.30	0	6,6,6	0.14	0
2	SO4	B	478	-	4,4,4	0.26	0	6,6,6	0.11	0
2	SO4	D	478	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	A	477	-	4,4,4	0.26	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.