



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:22 AM GMT

PDB ID : 2GV8
Title : Crystal structure of flavin-containing monooxygenase (FMO) from *S.pombe* and NADPH cofactor complex
Authors : Eswaramoorthy, S.; Swaminathan, S.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2006-05-02
Resolution : 2.10 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

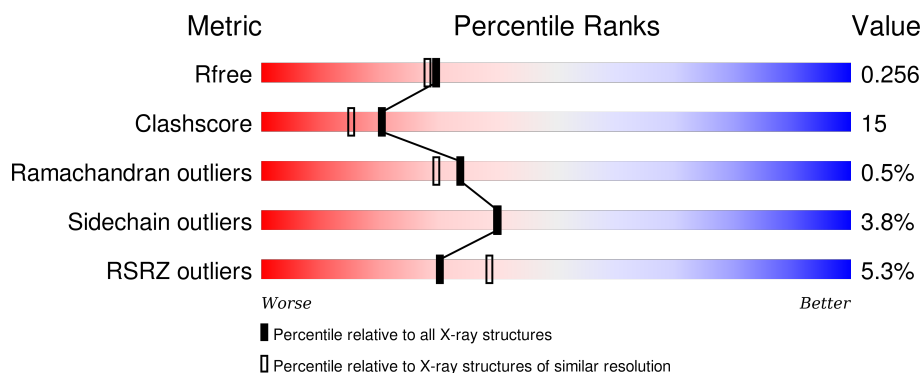
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
R_{free}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	447	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>
1	B	447	<div> <div>9%</div> <div> <div></div> <div>72%</div> <div>25%</div> <div>..</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7618 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.

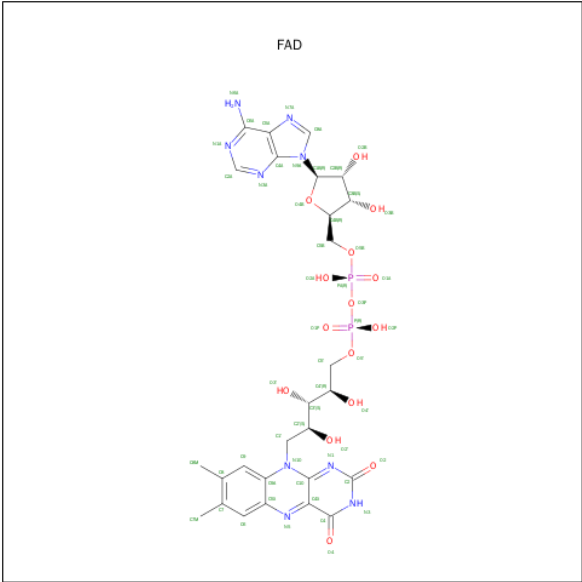
- Molecule 1 is a protein called monooxygenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	Se	0	0	0
			3486	2259	578	641	4	4			
1	B	442	Total	C	N	O	S	Se	0	0	0
			3486	2259	578	641	4	4			

There are 10 discrepancies between the modelled and reference sequences:

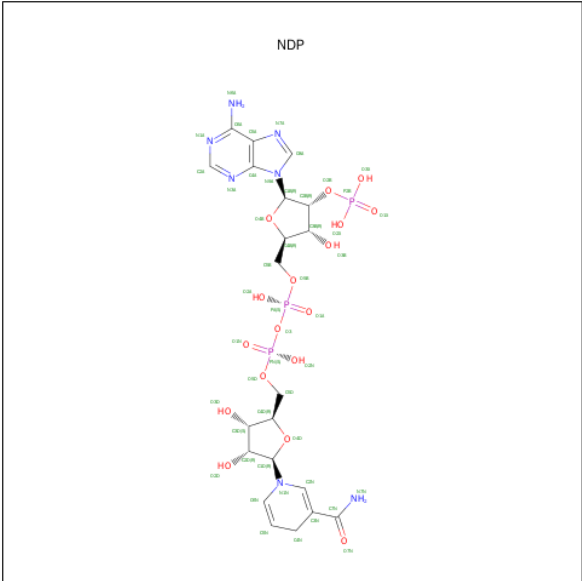
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
A	97	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
A	377	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
A	386	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
A	433	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
B	97	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
B	377	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
B	386	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4
B	433	MSE	MET	MODIFIED RESIDUE	UNP Q9HFE4

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



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

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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

