



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:08 AM GMT

PDB ID : 3DJJ
Title : Catalytic cycle of human glutathione reductase near 1 Å resolution
Authors : Berkholz, D.S.; Faber, H.R.; Savvides, S.N.; Karplus, P.A.
Deposited on : 2008-06-23
Resolution : 1.10 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

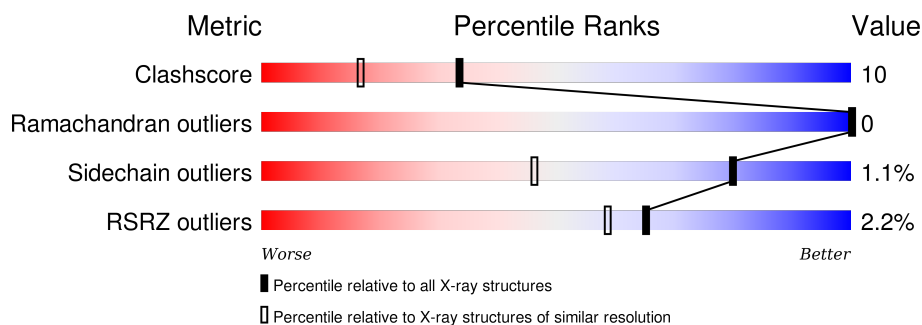
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.10 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	102246	1055 (1.14-1.06)
Ramachandran outliers	100387	1016 (1.14-1.06)
Sidechain outliers	100360	1014 (1.14-1.06)
RSRZ outliers	91569	1009 (1.14-1.06)

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	478	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	485	-	-	-	X
2	PO4	A	487	-	-	X	X
6	GOL	A	602	-	-	-	X
6	GOL	A	603	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	A	604	-	-	-	X
6	GOL	A	605	-	-	-	X
6	GOL	A	606	-	-	-	X
6	GOL	A	607	-	-	X	X
6	GOL	A	608	-	-	X	X

2 Entry composition [i](#)

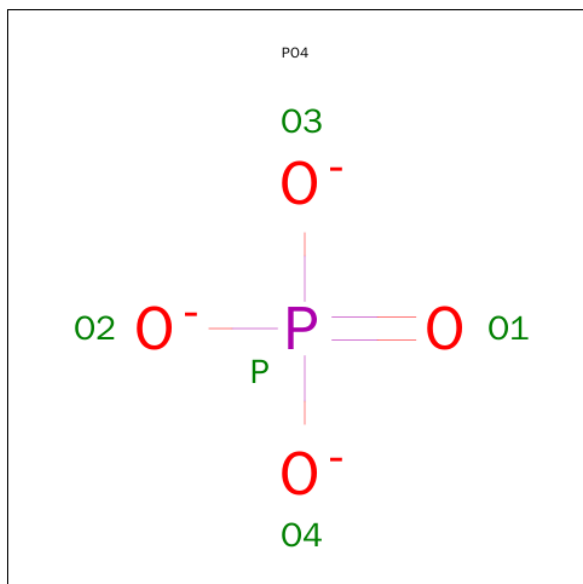
There are 7 unique types of molecules in this entry. The entry contains 4923 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutathione reductase, mitochondrial precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	462	Total	C	N	O	S	0	70	0
			3842	2444	646	720	32			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



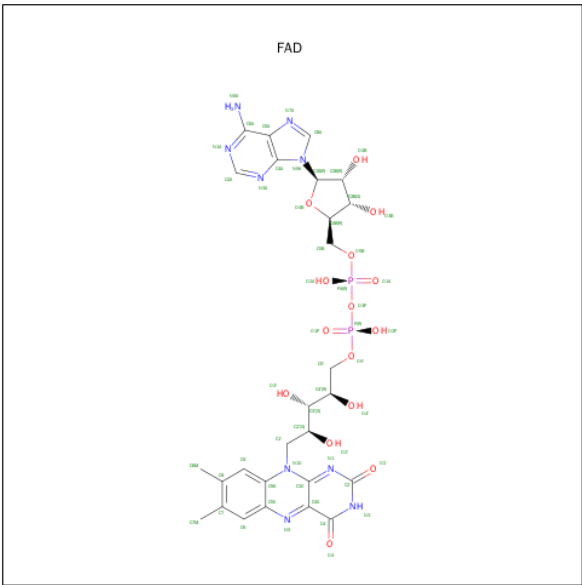
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



