



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 08:44 pm GMT

PDB ID : 3AX7
Title : Bovine Xanthine Oxidase, protease cleaved form
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Deposited on : 2011-03-30
Resolution : 2.34 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
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

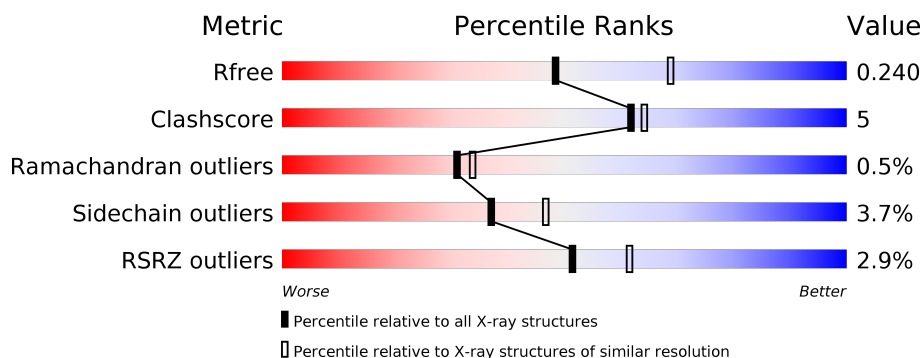
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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}	111664	1763 (2.36-2.32)
Clashscore	122126	1858 (2.36-2.32)
Ramachandran outliers	120053	1834 (2.36-2.32)
Sidechain outliers	120020	1835 (2.36-2.32)
RSRZ outliers	108989	1737 (2.36-2.32)

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. 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	1332	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>8%</div> </div> </div>
1	B	1332	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>9%</div> </div> </div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 19746 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.

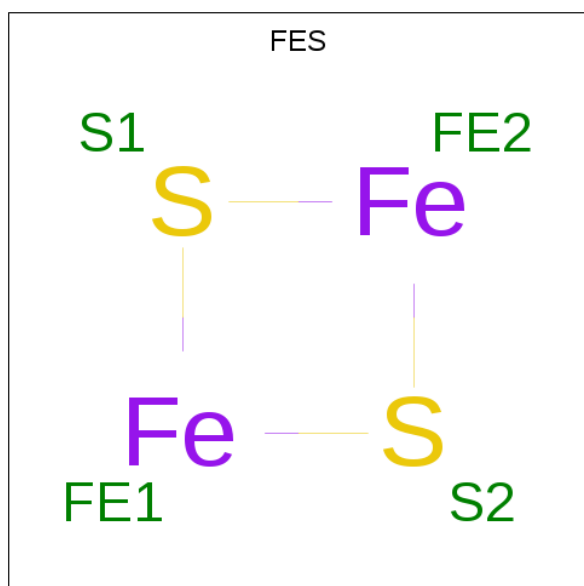
- Molecule 1 is a protein called Xanthine dehydrogenase/oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1225	Total	C	N	O	S	0	0	0
			9476	6013	1632	1771	60			
1	B	1218	Total	C	N	O	S	0	0	0
			9433	5988	1623	1763	59			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	552	HIS	ASP	CONFLICT	UNP P80457
B	552	HIS	ASP	CONFLICT	UNP P80457

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



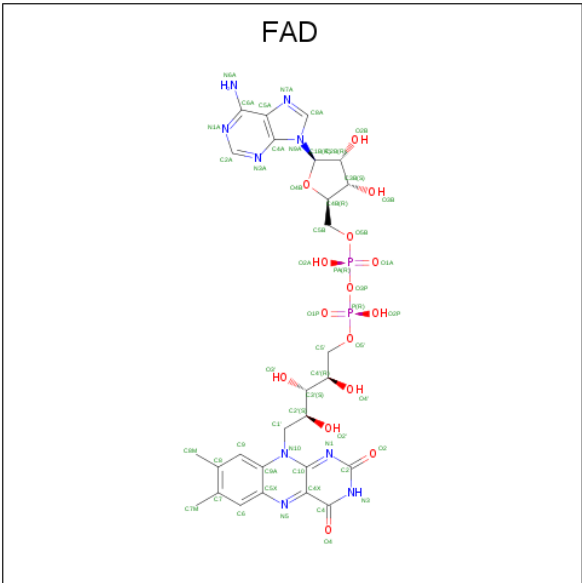
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		

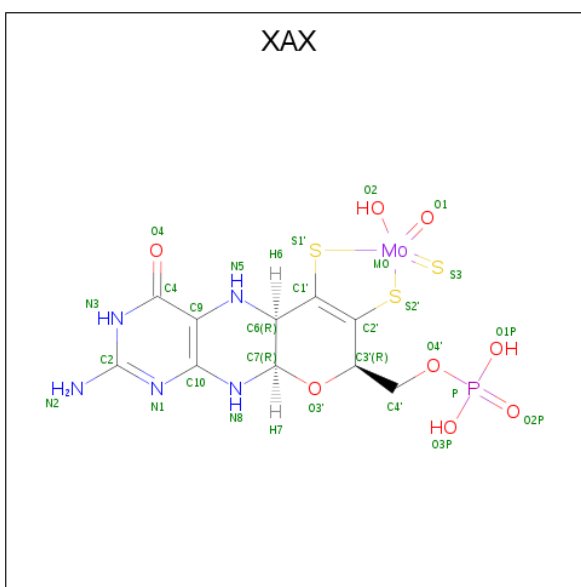
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		

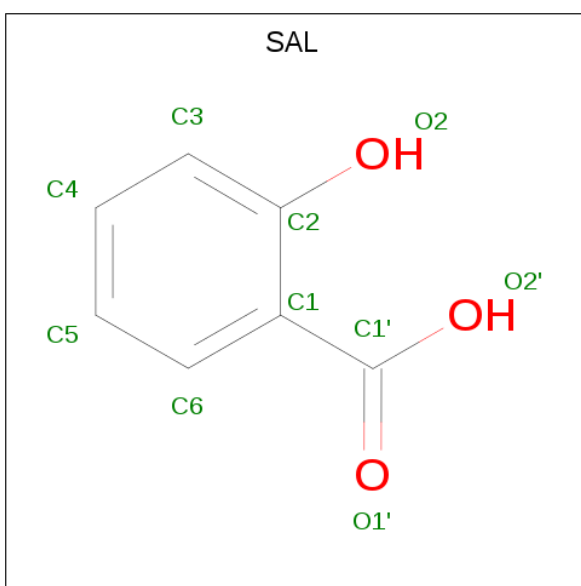
- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).





