



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 05:34 PM GMT

PDB ID : 1VDV
Title : Bovine Milk Xanthine Dehydrogenase Y-700 Bound Form
Authors : Fukunari, A.; Okamoto, K.; Nishino, T.; Eger, B.T.; Pai, E.F.; Kamezawa, M.; Yamada, I.; Kato, N.
Deposited on : 2004-03-25
Resolution : 1.98 Å(reported)

This is a wwPDB validation summary 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>

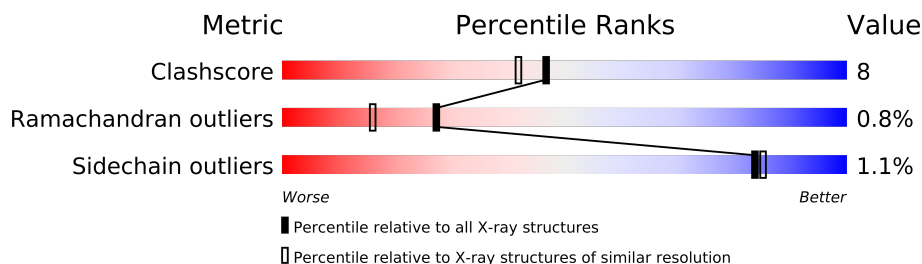
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
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 1.98 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	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1332	
1	B	1332	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 22610 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 Xanthine dehydrogenase/oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1299	Total	C	N	O	S	0	0	0
			10077	6404	1728	1884	61			
1	B	1296	Total	C	N	O	S	0	0	0
			10054	6391	1724	1878	61			

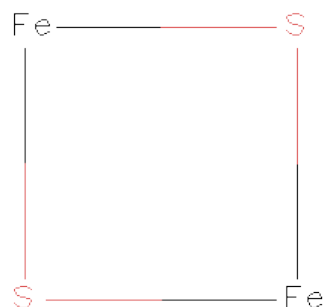
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P80457
B	1	MET	-	INITIATING METHIONINE	UNP P80457

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

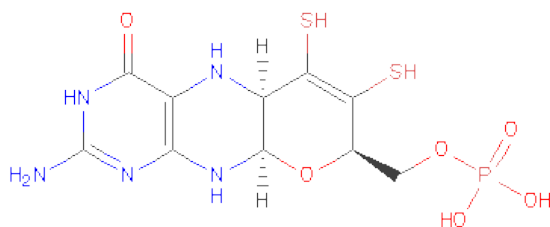
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	2	Total	Ca	0	0
			2	2		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



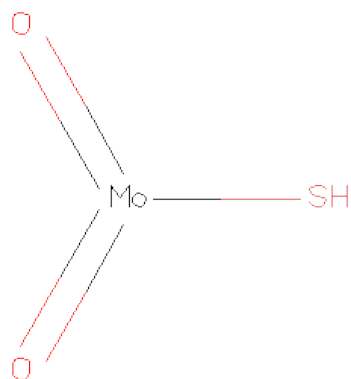
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: C₁₀H₁₄N₅O₆PS₂).



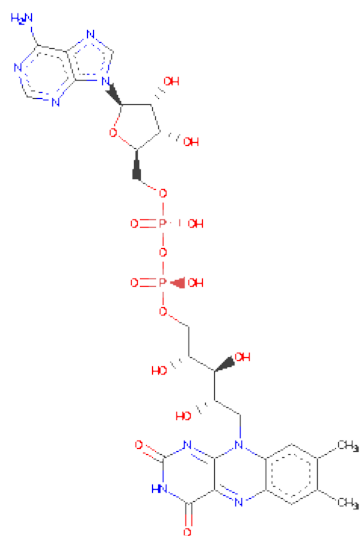
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 5 is DIOXOTHIOMOLYBDENUM(VI)ION (three-letter code: MOS) (formula: HMoO_2S).



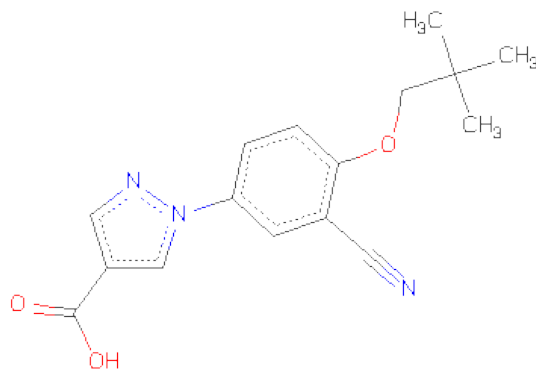
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	Mo	O	S	0	0
			4	1	2	1		
5	B	1	Total	Mo	O	S	0	0
			4	1	2	1		

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
6	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 7 is 1-[3-CYANO-4-(NEOPENTYLOXY)PHENYL]-1H-PYRAZOLE-4-CARBOXYLICACID (three-letter code: YSH) (formula: C₁₆H₁₇N₃O₃).