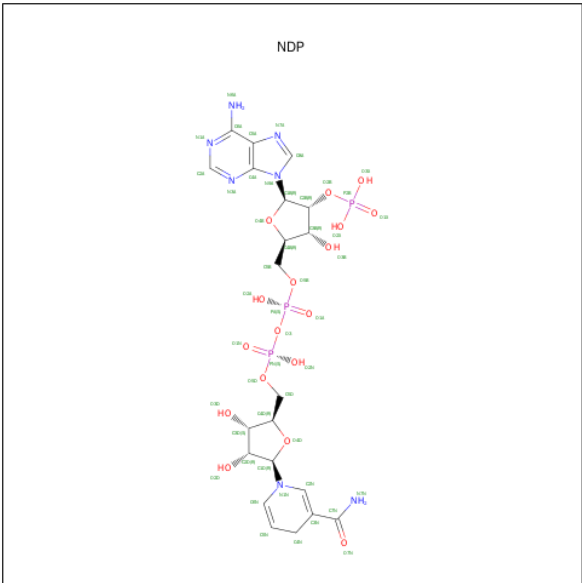
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		
3	A	1	Total	O	0	0
			1	1		
3	A	1	Total	O	0	0
			1	1		
3	A	1	Total	O	0	0
			1	1		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 5 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

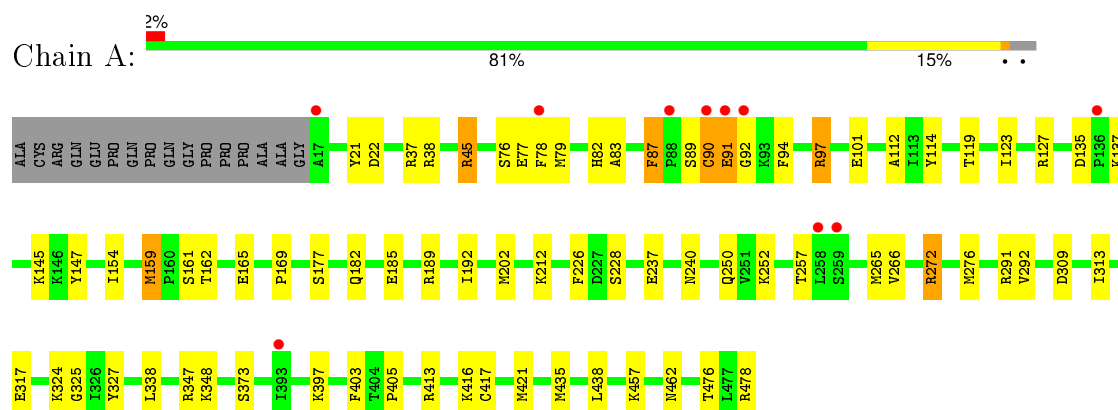
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	878	Total	O	0	35
			903	903		

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: Glutathione reductase, mitochondrial precursor



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.67Å 62.36Å 84.16Å 90.00° 122.29° 90.00°	Depositor
Resolution (Å)	100.00 – 1.10 41.26 – 1.10	Depositor EDS
% Data completeness (in resolution range)	90.9 (100.00-1.10) 85.4 (41.26-1.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.06 (at 1.10Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.113 , 0.147 0.121 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 67.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 184585 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	4923	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.84% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, PO4, SO4, FAD, NDP

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	0.76	1/4126 (0.0%)	1.29	36/5570 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	ARG	CD-NE	-5.32	1.37	1.46