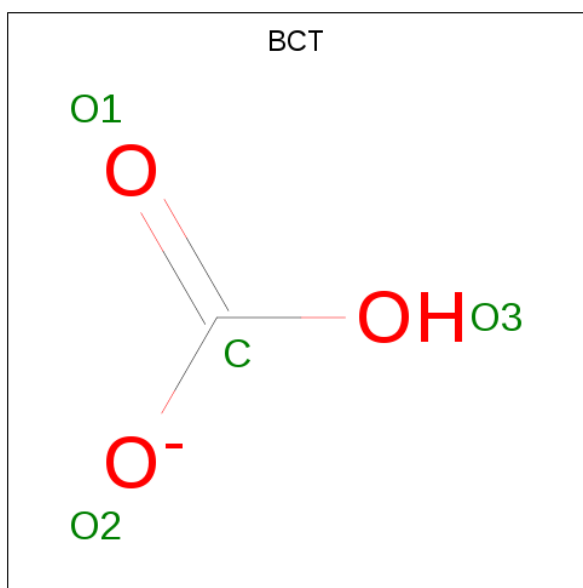
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	A	1	Total	C	Mo	N	O	P	S	0	0
			28	10	1	5	8	1	3		
4	B	1	Total	C	Mo	N	O	P	S	0	0
			28	10	1	5	8	1	3		

- Molecule 5 is 2-HYDROXYBENZOIC ACID (three-letter code: SAL) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	7	3		
5	B	1	Total	C	O	0	0
			10	7	3		

- Molecule 6 is BICARBONATE ION (three-letter code: BCT) (formula: CHO_3^-).



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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

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

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		
8	A	1	Total	Ca	0	0
			1	1		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	316	Total	O	0	0
			316	316		
9	B	283	Total	O	0	0
			283	283		

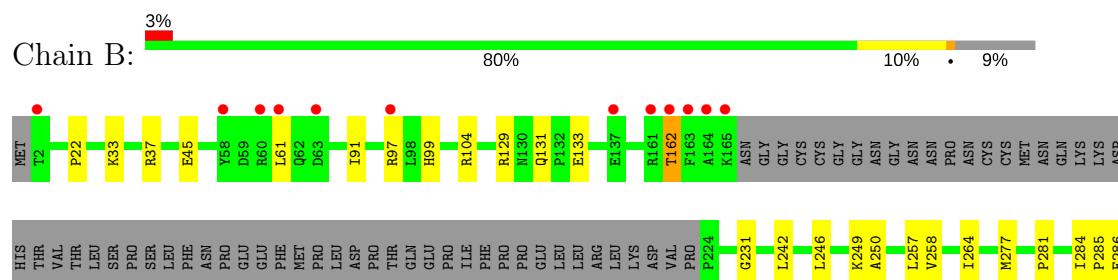
3 Residue-property plots

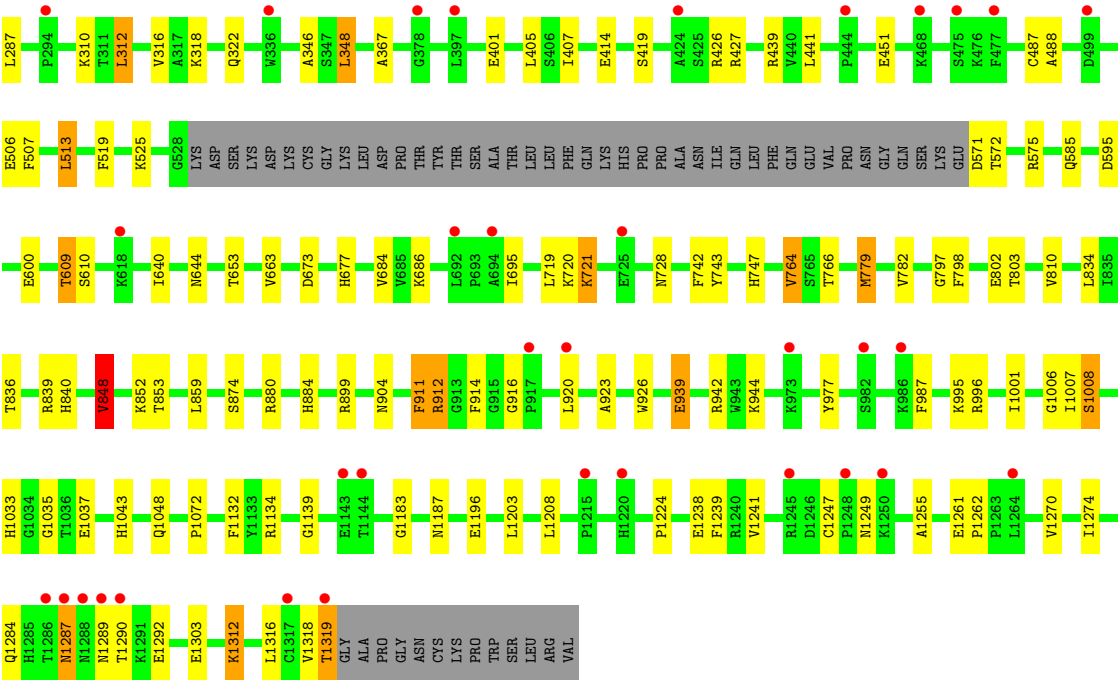
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Xanthine dehydrogenase/oxidase