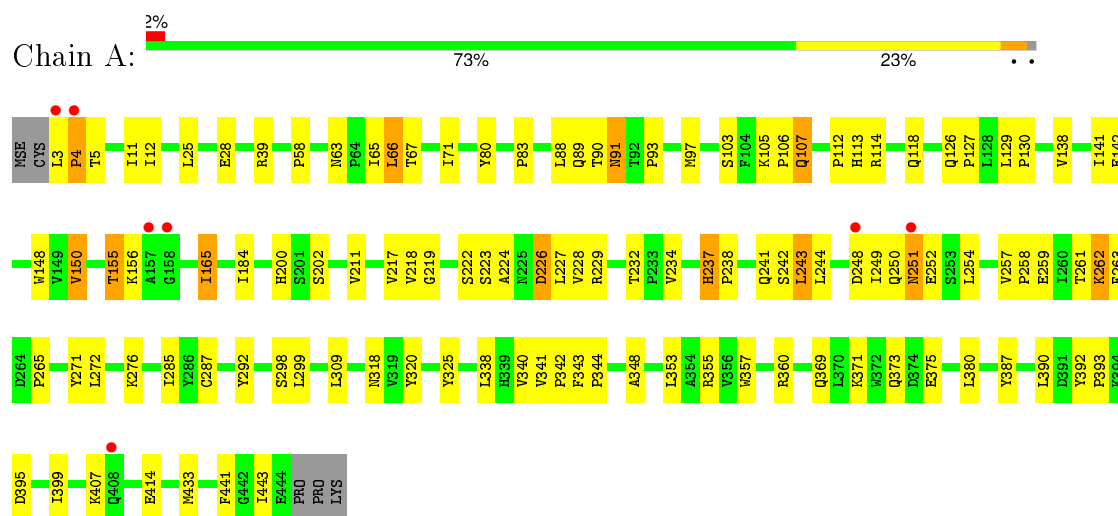
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	231	Total	O	0	0
			231	231		
5	B	201	Total	O	0	0
			201	201		

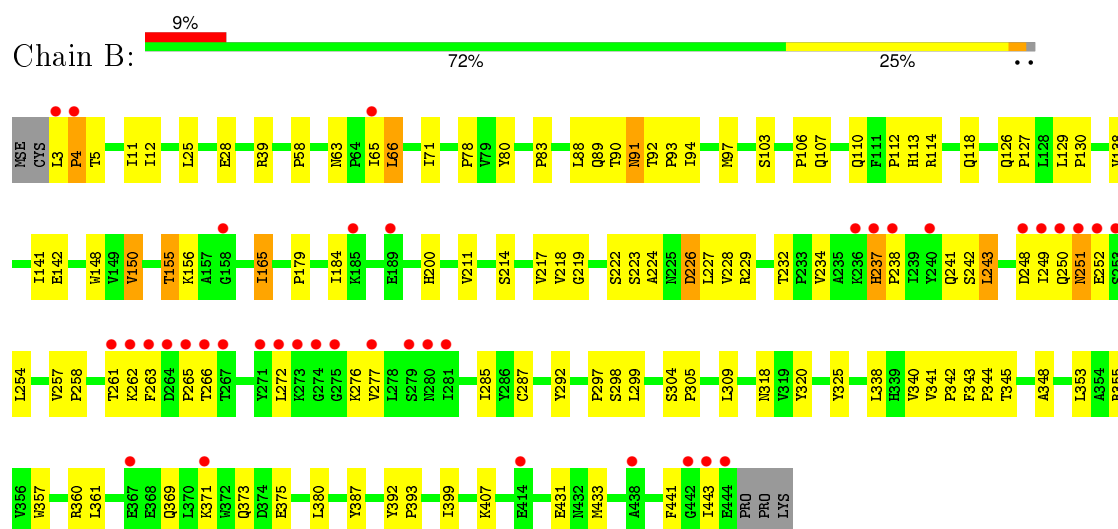
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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: monooxygenase



• Molecule 1: monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.31Å 72.53Å 80.37Å 98.59° 107.40° 101.72°	Depositor
Resolution (Å)	50.00 – 2.10 40.54 – 2.09	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.10) 83.2 (40.54-2.09)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.08Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.259 0.231 , 0.256	Depositor DCC
R_{free} test set	1940 reflections (3.06%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 68018 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7618	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.41% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.36	0/3583	0.65	2/4880 (0.0%)
1	B	0.35	0/3583	0.64	0/4880
All	All	0.35	0/7166	0.65	2/9760 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	GLN	CA-CB-CG	-7.24	97.48	113.40
1	A	107	GLN	CB-CG-CD	5.38	125.59	111.60

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	3486	0	3483	108	0
1	B	3486	0	3483	101	0
2	A	53	0	31	5	0
2	B	53	0	31	5	0
3	A	48	0	26	4	0
3	B	48	0	26	4	0
4	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
5	A	231	0	0	12	0
5	B	201	0	0	5	0
All	All	7618	0	7096	208	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 15.