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ARG	CD-NE-CZ	17.59	148.23	123.60
1	A	114	TYR	CB-CG-CD1	11.50	127.90	121.00
1	A	272[A]	ARG	CD-NE-CZ	8.82	135.94	123.60
1	A	272[B]	ARG	CD-NE-CZ	8.82	135.94	123.60
1	A	127	ARG	NE-CZ-NH1	8.70	124.65	120.30
1	A	347	ARG	NE-CZ-NH1	-8.62	115.99	120.30
1	A	309[A]	ASP	CB-CG-OD1	8.46	125.91	118.30
1	A	309[B]	ASP	CB-CG-OD1	8.46	125.91	118.30
1	A	82[A]	HIS	CA-CB-CG	7.85	126.95	113.60
1	A	82[B]	HIS	CA-CB-CG	7.85	126.95	113.60
1	A	291	ARG	NE-CZ-NH2	7.61	124.11	120.30
1	A	272[A]	ARG	NE-CZ-NH2	7.61	124.11	120.30
1	A	272[B]	ARG	NE-CZ-NH2	7.61	124.11	120.30
1	A	37	ARG	NE-CZ-NH1	-7.02	116.79	120.30
1	A	97	ARG	NE-CZ-NH2	6.99	123.80	120.30
1	A	21	TYR	CG-CD1-CE1	6.97	126.88	121.30
1	A	45	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	435	MET	CG-SD-CE	-6.75	89.40	100.20
1	A	135	ASP	CB-CG-OD1	6.14	123.83	118.30
1	A	265	MET	CA-CB-CG	6.09	123.66	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	TYR	CG-CD2-CE2	6.09	126.17	121.30
1	A	38	ARG	NE-CZ-NH2	6.07	123.34	120.30
1	A	265	MET	CG-SD-CE	6.03	109.84	100.20
1	A	317	GLU	OE1-CD-OE2	5.97	130.46	123.30
1	A	373[A]	SER	N-CA-CB	-5.95	101.58	110.50
1	A	373[B]	SER	N-CA-CB	-5.95	101.58	110.50
1	A	397	LYS	CB-CG-CD	5.86	126.82	111.60
1	A	127	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	A	237	GLU	OE1-CD-OE2	-5.58	116.61	123.30
1	A	21	TYR	CB-CG-CD1	5.48	124.29	121.00
1	A	462[A]	ASN	CA-CB-CG	5.30	125.07	113.40
1	A	462[B]	ASN	CA-CB-CG	5.30	125.07	113.40
1	A	416	LYS	CA-CB-CG	5.29	125.03	113.40
1	A	189	ARG	NE-CZ-NH2	5.22	122.91	120.30
1	A	87	PHE	CB-CG-CD2	5.17	124.42	120.80
1	A	94	PHE	CG-CD2-CE2	5.04	126.35	120.80

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	3842	0	3880	68	0
2	A	25	0	0	4	0
3	A	4	0	0	0	0
4	A	53	0	31	0	0
5	A	48	0	26	2	0
6	A	48	0	60	21	0
7	A	903	0	0	51	0
All	All	4923	0	3997	83	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 10.