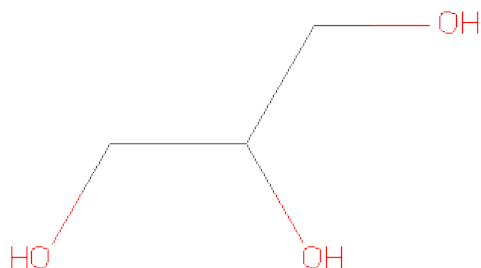
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			22	16	3	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			22	16	3	3		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



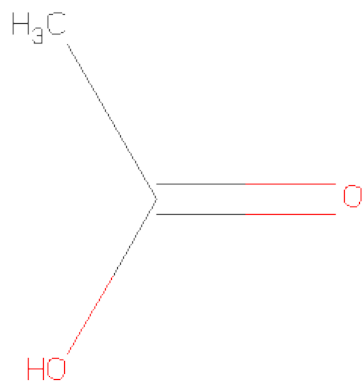
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total 4	C 2	O 2	0	0
9	B	1	Total 4	C 2	O 2	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1086	Total 1086	O 1086	0	0
10	B	1033	Total 1033	O 1033	0	0

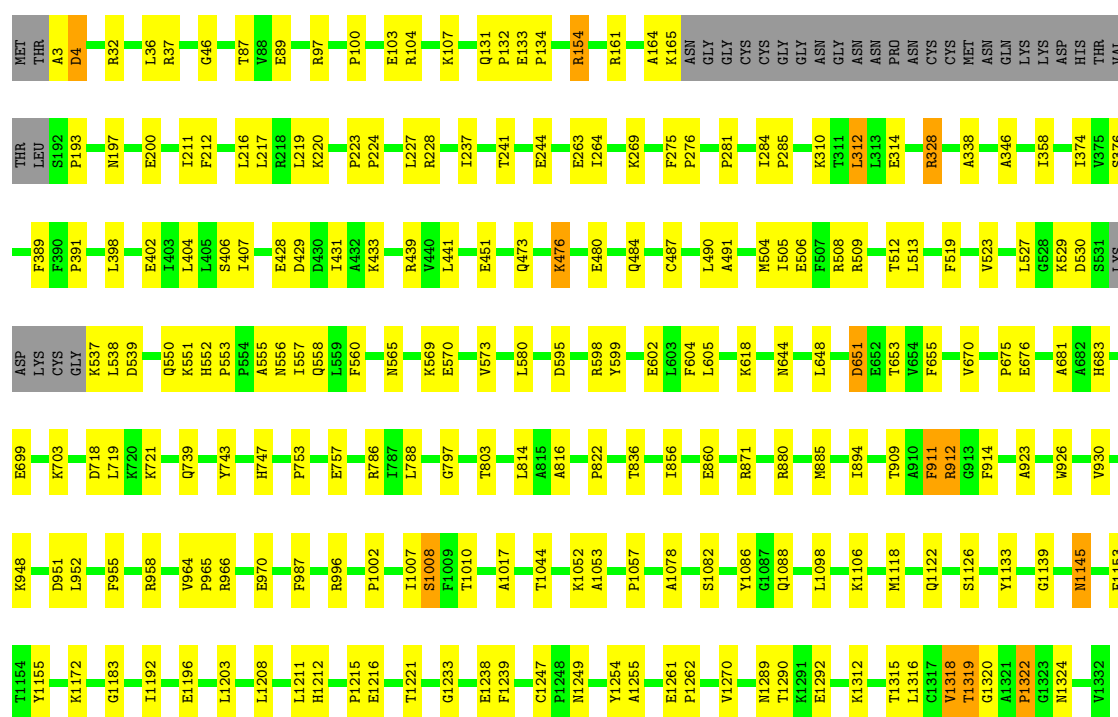
3 Residue-property plots

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.

Note EDS was not executed.

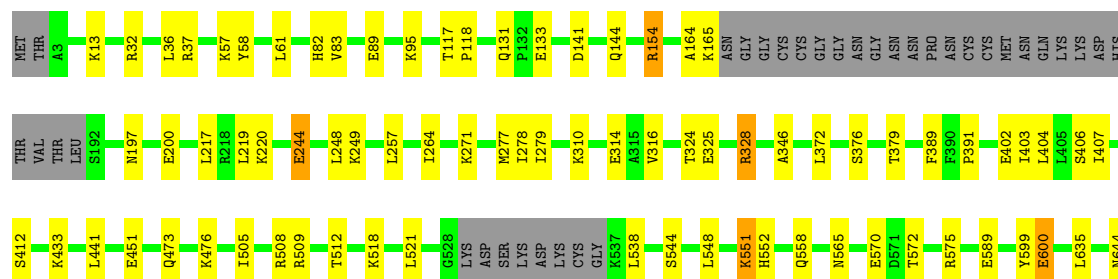
• Molecule 1: Xanthine dehydrogenase/oxidase