All (208) 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:114:ARG:HH11	1:A:118:GLN:HE22	1.13	0.95
1:A:244:LEU:HD23	1:A:259:GLU:OE1	1.69	0.93
1:B:114:ARG:HH11	1:B:118:GLN:HE22	1.11	0.92
1:A:262:LYS:HE2	1:A:271:TYR:CG	2.06	0.91
1:A:259:GLU:HG2	5:A:646:HOH:O	1.82	0.79
1:A:407:LYS:HD3	5:A:730:HOH:O	1.85	0.76
1:B:241:GLN:HG2	1:B:243:LEU:CD2	2.17	0.75
1:B:93:PRO:HD2	1:B:433:MSE:HE2	1.68	0.75
1:A:262:LYS:HD3	1:A:271:TYR:HB2	1.67	0.74
1:A:93:PRO:HD2	1:A:433:MSE:HE2	1.69	0.73
1:A:106:PRO:HG2	1:B:106:PRO:HG2	1.68	0.73
1:A:262:LYS:CD	1:A:271:TYR:HB2	2.19	0.72
1:A:241:GLN:HG2	1:A:243:LEU:CD2	2.20	0.71
1:B:238:PRO:HB3	1:B:252:GLU:O	1.91	0.70
1:A:414:GLU:HG2	5:A:727:HOH:O	1.92	0.69
1:A:155:THR:HG21	5:A:561:HOH:O	1.92	0.68
1:B:63:ASN:OD1	1:B:65:ILE:HG22	1.93	0.68
1:B:114:ARG:NH1	1:B:118:GLN:HE22	1.89	0.67
1:A:238:PRO:HB3	1:A:252:GLU:O	1.95	0.67
1:A:63:ASN:OD1	1:A:65:ILE:HG22	1.95	0.66
1:B:249:ILE:HG21	1:B:254:LEU:HD23	1.78	0.66
1:B:249:ILE:HG23	1:B:251:ASN:OD1	1.97	0.65
1:A:67:THR:HG23	5:A:713:HOH:O	1.96	0.65
1:A:249:ILE:HG21	1:A:254:LEU:HD23	1.78	0.65
1:B:222:SER:OG	3:B:501:NDP:H2D	1.97	0.64
1:B:407:LYS:HD3	5:B:581:HOH:O	1.97	0.64
1:B:227:LEU:HD21	1:B:285:ILE:HG21	1.80	0.64
1:A:227:LEU:HD21	1:A:285:ILE:HG21	1.79	0.63
1:A:222:SER:OG	3:A:501:NDP:H2D	1.98	0.63
1:A:249:ILE:HG23	1:A:251:ASN:OD1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:GLU:HB3	1:A:298:SER:CB	2.28	0.63
1:B:142:GLU:HB3	1:B:298:SER:CB	2.28	0.63
1:B:114:ARG:HH11	1:B:118:GLN:NE2	1.92	0.63
1:A:262:LYS:HE2	1:A:271:TYR:CD2	2.35	0.62
1:B:106:PRO:O	1:B:107:GLN:HB2	1.99	0.61
1:A:232:THR:O	1:A:237:HIS:HE1	1.83	0.61
1:B:272:LEU:HD12	1:B:276:LYS:HG3	1.83	0.61
1:B:232:THR:O	1:B:237:HIS:HE1	1.84	0.60
1:B:263:PHE:O	1:B:265:PRO:HD3	2.01	0.60
1:A:114:ARG:NH1	1:A:118:GLN:HE22	1.92	0.60
1:A:262:LYS:CE	1:A:271:TYR:CG	2.82	0.60
1:B:251:ASN:N	1:B:251:ASN:OD1	2.35	0.60
1:A:251:ASN:N	1:A:251:ASN:OD1	2.34	0.60
1:B:155:THR:HG21	5:B:527:HOH:O	2.01	0.60
1:A:39:ARG:HD2	5:A:627:HOH:O	2.02	0.59
1:B:93:PRO:CD	1:B:433:MSE:HE2	2.32	0.59
1:B:165:ILE:O	1:B:165:ILE:HG12	2.01	0.59