All (83) 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:A:91[A]:GLU:N	7:A:1807[A]:HOH:O	1.76	1.19
1:A:78[B]:PHE:CG	7:A:2824:HOH:O	2.22	0.92
2:A:486:PO4:P	7:A:1622:HOH:O	2.38	0.81
1:A:257:THR:HA	7:A:1366:HOH:O	1.84	0.78
6:A:601:GOL:H32	7:A:1300:HOH:O	1.86	0.75
1:A:476[B]:THR:HG21	7:A:1303:HOH:O	1.86	0.74
1:A:338:LEU:HD21	7:A:1300:HOH:O	1.90	0.70
1:A:78[B]:PHE:CD1	7:A:2824:HOH:O	2.41	0.70
1:A:292[B]:VAL:HG13	7:A:1694:HOH:O	1.92	0.68
6:A:607:GOL:H31	7:A:1316:HOH:O	1.94	0.68
1:A:276[B]:MET:HE1	7:A:3149:HOH:O	1.94	0.67
1:A:266[B]:VAL:HG22	1:A:276[B]:MET:SD	2.35	0.66
6:A:604:GOL:H31	7:A:1695:HOH:O	1.96	0.65
1:A:161[A]:SER:OG	1:A:292[A]:VAL:HG13	1.97	0.65
1:A:137:LYS:HE3	7:A:1523:HOH:O	1.96	0.65
1:A:324[B]:LYS:HD2	7:A:1210:HOH:O	1.95	0.64
5:A:480:NDP:H2D	7:A:1300:HOH:O	1.97	0.64
1:A:292[B]:VAL:CG1	7:A:1694:HOH:O	2.44	0.64
1:A:91[B]:GLU:HG2	7:A:1701:HOH:O	1.98	0.63
1:A:324[B]:LYS:HE3	7:A:1258:HOH:O	1.97	0.63
1:A:324[B]:LYS:HG3	7:A:3788:HOH:O	2.00	0.61
1:A:250:GLN:HG2	7:A:1257:HOH:O	1.99	0.61
1:A:92[B]:GLY:HA3	7:A:1613:HOH:O	2.01	0.60
6:A:607:GOL:H11	7:A:9004[B]:HOH:O	2.01	0.59
1:A:91[B]:GLU:CG	7:A:1701:HOH:O	2.51	0.57
1:A:438:LEU:HD21	7:A:1794:HOH:O	2.04	0.57
1:A:162[B]:THR:HG21	7:A:1797:HOH:O	2.05	0.57
1:A:421:MET:SD	1:A:457[B]:LYS:HD3	2.45	0.56
1:A:101[A]:GLU:HG3	7:A:2792[A]:HOH:O	2.05	0.56
6:A:601:GOL:HO2	6:A:608:GOL:HO1	1.52	0.56
1:A:405:PRO:HG3	1:A:417[B]:CYS:SG	2.46	0.56
1:A:212[A]:LYS:HD3	7:A:3423:HOH:O	2.05	0.56
1:A:403:PHE:O	1:A:417[B]:CYS:HB2	2.06	0.55
1:A:97:ARG:HG3	7:A:1328:HOH:O	2.06	0.55
1:A:145[A]:LYS:HE2	1:A:147:TYR:OH	2.07	0.54
1:A:90[A]:CYS:C	7:A:1807[A]:HOH:O	2.24	0.54
1:A:226:PHE:HA	6:A:608:GOL:H32	1.90	0.54
1:A:325:GLY:HA2	7:A:1203:HOH:O	2.09	0.52
1:A:212[A]:LYS:HD2	7:A:1164:HOH:O	2.08	0.52
2:A:487:PO4:O4	6:A:607:GOL:O1	2.28	0.52
1:A:119:THR:HA	7:A:1576:HOH:O	2.11	0.51
1:A:177:SER:HA	1:A:202[B]:MET:HE3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:ASN:HB3	7:A:1447:HOH:O	2.11	0.50
1:A:112:ALA:HA	6:A:607:GOL:H12	1.94	0.50
1:A:226:PHE:CE1	6:A:608:GOL:H11	2.46	0.50
1:A:324[A]:LYS:HG3	6:A:603:GOL:H31	1.93	0.49
6:A:606:GOL:H12	7:A:1571:HOH:O	2.13	0.49
1:A:76[A]:SER:OG	7:A:2730[A]:HOH:O	2.19	0.48
2:A:487:PO4:P	6:A:607:GOL:O1	2.72	0.47
6:A:608:GOL:H31	7:A:1159:HOH:O	2.15	0.46
1:A:272[A]:ARG:HD3	7:A:1245:HOH:O	2.14	0.46
1:A:77[A]:GLU:HG3	7:A:3430[A]:HOH:O	2.15	0.46
1:A:83:ALA:HA	1:A:87:PHE:O	2.16	0.45
1:A:77[B]:GLU:OE2	1:A:413:ARG:NH2	2.49	0.45
1:A:123:ILE:N	7:A:1576:HOH:O	2.50	0.45
1:A:154:ILE:HG21	1:A:313[B]:ILE:CD1	2.47	0.45
1:A:182[A]:GLN:NE2	7:A:3192:HOH:O	2.49	0.44
1:A:327:TYR:OH	6:A:603:GOL:H2	2.18	0.44
1:A:97:ARG:NH1	1:A:185:GLU:OE2	2.50	0.44
6:A:608:GOL:H31	7:A:2763[A]:HOH:O	2.17	0.44
1:A:79[B]:MET:HB3	1:A:79[B]:MET:HE3	1.81	0.44
2:A:487:PO4:P	6:A:607:GOL:HO2	2.41	0.44
1:A:159[A]:MET:HE2	1:A:159[A]:MET:HB2	1.96	0.43
1:A:348[B]:LYS:NZ	7:A:1586:HOH:O	2.50	0.43
1:A:165[B]:GLU:CD	1:A:169:PRO:HA	2.39	0.43
1:A:478:ARG:HG2	7:A:1358:HOH:O	2.19	0.43
1:A:22[B]:ASP:OD2	1:A:45:ARG:NH2	2.50	0.43
1:A:89[B]:SER:O	1:A:90[B]:CYS:HB2	2.19	0.42
1:A:276[B]:MET:HE2	7:A:1685:HOH:O	2.17	0.42
1:A:228:SER:OG	6:A:602:GOL:H12	2.18	0.42
5:A:480:NDP:H2A	7:A:1257:HOH:O	2.18	0.42
1:A:90[A]:CYS:HA	7:A:1807[A]:HOH:O	2.20	0.42
1:A:226:PHE:CZ	6:A:608:GOL:H11	2.54	0.42
1:A:79[B]:MET:HG2	1:A:90[B]:CYS:O	2.20	0.41
1:A:325:GLY:H	6:A:603:GOL:H2	1.84	0.41
1:A:325:GLY:H	6:A:603:GOL:C2	2.34	0.41
1:A:272[B]:ARG:NH2	7:A:1718:HOH:O	2.50	0.41
1:A:438:LEU:HD11	7:A:1794:HOH:O	2.20	0.41
1:A:78[B]:PHE:CD2	7:A:2824:HOH:O	2.63	0.40
1:A:90[A]:CYS:CA	7:A:1807[A]:HOH:O	2.69	0.40
1:A:226:PHE:CD1	6:A:608:GOL:H11	2.57	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	530/478 (111%)	511 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	447/393 (114%)	439 (98%)	8 (2%)	66	26