Chain A:



• Molecule 1: Xanthine dehydrogenase/oxidase

Chain B:



L1316	G1087	R895	N650
G1317	Q1088	G896	T653
V1318	L1089	T897	G854
T1319	N1088	G898	F855
G1320	P1109	R899	A856
A1321	F1132	T909	K657
P1322	Y1133	A910	D658
G1323	G1139	R912	E676
N1324	N1145	G913	E699
C1325	K1172	F914	L712
K1326	N1173	V926	K713
V1332	T1192	V930	L719
	E1196	K948	F723
	F1199	D951	A726
	L1203	L952	T736
	T1221	F955	Y743
	T1226	R958	H747
	P1236	V964	P753
	E1238	P965	E757
	F1239	F987	K778
	N1249	C992	R786
	A1255	W993	G797
	E1261	K994	L814
	P1262	R996	A815
	G1267	P1002	A816
	A1281	L1007	E817
	Q1284	S1008	K818
	H1285	T1010	M826
	T1286	A1017	T836
	N1287	L1030	K847
	N1288	Q1048	V857
	T1289	A1053	E860
	T1290	P1057	R871
	V1291	A1078	H875
	E1292	S1082	
	S1298	V1085	P880
	K1312		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.82Å 123.94Å 148.89Å 90.00° 91.16° 90.00°	Depositor
Resolution (Å)	20.00 – 1.98	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.98)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.178 , 0.215	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	22610	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, YSH, MOS, CA, FES, ACY, FAD, MTE

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	0/10298	0.60	0/13939
1	B	0.31	0/10275	0.60	0/13909
All	All	0.32	0/20573	0.60	0/27848

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	10077	0	10076	172	0
1	B	10054	0	10053	155	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	8	0	0	1	0
3	B	8	0	0	0	0
4	A	24	0	10	1	0
4	B	24	0	10	1	0
5	A	4	0	0	1	0
5	B	4	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	53	0	31	4	0
6	B	53	0	31	3	0
7	A	22	0	16	3	0
7	B	22	0	16	3	0
8	A	66	0	88	8	0
8	B	60	0	80	8	0
9	A	4	0	3	4	0
9	B	4	0	3	4	0
10	A	1086	0	0	9	0
10	B	1033	0	0	7	0
All	All	22610	0	20417	331	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 8.

The worst 5 of 331 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:B:5102:YSH:C1	7:B:5102:YSH:N2	1.70	1.52
7:A:5101:YSH:C1	7:A:5101:YSH:N2	1.68	1.51
1:A:3:ALA:HB1	1:A:228:ARG:H	1.20	1.06
1:A:537:LYS:HG2	1:A:538:LEU:H	1.28	0.98
1:A:955:PHE:HA	1:A:1145:ASN:HD21	1.30	0.97

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	1293/1332 (97%)	1244 (96%)	41 (3%)	8 (1%)	33 23
1	B	1290/1332 (97%)	1234 (96%)	44 (3%)	12 (1%)	25 13
All	All	2583/2664 (97%)	2478 (96%)	85 (3%)	20 (1%)	27 16

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	1008	SER
1	B	1008	SER
1	B	1287	ASN
1	B	1324	ASN

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	1101/1128 (98%)	1086 (99%)	15 (1%)	78	79
1	B	1098/1128 (97%)	1088 (99%)	10 (1%)	87	89
All	All	2199/2256 (98%)	2174 (99%)	25 (1%)	84	85

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1002	PRO
1	A	1208	LEU
1	B	1145	ASN
1	A	1145	ASN
1	A	1239	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1284	GLN
1	B	131	GLN
1	B	1145	ASN
1	A	1324	ASN
1	B	146	ASN