• Molecule 1: Xanthine dehydrogenase/oxidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	133.48Å 73.15Å 146.27Å 90.00° 98.18° 90.00°	Depositor
Resolution (Å)	36.37 – 2.34 36.37 – 2.34	Depositor EDS
% Data completeness (in resolution range)	93.8 (36.37-2.34) 93.8 (36.37-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.40 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.194 , 0.240 0.195 , 0.240	Depositor DCC
R_{free} test set	5554 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19746	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: XAX, GOL, SAL, CA, FES, BCT, FAD

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	0.64	0/9675	0.69	6/13085 (0.0%)
1	B	0.62	0/9631	0.68	6/13026 (0.0%)
All	All	0.63	0/19306	0.68	12/26111 (0.0%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	839	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	B	942	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	A	779	MET	CG-SD-CE	-5.94	90.69	100.20
1	A	1325	CYS	N-CA-C	5.65	126.26	111.00
1	A	439	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	B	942	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	B	848	VAL	CB-CA-C	-5.34	101.25	111.40
1	A	386	ASP	CB-CG-OD1	5.21	122.98	118.30
1	B	839	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	A	427	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	A	621	ASP	CB-CG-OD1	5.09	122.89	118.30
1	B	513	LEU	CA-CB-CG	5.06	126.94	115.30

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	9476	0	9483	91	0
1	B	9433	0	9439	97	0
2	A	8	0	0	0	0
2	B	8	0	0	0	0
3	A	53	0	31	1	0
3	B	53	0	31	3	0
4	A	28	0	10	0	0
4	B	28	0	10	1	0
5	A	10	0	5	1	0
5	B	10	0	4	1	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	18	0	24	0	0
7	B	12	0	16	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	316	0	0	3	0
9	B	283	0	0	9	0
All	All	19746	0	19053	185	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 5.