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90[A]	CYS
1	A	90[B]	CYS
1	A	91[A]	GLU
1	A	91[B]	GLU
1	A	159[A]	MET
1	A	159[B]	MET
1	A	252[A]	LYS
1	A	252[B]	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 19 ligands modelled in this entry, 4 are modelled with single atom - leaving 15 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	$\# Z > 2$
4	FAD	A	479	-	48,58,58	1.55	6 (12%)	54,89,89	1.81	8 (14%)
5	NDP	A	480	-	42,52,52	1.31	5 (11%)	55,80,80	1.10	4 (7%)
2	PO4	A	481	-	4,4,4	0.41	0	6,6,6	0.26	0
2	PO4	A	482	-	4,4,4	0.63	0	6,6,6	0.28	0
2	PO4	A	485	-	4,4,4	0.65	0	6,6,6	0.28	0
2	PO4	A	486	-	4,4,4	0.83	0	6,6,6	0.33	0
2	PO4	A	487	-	4,4,4	0.93	0	6,6,6	0.32	0
6	GOL	A	601	-	5,5,5	0.67	0	5,5,5	1.34	1 (20%)
6	GOL	A	602	-	5,5,5	1.07	0	5,5,5	1.11	0
6	GOL	A	603	-	5,5,5	0.84	0	5,5,5	5.30	1 (20%)
6	GOL	A	604	-	5,5,5	1.28	0	5,5,5	1.08	0
6	GOL	A	605	-	5,5,5	0.93	0	5,5,5	1.59	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	A	606	-	5,5,5	0.43	0	5,5,5	6.78	1 (20%)
6	GOL	A	607	-	5,5,5	0.86	0	5,5,5	0.57	0
6	GOL	A	608	-	5,5,5	0.58	0	5,5,5	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FAD	A	479	-	-	0/30/50/50	0/6/6/6
5	NDP	A	480	-	-	0/30/77/77	0/5/5/5
2	PO4	A	481	-	-	0/0/0/0	0/0/0/0
2	PO4	A	482	-	-	0/0/0/0	0/0/0/0
2	PO4	A	485	-	-	0/0/0/0	0/0/0/0
2	PO4	A	486	-	-	0/0/0/0	0/0/0/0
2	PO4	A	487	-	-	0/0/0/0	0/0/0/0
6	GOL	A	601	-	-	0/4/4/4	0/0/0/0
6	GOL	A	602	-	-	0/4/4/4	0/0/0/0
6	GOL	A	603	-	-	0/4/4/4	0/0/0/0
6	GOL	A	604	-	-	0/4/4/4	0/0/0/0
6	GOL	A	605	-	-	0/4/4/4	0/0/0/0
6	GOL	A	606	-	-	0/4/4/4	0/0/0/0
6	GOL	A	607	-	-	0/4/4/4	0/0/0/0
6	GOL	A	608	-	-	0/4/4/4	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	480	NDP	C2D-C3D	-3.20	1.44	1.53
4	A	479	FAD	C1'-N10	-2.90	1.45	1.48
5	A	480	NDP	PN-O2N	-2.32	1.45	1.54
5	A	480	NDP	PA-O2A	-2.16	1.45	1.54
4	A	479	FAD	C8M-C8	2.14	1.55	1.51
4	A	479	FAD	C4X-N5	2.71	1.37	1.33
5	A	480	NDP	C6N-C5N	2.86	1.38	1.33
4	A	479	FAD	C9A-N10	3.42	1.43	1.38
5	A	480	NDP	O4B-C1B	3.49	1.45	1.41
4	A	479	FAD	C4-N3	3.96	1.40	1.33
4	A	479	FAD	O4B-C1B	5.92	1.48	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	606	GOL	C3-C2-C1	-15.14	51.74	111.12
6	A	603	GOL	C3-C2-C1	-11.65	65.44	111.12
4	A	479	FAD	C4X-C4-N3	-5.88	115.56	123.59
4	A	479	FAD	C4B-O4B-C1B	-4.07	105.25	109.72
6	A	605	GOL	C3-C2-C1	-3.40	97.80	111.12
5	A	480	NDP	N3A-C2A-N1A	-2.78	126.76	128.89
4	A	479	FAD	C4-C4X-C10	-2.76	118.18	119.94
5	A	480	NDP	C1D-N1N-C2N	-2.66	116.27	120.91
6	A	601	GOL	C3-C2-C1	-2.63	100.81	111.12
4	A	479	FAD	O4'-C4'-C5'	-2.12	105.58	110.19
4	A	479	FAD	O5B-PA-O1A	2.15	117.94	109.62
5	A	480	NDP	C2A-N1A-C6A	2.16	122.63	118.77
5	A	480	NDP	C3D-C2D-C1D	2.22	105.86	101.40
4	A	479	FAD	C5X-C9A-N10	2.30	119.37	117.62
4	A	479	FAD	C1'-N10-C9A	2.85	122.06	118.86
4	A	479	FAD	C4-N3-C2	7.85	122.04	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	480	NDP	2	0
2	A	486	PO4	1	0
2	A	487	PO4	3	0
6	A	601	GOL	2	0
6	A	602	GOL	1	0
6	A	603	GOL	4	0
6	A	604	GOL	1	0
6	A	606	GOL	1	0
6	A	607	GOL	6	0
6	A	608	GOL	7	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	462/478 (96%)	-0.15	10 (2%) 65 59	10, 15, 30, 63	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90[A]	CYS	8.8
1	A	91[A]	GLU	6.9
1	A	92[A]	GLY	4.8
1	A	136	PRO	3.5
1	A	17	ALA	3.3
1	A	78[A]	PHE	3.1
1	A	259[A]	SER	3.0
1	A	393	ILE	2.5
1	A	258	LEU	2.2
1	A	88[A]	PRO	2.2