1:A:262:LYS:HE2	1:A:271:TYR:CD1	2.38	0.59
1:A:318:ASN:H	1:A:373:GLN:HE22	1.51	0.58
1:B:91:ASN:C	1:B:91:ASN:HD22	2.06	0.58
1:B:318:ASN:H	1:B:373:GLN:HE22	1.51	0.58
1:A:272:LEU:HD12	1:A:276:LYS:HG3	1.84	0.58
1:B:88:LEU:HD11	2:B:500:FAD:H6	1.86	0.58
1:B:58:PRO:HG3	1:B:66:LEU:CD2	2.34	0.58
1:A:414:GLU:CG	5:A:727:HOH:O	2.52	0.57
1:B:241:GLN:HG2	1:B:243:LEU:HD21	1.84	0.57
1:A:441:PHE:O	1:A:443:ILE:HG23	2.05	0.57
1:A:165:ILE:O	1:A:165:ILE:HG12	2.03	0.57
1:A:93:PRO:CD	1:A:433:MSE:HE2	2.33	0.57
1:A:371:LYS:HE3	1:A:375:GLU:OE1	2.05	0.57
1:A:88:LEU:HD11	2:A:500:FAD:H6	1.86	0.57
1:A:241:GLN:HG2	1:A:243:LEU:HD21	1.85	0.57
1:B:441:PHE:O	1:B:443:ILE:HG23	2.05	0.57
1:B:371:LYS:HE3	1:B:375:GLU:OE1	2.05	0.56
1:A:91:ASN:HD22	1:A:91:ASN:C	2.09	0.56
1:B:58:PRO:HG3	1:B:66:LEU:HD21	1.88	0.55
1:A:58:PRO:HG3	1:A:66:LEU:CD2	2.35	0.55
1:B:343:PHE:HB2	1:B:344:PRO:HD3	1.88	0.55
1:A:222:SER:HB2	5:A:562:HOH:O	2.07	0.55
1:A:299:LEU:HB3	1:A:309:LEU:HD12	1.90	0.54
1:B:241:GLN:HG2	1:B:243:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:PHE:O	1:A:265:PRO:HD3	2.08	0.54
1:A:114:ARG:HH11	1:A:118:GLN:NE2	1.95	0.54
1:B:71:ILE:HD12	1:B:71:ILE:N	2.23	0.54
1:A:5:THR:HG23	5:A:699:HOH:O	2.07	0.53
1:A:58:PRO:HG3	1:A:66:LEU:HD21	1.90	0.53
1:A:343:PHE:HB2	1:A:344:PRO:HD3	1.90	0.53
1:B:179:PRO:HB3	1:B:200:HIS:CE1	2.43	0.53
1:A:71:ILE:HD12	1:A:71:ILE:N	2.24	0.53
1:A:200:HIS:CD2	1:A:202:SER:H	2.26	0.53
1:A:392:TYR:CD1	1:A:393:PRO:HA	2.44	0.53
1:B:299:LEU:HB3	1:B:309:LEU:HD12	1.90	0.53
1:B:341:VAL:O	1:B:344:PRO:HD2	2.09	0.52
1:B:340:VAL:O	1:B:342:PRO:HD3	2.10	0.52
1:A:341:VAL:O	1:A:344:PRO:HD2	2.10	0.52
1:A:224:ALA:O	1:A:228:VAL:HG23	2.10	0.52
1:B:224:ALA:O	1:B:228:VAL:HG23	2.10	0.51
1:B:392:TYR:CD1	1:B:393:PRO:HA	2.45	0.51
1:B:218:VAL:HG22	1:B:242:SER:HB3	1.93	0.51
1:A:39:ARG:HD3	1:A:80:TYR:CE1	2.46	0.51
1:A:218:VAL:HG22	1:A:242:SER:HB3	1.91	0.51
1:B:217:VAL:O	1:B:241:GLN:HA	2.11	0.51
1:B:223:SER:HA	3:B:501:NDP:H5N	1.92	0.50
1:A:83:PRO:HG2	2:A:500:FAD:HM82	1.93	0.50
1:B:83:PRO:HG2	2:B:500:FAD:HM82	1.93	0.50
1:A:243:LEU:N	1:A:243:LEU:HD23	2.27	0.50
1:A:241:GLN:HG2	1:A:243:LEU:HD23	1.93	0.50