All (185) 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:779:MET:SD	9:B:1452:HOH:O	2.09	1.10
1:A:884:HIS:HE1	1:A:1006:GLY:H	1.17	0.92
1:A:720:LYS:O	1:A:721:LYS:HB2	1.70	0.90
1:A:131:GLN:HE21	1:A:133:GLU:H	1.14	0.88
1:A:995:LYS:NZ	1:A:1284:GLN:HE21	1.72	0.86
1:B:884:HIS:HE1	1:B:1006:GLY:H	1.18	0.86
1:A:995:LYS:HZ1	1:A:1284:GLN:HE21	1.20	0.84
1:B:131:GLN:HE21	1:B:133:GLU:H	1.25	0.84
1:B:640:ILE:HG12	1:B:779:MET:HE1	1.60	0.83
1:B:779:MET:CG	9:B:1452:HOH:O	2.25	0.83
1:A:695:ILE:H	1:A:904:ASN:HD22	1.26	0.83
1:B:695:ILE:H	1:B:904:ASN:HD22	1.25	0.82
1:B:764:VAL:HG22	1:B:766:THR:HG22	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:GLN:NE2	1:B:133:GLU:H	1.78	0.80
1:A:884:HIS:CE1	1:A:1006:GLY:H	1.99	0.79
1:A:1324:ASN:O	1:A:1325:CYS:HB3	1.88	0.74
1:B:884:HIS:CE1	1:B:1006:GLY:H	2.06	0.73
1:A:1088:GLN:HG2	1:A:1133:TYR:CD1	2.23	0.73
1:A:1324:ASN:O	1:A:1325:CYS:CB	2.35	0.73
1:B:720:LYS:O	1:B:721:LYS:CB	2.37	0.72
1:A:623:SER:HA	1:A:626:GLN:HE21	1.53	0.71
1:A:851:MET:HE3	1:A:857:VAL:HG21	1.74	0.70
1:B:609:THR:HG22	9:B:1483:HOH:O	1.95	0.67
1:A:571:ASP:N	9:A:1563:HOH:O	2.27	0.67
1:A:840:HIS:HE1	1:A:874:SER:OG	1.77	0.66
1:B:33:LYS:HB3	1:B:33:LYS:NZ	2.10	0.66
1:A:1033:HIS:HD2	1:A:1035:GLY:H	1.42	0.66
1:B:1287:ASN:HA	9:B:1573:HOH:O	1.97	0.65
1:B:852:LYS:HE2	9:B:1530:HOH:O	1.96	0.64
1:B:939:GLU:HG2	1:B:977:TYR:CE2	2.33	0.64
1:B:131:GLN:HE21	1:B:133:GLU:N	1.96	0.63
1:A:673:ASP:OD2	1:A:677:HIS:HD2	1.82	0.62
1:B:1048:GLN:HE22	1:B:1187:ASN:HD22	1.46	0.62
1:B:995:LYS:NZ	1:B:1284:GLN:HE21	1.98	0.62
1:B:764:VAL:HG22	1:B:766:THR:CG2	2.30	0.62
1:B:673:ASP:OD2	1:B:677:HIS:HD2	1.83	0.61
1:A:159:GLY:O	1:A:162:THR:HG22	2.00	0.61
1:A:851:MET:CE	1:A:857:VAL:HG21	2.30	0.61
1:B:779:MET:HG2	9:B:1452:HOH:O	1.97	0.61
1:A:1048:GLN:HE22	1:A:1187:ASN:HD22	1.49	0.60
1:B:720:LYS:O	1:B:721:LYS:HB2	2.01	0.60
1:A:844:ALA:HB2	1:A:922:ILE:HD13	1.84	0.60
1:A:356:SER:OG	1:A:358:ILE:HD13	2.03	0.59
1:A:1033:HIS:CD2	1:A:1035:GLY:H	2.19	0.59
1:A:131:GLN:NE2	1:A:133:GLU:H	1.95	0.59
1:A:1279:ARG:NH2	1:A:1290:THR:O	2.32	0.58
1:B:610:SER:O	1:B:663:VAL:O	2.22	0.58
1:A:1324:ASN:HD22	1:A:1324:ASN:N	2.01	0.57
1:B:571:ASP:N	9:B:1348:HOH:O	2.35	0.57
1:B:1289:ASN:HB2	1:B:1292:GLU:HB2	1.86	0.57
1:A:1324:ASN:ND2	1:A:1324:ASN:N	2.52	0.57
1:A:1203:LEU:C	1:A:1203:LEU:HD12	2.24	0.57
1:A:439:ARG:NH2	1:A:451:GLU:OE1	2.32	0.57
1:B:728:ASN:HD21	1:B:852:LYS:HE3	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:GLN:HG2	1:B:414:GLU:OE2	2.05	0.56
1:B:441:LEU:HB3	1:B:451:GLU:HG3	1.87	0.56
1:B:995:LYS:HZ1	1:B:1284:GLN:HE21	1.51	0.56
1:B:695:ILE:H	1:B:904:ASN:ND2	2.01	0.56
1:B:264:ILE:HD11	3:B:1335:FAD:H3B	1.87	0.56
1:A:131:GLN:HE21	1:A:133:GLU:N	1.94	0.56
1:B:1033:HIS:HD2	1:B:1035:GLY:H	1.54	0.56
1:B:798:PHE:HA	4:B:3003:XAX:HN5	1.70	0.56
1:A:601:ASN:O	1:A:821:HIS:HD2	1.89	0.56
1:A:609:THR:HG23	1:A:664:GLY:HA2	1.88	0.55
1:B:1312:LYS:HB2	1:B:1318:VAL:HB	1.89	0.55
1:B:853:THR:HG23	1:B:944:LYS:NZ	2.21	0.55
1:B:640:ILE:HG12	1:B:779:MET:CE	2.35	0.55
1:A:1326:LYS:CG	1:A:1326:LYS:O	2.55	0.55
1:B:439:ARG:NH2	1:B:451:GLU:OE1	2.39	0.55
1:A:1088:GLN:HG2	1:A:1133:TYR:CE1	2.42	0.54
1:A:468:LYS:O	1:A:472:LYS:HD2	2.07	0.54
1:B:37:ARG:HD3	1:B:595:ASP:O	2.07	0.54
1:A:1128:SER:HB2	1:B:1072:PRO:HG3	1.89	0.54
1:A:764:VAL:HG22	1:A:766:THR:HG22	1.90	0.53
1:B:1183:GLY:HA2	1:B:1247:CYS:O	2.08	0.53
1:A:856:ILE:HD12	1:A:945:ASN:CG	2.29	0.53
1:A:1324:ASN:HD22	1:A:1324:ASN:H	1.55	0.52
1:A:884:HIS:HE1	1:A:1006:GLY:N	1.96	0.52
1:A:1249:ASN:O	1:A:1255:ALA:HA	2.09	0.52
1:A:802:GLU:OE1	5:A:1336:SAL:H4	2.10	0.52
1:B:258:VAL:HG22	1:B:264:ILE:HG13	1.92	0.52
1:B:312:LEU:O	1:B:316:VAL:HG23	2.09	0.52
1:B:853:THR:HG23	1:B:944:LYS:HZ3	1.74	0.52
1:A:338:ALA:HB2	3:A:1335:FAD:C6	2.40	0.52
1:B:284:ILE:HB	1:B:287:LEU:HD12	1.91	0.51
1:B:1048:GLN:NE2	1:B:1187:ASN:HD22	2.09	0.51
1:B:609:THR:CG2	9:B:1483:HOH:O	2.56	0.50
1:A:1126:SER:HB2	1:B:1132:PHE:CD1	2.46	0.50
1:A:257:LEU:HD13	1:A:281:PRO:HG3	1.94	0.50
1:B:250:ALA:HA	1:B:401:GLU:HG2	1.93	0.50
1:B:242:LEU:O	1:B:246:LEU:HG	2.11	0.50
1:A:1324:ASN:O	1:A:1325:CYS:SG	2.70	0.49
1:A:1183:GLY:HA2	1:A:1247:CYS:O	2.11	0.49
1:B:346:ALA:HB1	3:B:1335:FAD:H4'	1.94	0.49