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. 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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	GOL	A	607	6/6	0.84	0.27	18.23	29,49,59,87	0
2	PO4	A	487	5/5	0.83	0.24	13.66	29,45,63,67	0
6	GOL	A	602	6/6	0.94	0.20	13.00	20,29,60,87	0
6	GOL	A	605	6/6	0.87	0.21	10.26	28,29,30,35	0
6	GOL	A	608	6/6	0.80	0.22	8.04	30,40,52,57	0
6	GOL	A	606	6/6	0.72	0.28	7.97	64,77,80,80	0
6	GOL	A	603	6/6	0.74	0.26	5.25	37,46,50,51	0
6	GOL	A	604	6/6	0.98	0.13	4.74	12,24,32,65	0
2	PO4	A	485	5/5	0.90	0.14	4.02	29,31,39,43	5
2	PO4	A	482	5/5	0.90	0.24	1.98	42,57,69,73	0
6	GOL	A	601	6/6	0.94	0.10	0.75	18,20,22,23	0
4	FAD	A	479	53/53	0.99	0.06	-0.45	9,11,14,16	0
5	NDP	A	480	48/48	0.99	0.04	-1.26	9,12,14,17	0
3	SO4	A	3584	1/5	0.73	0.45	-	63,63,63,63	0
3	SO4	A	3585	1/5	0.72	0.07	-	54,54,54,54	0
2	PO4	A	486	5/5	0.88	0.46	-	52,54,61,63	5
3	SO4	A	3586	1/5	0.85	0.29	-	44,44,44,44	0
2	PO4	A	481	5/5	0.99	0.10	-	21,29,38,44	0
3	SO4	A	3587	1/5	0.18	0.45	-	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.