1:A:249:ILE:CG2	1:A:251:ASN:OD1	2.59	0.50
1:B:249:ILE:CG2	1:B:251:ASN:OD1	2.60	0.50
1:A:67:THR:HA	5:A:713:HOH:O	2.11	0.50
1:B:242:SER:O	3:B:501:NDP:H2A	2.11	0.50
1:A:223:SER:HA	3:A:501:NDP:H5N	1.93	0.50
1:A:340:VAL:O	1:A:342:PRO:HD3	2.12	0.50
1:B:211:VAL:HG12	1:B:234:VAL:HB	1.94	0.49
1:A:217:VAL:O	1:A:241:GLN:HA	2.13	0.49
1:A:97:MSE:HE1	1:A:112:PRO:HD2	1.94	0.49
1:A:211:VAL:HG12	1:A:234:VAL:HB	1.94	0.49
1:B:11:ILE:HD11	1:B:25:LEU:HD12	1.94	0.49
1:B:237:HIS:HD2	1:B:252:GLU:OE2	1.96	0.49
1:B:97:MSE:O	1:B:343:PHE:HB2	2.12	0.49
1:B:39:ARG:HD3	1:B:80:TYR:CE1	2.47	0.49
1:B:141:ILE:O	1:B:298:SER:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:TYR:OH	1:B:338:LEU:HD13	2.12	0.49
1:A:141:ILE:O	1:A:298:SER:HB2	2.13	0.48
1:A:248:ASP:O	1:A:250:GLN:HG2	2.13	0.48
1:A:226:ASP:OD1	1:A:229:ARG:NH2	2.46	0.48
1:B:257:VAL:HB	1:B:258:PRO:HD2	1.96	0.48
1:A:106:PRO:O	1:A:107:GLN:HB2	2.13	0.48
1:B:226:ASP:OD1	1:B:229:ARG:NH2	2.46	0.48
1:B:248:ASP:O	1:B:250:GLN:HG2	2.12	0.48
1:B:380:LEU:HD11	1:B:387:TYR:HA	1.95	0.48
1:A:242:SER:O	3:A:501:NDP:H2A	2.13	0.48
1:B:97:MSE:HE1	1:B:112:PRO:HD2	1.96	0.48
1:B:39:ARG:HG2	2:B:500:FAD:N3A	2.28	0.48
1:B:243:LEU:HD23	1:B:243:LEU:N	2.29	0.47
1:A:237:HIS:HD2	1:A:252:GLU:OE2	1.97	0.47
1:A:3:LEU:O	1:A:5:THR:N	2.47	0.47
1:B:3:LEU:O	1:B:5:THR:N	2.47	0.47
1:A:39:ARG:HG2	2:A:500:FAD:N3A	2.29	0.47
1:B:39:ARG:HD2	5:B:570:HOH:O	2.14	0.47
1:B:106:PRO:O	1:B:107:GLN:CB	2.63	0.47
1:A:257:VAL:HB	1:A:258:PRO:HD2	1.97	0.46
1:A:355:ARG:HH11	1:A:355:ARG:HG3	1.79	0.46
1:A:97:MSE:O	1:A:343:PHE:HB2	2.15	0.46
1:B:214:SER:HA	5:B:649:HOH:O	2.15	0.46
1:A:11:ILE:HD11	1:A:25:LEU:HD12	1.96	0.46
1:A:219:GLY:HA2	3:A:501:NDP:N3A	2.31	0.46
1:B:39:ARG:HD3	1:B:80:TYR:CD1	2.51	0.46
1:A:5:THR:HA	5:A:699:HOH:O	2.15	0.46
1:A:292:TYR:OH	1:A:338:LEU:HD13	2.15	0.46
1:B:320:TYR:CG	1:B:369:GLN:HG2	2.50	0.46
1:A:309:LEU:HD21	1:A:325:TYR:CD1	2.51	0.46
1:B:348:ALA:HB2	1:B:399:ILE:HG23	1.98	0.45
1:A:320:TYR:CG	1:A:369:GLN:HG2	2.51	0.45
1:A:380:LEU:HD11	1:A:387:TYR:HA	1.98	0.45
1:B:222:SER:O	1:B:226:ASP:HB2	2.17	0.45
1:B:355:ARG:HG3	1:B:355:ARG:HH11	1.80	0.45