1:A:74:LEU:O	1:A:76:PRO:HD3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:ARG:HD3	1:A:1212:HIS:CD2	2.48	0.49
1:A:356:SER:OG	1:A:358:ILE:CD1	2.61	0.49
1:B:802:GLU:OE1	5:B:1336:SAL:H4	2.13	0.49
1:A:423:GLN:HG2	1:A:425:SER:H	1.78	0.48
1:B:1316:LEU:O	1:B:1319:THR:HB	2.13	0.48
1:B:488:ALA:HA	1:B:1319:THR:OG1	2.13	0.48
1:A:958:ARG:HG2	1:A:960:GLU:HG2	1.94	0.48
1:B:91:ILE:O	1:B:99:HIS:HB2	2.13	0.48
1:A:719:LEU:HD11	1:A:895:ARG:HB2	1.94	0.48
1:B:104:ARG:CZ	1:B:162:THR:HG21	2.44	0.48
1:B:45:GLU:CD	1:B:1224:PRO:HD2	2.34	0.48
1:B:1196:GLU:HG3	1:B:1241:VAL:HG21	1.96	0.47
1:A:112:GLN:HB3	1:A:1039:GLY:O	2.13	0.47
1:A:146:ASN:ND2	1:A:341:GLN:HE22	2.11	0.47
1:A:81:HIS:CD2	1:A:227:LEU:HD11	2.49	0.47
1:B:779:MET:HG2	1:B:810:VAL:HG13	1.96	0.47
1:B:1033:HIS:CD2	1:B:1035:GLY:H	2.32	0.47
1:B:1249:ASN:O	1:B:1255:ALA:HA	2.15	0.47
1:B:348:LEU:HD13	1:B:407:ILE:HD13	1.97	0.47
1:A:640:ILE:HG12	1:A:779:MET:HE1	1.97	0.47
1:A:840:HIS:CE1	1:A:874:SER:OG	2.64	0.47
1:B:840:HIS:HE1	1:B:874:SER:OG	1.98	0.47
1:B:33:LYS:HB3	1:B:33:LYS:HZ3	1.78	0.46
1:B:507:PHE:HB2	1:B:1303:GLU:HG3	1.97	0.46
1:B:585:GLN:NE2	9:B:1365:HOH:O	2.47	0.46
1:B:880:ARG:O	1:B:884:HIS:HD2	1.98	0.46
1:B:572:THR:HA	1:B:575:ARG:HD3	1.98	0.46
1:A:848:VAL:HG13	1:A:859:LEU:HD13	1.97	0.46
1:A:143:PHE:HB3	1:A:1232:PHE:CE1	2.51	0.46
1:A:764:VAL:HG22	1:A:766:THR:CG2	2.45	0.46
1:B:419:SER:HB2	1:B:519:PHE:CD1	2.51	0.46
1:B:853:THR:O	1:B:944:LYS:NZ	2.42	0.45
1:A:319:LEU:HB3	1:A:320:PRO:HD2	1.97	0.45
1:B:916:GLY:O	1:B:920:LEU:HG	2.16	0.45
1:B:1270:VAL:O	1:B:1274:ILE:HG13	2.17	0.45
1:A:59:ASP:OD1	1:A:62:GLN:HG2	2.17	0.45
1:B:284:ILE:HA	1:B:285:PRO:HD3	1.88	0.45
1:B:880:ARG:HD2	1:B:914:PHE:HB3	1.97	0.45
1:A:880:ARG:HD2	1:A:914:PHE:HB3	1.97	0.45
1:B:644:ASN:O	1:B:653:THR:HA	2.17	0.45
1:A:367:ALA:O	1:A:439:ARG:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:LEU:O	3:B:1335:FAD:H2B	2.16	0.45
1:A:1048:GLN:NE2	1:A:1187:ASN:HD22	2.14	0.44
1:A:1176:THR:HG21	1:A:1199:PHE:CZ	2.52	0.44
1:B:987:PHE:CD2	1:B:996:ARG:HG3	2.52	0.44
1:A:1285:HIS:O	1:A:1325:CYS:CB	2.65	0.44
1:B:923:ALA:HA	1:B:926:TRP:NE1	2.33	0.44
1:B:318:LYS:HD3	1:B:318:LYS:HA	1.85	0.44
1:A:1175:ARG:HG2	9:A:1427:HOH:O	2.16	0.44
1:B:911:PHE:O	1:B:912:ARG:C	2.56	0.44
1:A:1128:SER:HB2	1:B:1072:PRO:CG	2.48	0.44
1:A:585:GLN:NE2	9:A:1476:HOH:O	2.50	0.43
1:A:1285:HIS:O	1:A:1325:CYS:HB2	2.18	0.43
1:B:884:HIS:HE1	1:B:1006:GLY:N	2.00	0.43
1:A:719:LEU:HD11	1:A:895:ARG:CB	2.49	0.43
1:A:779:MET:HG3	1:A:780:LEU:HG	2.01	0.43
1:A:614:HIS:HD2	1:A:693:PRO:O	2.00	0.43
1:A:661:THR:O	1:A:904:ASN:HA	2.19	0.42
1:A:37:ARG:HD3	1:A:595:ASP:O	2.18	0.42
1:A:880:ARG:O	1:A:884:HIS:HD2	2.02	0.42
1:B:1203:LEU:HD13	1:B:1270:VAL:HG21	2.01	0.42
1:A:600:GLU:HG3	1:A:601:ASN:N	2.34	0.42
1:A:1312:LYS:HG3	1:A:1318:VAL:HB	2.00	0.42
1:A:1261:GLU:N	1:A:1262:PRO:CD	2.83	0.42
1:B:33:LYS:HZ2	1:B:33:LYS:HB3	1.84	0.42
1:B:22:PRO:HD2	1:B:231:GLY:HA3	2.01	0.42
1:B:1037:GLU:HB2	1:B:1043:HIS:CD2	2.55	0.42
1:B:281:PRO:HB2	1:B:287:LEU:HD13	2.01	0.42
1:B:487:CYS:HB3	1:B:513:LEU:HD13	2.00	0.42
1:A:856:ILE:HD12	1:A:945:ASN:OD1	2.19	0.42
1:B:802:GLU:HG2	1:B:803:THR:HG23	2.02	0.42
1:B:1261:GLU:N	1:B:1262:PRO:CD	2.83	0.41
1:A:995:LYS:HZ2	1:A:1284:GLN:HE21	1.64	0.41
1:A:948:LYS:HE2	1:A:948:LYS:HB3	1.79	0.41
1:A:271:LYS:HG3	1:A:271:LYS:O	2.20	0.41
1:A:117:THR:N	1:A:118:PRO:CD	2.83	0.41
1:A:474:LEU:O	1:A:475:SER:HB2	2.21	0.41
1:B:747:HIS:CD2	1:B:836:THR:HG21	2.55	0.41
1:A:970:GLU:HG2	1:A:1179:VAL:HG21	2.03	0.41
1:B:286:GLU:HB3	1:B:405:LEU:HD11	2.02	0.41
1:B:720:LYS:O	1:B:721:LYS:HB3	2.17	0.41
1:B:1007:ILE:O	1:B:1008:SER:CB	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:367:ALA:O	1:B:439:ARG:HD3	2.21	0.41
1:B:663:VAL:HG12	1:B:834:LEU:HD11	2.02	0.41
1:B:728:ASN:ND2	1:B:852:LYS:HE3	2.33	0.41
1:A:601:ASN:O	1:A:821:HIS:CD2	2.72	0.40
1:A:695:ILE:H	1:A:904:ASN:ND2	2.05	0.40
1:A:754:LYS:HE2	1:A:761:GLU:HB2	2.04	0.40
1:A:733:GLU:HA	1:A:844:ALA:O	2.21	0.40
1:B:848:VAL:HG13	1:B:859:LEU:HD13	2.04	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	1219/1332 (92%)	1172 (96%)	39 (3%)	8 (1%)	24	24
1	B	1212/1332 (91%)	1162 (96%)	45 (4%)	5 (0%)	36	40
All	All	2431/2664 (91%)	2334 (96%)	84 (4%)	13 (0%)	31	34