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 ⓘ

Of 39 ligands modelled in this entry, 4 are monoatomic - leaving 35 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	FES	A	3001	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FES	A	3002	1	0,4,4	0.00	-	0,4,4	0.00	-
4	MTE	A	3003	5	26,26,26	4.74	16 (61%)	34,40,40	3.43	17 (50%)
5	MOS	A	3004	4	0,3,3	0.00	-	0,3,3	0.00	-
6	FAD	A	3005	-	58,58,58	2.35	20 (34%)	85,89,89	2.69	30 (35%)
8	GOL	A	5001	-	5,5,5	0.22	0	5,5,5	0.42	0
8	GOL	A	5002	-	5,5,5	0.16	0	5,5,5	0.37	0
8	GOL	A	5003	-	5,5,5	0.24	0	5,5,5	0.35	0
8	GOL	A	5004	-	5,5,5	0.21	0	5,5,5	0.35	0
8	GOL	A	5005	-	5,5,5	0.23	0	5,5,5	0.35	0
8	GOL	A	5006	-	5,5,5	0.15	0	5,5,5	0.44	0
8	GOL	A	5011	-	5,5,5	0.14	0	5,5,5	0.36	0
8	GOL	A	5016	-	5,5,5	0.19	0	5,5,5	0.51	0
8	GOL	A	5017	-	5,5,5	0.20	0	5,5,5	0.33	0
8	GOL	A	5018	-	5,5,5	0.28	0	5,5,5	0.29	0
8	GOL	A	5019	-	5,5,5	0.25	0	5,5,5	0.31	0
7	YSH	A	5101	-	23,23,23	6.69	14 (60%)	33,33,33	3.73	12 (36%)
9	ACY	A	5201	-	3,3,3	0.85	0	3,3,3	1.58	1 (33%)
3	FES	B	4001	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FES	B	4002	1	0,4,4	0.00	-	0,4,4	0.00	-
4	MTE	B	4003	5	26,26,26	4.56	17 (65%)	34,40,40	4.19	18 (52%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MOS	B	4004	4	0,3,3	0.00	-	0,3,3	0.00	-
6	FAD	B	4005	-	58,58,58	2.47	24 (41%)	85,89,89	2.65	29 (34%)
8	GOL	B	5007	-	5,5,5	0.20	0	5,5,5	0.34	0
8	GOL	B	5008	-	5,5,5	0.17	0	5,5,5	0.40	0
8	GOL	B	5009	-	5,5,5	0.24	0	5,5,5	0.31	0
8	GOL	B	5012	-	5,5,5	0.15	0	5,5,5	0.46	0
8	GOL	B	5013	-	5,5,5	0.16	0	5,5,5	0.30	0
8	GOL	B	5014	-	5,5,5	0.14	0	5,5,5	0.40	0
8	GOL	B	5015	-	5,5,5	0.19	0	5,5,5	0.32	0
8	GOL	B	5020	-	5,5,5	0.18	0	5,5,5	0.35	0
8	GOL	B	5021	-	5,5,5	0.19	0	5,5,5	0.40	0
8	GOL	B	5022	-	5,5,5	0.16	0	5,5,5	0.37	0
7	YSH	B	5102	-	23,23,23	6.83	14 (60%)	33,33,33	3.71	12 (36%)
9	ACY	B	5202	-	3,3,3	0.94	0	3,3,3	1.52	1 (33%)

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
3	FES	A	3001	1	-	0/0/4/4	0/0/1/1
3	FES	A	3002	1	-	0/0/4/4	0/0/1/1
4	MTE	A	3003	5	-	0/6/34/34	0/0/3/3
5	MOS	A	3004	4	-	0/0/0/0	0/0/0/0
6	FAD	A	3005	-	-	0/34/50/50	0/1/6/6
8	GOL	A	5001	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5002	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5003	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5004	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5005	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5006	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5011	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5016	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5017	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5018	-	-	0/4/4/4	0/0/0/0
8	GOL	A	5019	-	-	0/4/4/4	0/0/0/0
7	YSH	A	5101	-	-	0/16/16/16	0/2/2/2
9	ACY	A	5201	-	-	0/0/0/0	0/0/0/0
3	FES	B	4001	1	-	0/0/4/4	0/0/1/1
3	FES	B	4002	1	-	0/0/4/4	0/0/1/1
4	MTE	B	4003	5	-	0/6/34/34	0/0/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MOS	B	4004	4	-	0/0/0/0	0/0/0/0
6	FAD	B	4005	-	-	0/34/50/50	0/1/6/6
8	GOL	B	5007	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5008	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5009	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5012	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5013	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5014	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5015	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5020	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5021	-	-	0/4/4/4	0/0/0/0
8	GOL	B	5022	-	-	0/4/4/4	0/0/0/0
7	YSH	B	5102	-	-	0/16/16/16	0/2/2/2
9	ACY	B	5202	-	-	0/0/0/0	0/0/0/0

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	5102	YSH	C1-N2	21.26	1.70	1.36
7	A	5101	YSH	C1-N2	20.58	1.68	1.36
7	B	5102	YSH	C11-C6	14.26	1.62	1.38
7	A	5101	YSH	C11-C6	14.18	1.62	1.38
4	A	3003	MTE	C9-C10	13.70	1.61	1.41

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	5102	YSH	C4-N3-N2	15.05	114.44	103.70
7	A	5101	YSH	C4-N3-N2	14.56	114.09	103.70
6	A	3005	FAD	N3A-C2A-N1A	-13.20	117.67	128.71
6	B	4005	FAD	N3A-C2A-N1A	-13.04	117.81	128.71
7	A	5101	YSH	C6-N2-N3	11.21	128.73	118.87

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.