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	721	LYS
1	A	1008	SER
1	A	1325	CYS
1	B	1008	SER
1	B	721	LYS
1	B	912	ARG
1	A	527	LEU
1	A	912	ARG
1	A	797	GLY
1	B	797	GLY

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Mol	Chain	Res	Type
1	A	1139	GLY
1	A	1253	ILE
1	B	1139	GLY

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	1030/1128 (91%)	990 (96%)	40 (4%)	35	45
1	B	1026/1128 (91%)	990 (96%)	36 (4%)	39	49
All	All	2056/2256 (91%)	1980 (96%)	76 (4%)	37	47

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LYS
1	A	60	ARG
1	A	62	GLN
1	A	65	ILE
1	A	161	ARG
1	A	165	LYS
1	A	243	LYS
1	A	312	LEU
1	A	318	LYS
1	A	335	ARG
1	A	348	LEU
1	A	358	ILE
1	A	401	GLU
1	A	433	LYS
1	A	472	LYS
1	A	525	LYS
1	A	577	LEU
1	A	609	THR
1	A	657	LYS
1	A	684	VAL

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Mol	Chain	Res	Type
1	A	686	LYS
1	A	720	LYS
1	A	742	PHE
1	A	743	TYR
1	A	764	VAL
1	A	774	SER
1	A	779	MET
1	A	782	VAL
1	A	818	LYS
1	A	848	VAL
1	A	857	VAL
1	A	911	PHE
1	A	960	GLU
1	A	983	GLU
1	A	1001	ILE
1	A	1203	LEU
1	A	1238	GLU
1	A	1279	ARG
1	A	1287	ASN
1	A	1324	ASN
1	B	61	LEU
1	B	97	ARG
1	B	129	ARG
1	B	162	THR
1	B	249	LYS
1	B	277	MET
1	B	310	LYS
1	B	312	LEU
1	B	348	LEU
1	B	426	ARG
1	B	427	ARG
1	B	506	GLU
1	B	525	LYS
1	B	600	GLU
1	B	609	THR
1	B	684	VAL
1	B	686	LYS
1	B	719	LEU
1	B	742	PHE
1	B	743	TYR
1	B	764	VAL
1	B	779	MET

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Mol	Chain	Res	Type
1	B	782	VAL
1	B	848	VAL
1	B	899	ARG
1	B	911	PHE
1	B	939	GLU
1	B	1001	ILE
1	B	1134	ARG
1	B	1208	LEU
1	B	1238	GLU
1	B	1239	PHE
1	B	1287	ASN
1	B	1290	THR
1	B	1312	LYS
1	B	1319	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN
1	A	146	ASN
1	A	471	GLN
1	A	585	GLN
1	A	614	HIS
1	A	626	GLN
1	A	677	HIS
1	A	821	HIS
1	A	840	HIS
1	A	884	HIS
1	A	904	ASN
1	A	1033	HIS
1	A	1048	GLN
1	A	1212	HIS
1	A	1284	GLN
1	A	1287	ASN
1	A	1324	ASN
1	B	131	GLN
1	B	146	ASN
1	B	585	GLN
1	B	614	HIS
1	B	626	GLN
1	B	677	HIS
1	B	728	ASN

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Mol	Chain	Res	Type
1	B	821	HIS
1	B	840	HIS
1	B	884	HIS
1	B	904	ASN
1	B	1033	HIS
1	B	1048	GLN
1	B	1088	GLN
1	B	1284	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 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	$\# Z > 2$
2	FES	A	1333	1	0,4,4	0.00	-	0,4,4	0.00	-
2	FES	A	1334	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FAD	A	1335	-	51,58,58	1.28	5 (9%)	57,89,89	2.21	9 (15%)
5	SAL	A	1336	-	7,10,10	1.33	1 (14%)	9,13,13	1.57	3 (33%)
6	BCT	A	1337	-	0,3,3	0.00	-	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	A	1338	-	5,5,5	0.61	0	5,5,5	0.59	0
7	GOL	A	1339	-	5,5,5	0.34	0	5,5,5	0.36	0
7	GOL	A	1340	-	5,5,5	0.34	0	5,5,5	0.55	0
4	XAX	A	3003	-	23,31,31	2.72	7 (30%)	20,52,52	1.97	7 (35%)
2	FES	B	1333	1	0,4,4	0.00	-	0,4,4	0.00	-
2	FES	B	1334	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FAD	B	1335	-	51,58,58	1.37	6 (11%)	57,89,89	1.95	8 (14%)
5	SAL	B	1336	-	7,10,10	1.31	1 (14%)	9,13,13	1.48	2 (22%)
6	BCT	B	1337	-	0,3,3	0.00	-	0,3,3	0.00	-
7	GOL	B	1338	-	5,5,5	0.35	0	5,5,5	0.42	0
7	GOL	B	1339	-	5,5,5	0.35	0	5,5,5	0.41	0
4	XAX	B	3003	-	23,31,31	2.46	7 (30%)	20,52,52	2.47	11 (55%)

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	FES	A	1333	1	-	0/0/4/4	0/1/1/1
2	FES	A	1334	1	-	0/0/4/4	0/1/1/1
3	FAD	A	1335	-	-	0/28/50/50	0/6/6/6
5	SAL	A	1336	-	-	0/0/4/4	0/1/1/1
6	BCT	A	1337	-	-	0/0/0/0	0/0/0/0
7	GOL	A	1338	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1339	-	-	0/4/4/4	0/0/0/0
7	GOL	A	1340	-	-	0/4/4/4	0/0/0/0
4	XAX	A	3003	-	-	0/6/46/46	0/4/4/4
2	FES	B	1333	1	-	0/0/4/4	0/1/1/1
2	FES	B	1334	1	-	0/0/4/4	0/1/1/1
3	FAD	B	1335	-	-	0/28/50/50	0/6/6/6
5	SAL	B	1336	-	-	0/0/4/4	0/1/1/1
6	BCT	B	1337	-	-	0/0/0/0	0/0/0/0
7	GOL	B	1338	-	-	0/4/4/4	0/0/0/0
7	GOL	B	1339	-	-	0/4/4/4	0/0/0/0
4	XAX	B	3003	-	-	0/6/46/46	0/4/4/4

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3003	XAX	C1'-S1'	-5.37	1.65	1.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3003	XAX	C2'-S2'	-4.42	1.67	1.76
4	A	3003	XAX	C1'-S1'	-4.11	1.68	1.76
4	B	3003	XAX	C2'-S2'	-3.16	1.70	1.76
4	A	3003	XAX	C7-C6	2.30	1.55	1.53
3	A	1335	FAD	C4-N3	2.32	1.37	1.33
3	B	1335	FAD	C10-N1	2.42	1.36	1.33
4	B	3003	XAX	C7-C6	2.68	1.55	1.53
3	B	1335	FAD	C5X-N5	2.71	1.39	1.35
3	A	1335	FAD	C2A-N1A	2.86	1.39	1.33
5	A	1336	SAL	C1-C2	3.13	1.49	1.40
3	B	1335	FAD	C2A-N1A	3.14	1.39	1.33
5	B	1336	SAL	C1-C2	3.32	1.50	1.40
4	B	3003	XAX	C9-N5	3.41	1.45	1.38
3	A	1335	FAD	C2A-N3A	3.49	1.37	1.32
3	B	1335	FAD	C4-N3	3.52	1.39	1.33
3	A	1335	FAD	C10-N1	3.56	1.38	1.33
3	B	1335	FAD	C4X-N5	3.73	1.38	1.33
3	A	1335	FAD	C4X-N5	4.01	1.39	1.33
4	B	3003	XAX	C9-C10	4.11	1.49	1.41
4	B	3003	XAX	O4-C4	4.40	1.35	1.24
4	A	3003	XAX	O4-C4	4.51	1.35	1.24
3	B	1335	FAD	C2A-N3A	4.60	1.39	1.32
4	A	3003	XAX	C9-C10	4.83	1.50	1.41
4	A	3003	XAX	C9-N5	5.24	1.48	1.38
4	B	3003	XAX	C4-C9	6.16	1.48	1.41
4	A	3003	XAX	C4-C9	6.39	1.48	1.41

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1335	FAD	N3A-C2A-N1A	-11.76	118.80	128.86
3	B	1335	FAD	N3A-C2A-N1A	-9.60	120.64	128.86
4	B	3003	XAX	C4-C9-C10	-4.33	110.65	114.56
4	B	3003	XAX	N3-C2-N1	-3.50	119.87	125.43
3	A	1335	FAD	C4X-C4-N3	-3.13	119.02	123.47
4	A	3003	XAX	O3P-P-O4'	-3.11	98.46	106.73
4	A	3003	XAX	C2'-C1'-S1'	-2.62	118.66	120.15
4	B	3003	XAX	C2'-C1'-S1'	-2.61	118.67	120.15
3	B	1335	FAD	C4X-C4-N3	-2.47	119.96	123.47
3	A	1335	FAD	C1B-N9A-C4A	-2.41	122.48	126.64
5	A	1336	SAL	C4-C3-C2	-2.28	117.11	120.05
3	B	1335	FAD	C1'-N10-C10	-2.20	116.26	118.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1335	FAD	C4A-C5A-N7A	-2.17	107.31	109.41
5	B	1336	SAL	C4-C3-C2	-2.16	117.27	120.05
4	A	3003	XAX	N3-C2-N1	-2.15	122.02	125.43
4	B	3003	XAX	C1'-C2'-S2'	-2.14	118.94	120.15
4	B	3003	XAX	O3P-P-O4'	-2.06	101.25	106.73
4	B	3003	XAX	O4'-P-O2P	-2.00	100.86	106.47
3	A	1335	FAD	C6-C5X-C9A	2.01	121.70	119.01
4	B	3003	XAX	O3P-P-O2P	2.07	118.67	110.60
4	A	3003	XAX	N2-C2-N1	2.08	120.52	117.25
5	A	1336	SAL	C6-C1-C2	2.13	121.60	117.42
3	A	1335	FAD	C2A-N1A-C6A	2.20	122.50	118.75
4	B	3003	XAX	N2-C2-N1	2.26	120.79	117.25
3	B	1335	FAD	C4-C4X-N5	2.26	121.24	118.70
5	A	1336	SAL	C5-C4-C3	2.30	123.34	120.20
4	A	3003	XAX	N8-C10-N1	2.30	121.36	116.90
4	A	3003	XAX	C2-N1-C10	2.38	119.85	114.50
4	B	3003	XAX	O3'-C7-C6	2.59	110.69	108.96
5	B	1336	SAL	C5-C4-C3	2.60	123.77	120.20
3	A	1335	FAD	C5X-C9A-N10	3.00	120.01	117.71
4	B	3003	XAX	C2-N1-C10	3.05	121.35	114.50
3	B	1335	FAD	C4X-N5-C5X	3.45	120.38	116.76
3	A	1335	FAD	C4X-N5-C5X	3.67	120.60	116.76
3	B	1335	FAD	C4-N3-C2	4.70	119.14	115.14
4	A	3003	XAX	C4-N3-C2	4.75	122.89	116.06
3	A	1335	FAD	C1'-N10-C9A	4.83	122.60	118.31
4	B	3003	XAX	C4-N3-C2	5.69	124.24	116.06
3	B	1335	FAD	C1'-N10-C9A	6.07	123.70	118.31
3	A	1335	FAD	C4-N3-C2	6.41	120.60	115.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1335	FAD	1	0
5	A	1336	SAL	1	0
3	B	1335	FAD	3	0
5	B	1336	SAL	1	0
4	B	3003	XAX	1	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	1225/1332 (91%)	-0.01	24 (1%) 65 74	17, 27, 43, 62	0
1	B	1218/1332 (91%)	0.07	46 (3%) 40 51	17, 28, 44, 64	0
All	All	2443/2664 (91%)	0.03	70 (2%) 51 61	17, 28, 43, 64	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1287	ASN	6.3
1	A	58	TYR	5.8
1	B	1290	THR	5.5
1	B	165	LYS	5.5
1	B	2	THR	5.0
1	B	477	PHE	4.8
1	B	1288	ASN	4.7
1	B	164	ALA	4.2
1	A	165	LYS	4.0
1	A	61	LEU	3.9
1	B	162	THR	3.9
1	B	1250	LYS	3.8
1	A	2	THR	3.7
1	A	60	ARG	3.7
1	B	58	TYR	3.5
1	A	1246	ASP	3.4
1	B	618	LYS	3.3
1	A	720	LYS	3.2
1	B	1143	GLU	3.1
1	B	692	LEU	3.1
1	B	1248	PRO	3.1
1	B	725	GLU	3.1
1	A	724	SER	3.0
1	A	1247	CYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	97	ARG	3.0
1	B	1286	THR	3.0
1	B	336	TRP	3.0
1	A	378	GLY	2.9
1	B	1289	ASN	2.9
1	B	63	ASP	2.8
1	B	163	PHE	2.8
1	B	161	ARG	2.8
1	A	97	ARG	2.6
1	A	1245	ARG	2.6
1	B	1319	THR	2.6
1	B	468	LYS	2.6
1	B	60	ARG	2.5
1	B	1144	THR	2.5
1	B	499	ASP	2.5
1	A	983	GLU	2.5
1	B	986	LYS	2.5
1	B	444	PRO	2.4
1	B	1317	CYS	2.4
1	A	499	ASP	2.4
1	A	528	GLY	2.3
1	B	424	ALA	2.3
1	B	137	GLU	2.3
1	B	1264	LEU	2.3
1	A	1326	LYS	2.3
1	A	498	PRO	2.3
1	A	1215	PRO	2.3
1	B	973	LYS	2.3
1	A	164	ALA	2.3
1	B	294	PRO	2.2
1	B	920	LEU	2.2
1	B	475	SER	2.2
1	A	986	LYS	2.1
1	A	161	ARG	2.1
1	B	1220	HIS	2.1
1	B	982	SER	2.1
1	B	61	LEU	2.1
1	B	397	LEU	2.1
1	A	911	PHE	2.1
1	A	982	SER	2.1
1	B	1215	PRO	2.1
1	B	917	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	378	GLY	2.0
1	A	1325	CYS	2.0
1	B	1245	ARG	2.0
1	B	694	ALA	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
5	SAL	B	1336	10/10	0.87	0.18	35,37,38,40	0
5	SAL	A	1336	10/10	0.92	0.21	27,30,31,31	0
7	GOL	A	1340	6/6	0.95	0.13	40,40,40,41	0
7	GOL	B	1338	6/6	0.96	0.15	29,30,30,31	0
3	FAD	B	1335	53/53	0.96	0.14	23,28,30,31	0
7	GOL	A	1338	6/6	0.96	0.11	27,28,30,30	0
7	GOL	B	1339	6/6	0.96	0.13	19,25,27,27	0
7	GOL	A	1339	6/6	0.97	0.11	26,27,28,29	0
6	BCT	B	1337	4/4	0.97	0.14	17,17,18,20	0
3	FAD	A	1335	53/53	0.97	0.13	20,24,27,30	0
8	CA	B	1340	1/1	0.98	0.13	24,24,24,24	0
6	BCT	A	1337	4/4	0.99	0.21	20,21,22,22	0
4	XAX	B	3003	28/28	0.99	0.15	14,23,29,34	0
4	XAX	A	3003	28/28	0.99	0.15	15,20,25,33	0
2	FES	A	1333	4/4	0.99	0.10	20,20,21,24	0
2	FES	A	1334	4/4	0.99	0.09	19,21,21,22	0
2	FES	B	1333	4/4	0.99	0.11	20,20,21,23	0
8	CA	A	1341	1/1	0.99	0.10	22,22,22,22	0
2	FES	B	1334	4/4	1.00	0.10	20,21,22,23	0

6.5 Other polymers ⓘ

There are no such residues in this entry.