1:B:148:TRP:O	1:B:165:ILE:HA	2.17	0.45
1:A:39:ARG:HD3	1:A:80:TYR:CD1	2.52	0.45
1:B:71:ILE:CD1	1:B:71:ILE:N	2.80	0.45
1:B:237:HIS:CD2	1:B:252:GLU:OE2	2.69	0.45
1:A:89:GLN:HG2	1:A:113:HIS:HA	1.99	0.45
1:A:237:HIS:CD2	1:A:252:GLU:OE2	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:PHE:N	1:A:343:PHE:CD1	2.85	0.44
1:B:353:LEU:HD11	1:B:357:TRP:CE2	2.52	0.44
1:A:348:ALA:HB2	1:A:399:ILE:HG23	1.99	0.44
1:B:227:LEU:HD22	1:B:287:CYS:SG	2.58	0.44
1:A:227:LEU:CD2	1:A:285:ILE:HG21	2.47	0.44
1:B:343:PHE:N	1:B:343:PHE:CD1	2.84	0.44
1:A:371:LYS:O	1:A:375:GLU:HG3	2.17	0.44
1:B:28:GLU:OE1	1:B:360:ARG:HD3	2.17	0.44
1:A:251:ASN:HB2	1:A:252:GLU:H	1.56	0.44
1:B:219:GLY:HA2	3:B:501:NDP:N3A	2.31	0.44
1:A:83:PRO:CG	2:A:500:FAD:HM82	2.48	0.44
1:B:91:ASN:C	1:B:91:ASN:ND2	2.69	0.44
1:A:222:SER:O	1:A:226:ASP:HB2	2.17	0.44
1:B:257:VAL:CG2	1:B:272:LEU:HD13	2.47	0.44
1:B:90:THR:HA	2:B:500:FAD:O4	2.18	0.44
1:B:345:THR:HB	5:B:536:HOH:O	2.17	0.44
1:A:90:THR:HA	2:A:500:FAD:O4	2.17	0.44
1:A:360:ARG:NH1	5:A:656:HOH:O	2.26	0.44
1:B:407:LYS:HA	1:B:407:LYS:HD2	1.79	0.43
1:A:257:VAL:CG2	1:A:272:LEU:HD13	2.48	0.43
1:A:148:TRP:O	1:A:165:ILE:HA	2.18	0.43
1:B:309:LEU:HD21	1:B:325:TYR:CD1	2.53	0.43
1:A:355:ARG:NH1	1:A:355:ARG:HG3	2.33	0.43
1:B:83:PRO:CG	2:B:500:FAD:HM82	2.48	0.43
1:A:227:LEU:HD22	1:A:287:CYS:SG	2.59	0.43
1:B:371:LYS:O	1:B:375:GLU:HG3	2.18	0.43
1:A:91:ASN:ND2	1:A:91:ASN:C	2.72	0.43
1:B:355:ARG:HG3	1:B:355:ARG:NH1	2.34	0.43
1:A:126:GLN:HB3	1:A:127:PRO:CD	2.49	0.43
1:B:126:GLN:HB3	1:B:127:PRO:CD	2.49	0.43
1:A:184:ILE:HG22	1:A:262:LYS:HA	2.01	0.43
1:A:97:MSE:HA	1:A:341:VAL:CG1	2.49	0.43
1:B:89:GLN:HG2	1:B:113:HIS:HA	2.00	0.43
1:B:179:PRO:HB3	1:B:200:HIS:ND1	2.34	0.42
1:A:71:ILE:CD1	1:A:71:ILE:N	2.82	0.42
1:B:392:TYR:CE2	1:B:431:GLU:HG3	2.54	0.42
1:A:28:GLU:OE1	1:A:360:ARG:HD3	2.19	0.42
1:B:251:ASN:HB2	1:B:252:GLU:H	1.56	0.42
1:B:12:ILE:HD12	1:B:138:VAL:HG21	2.01	0.42
1:B:94:ILE:HG12	1:B:110:GLN:HA	2.01	0.42
1:A:353:LEU:HD11	1:A:357:TRP:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:THR:O	1:B:97:MSE:HE2	2.20	0.42
1:B:107:GLN:HA	1:B:107:GLN:OE1	2.19	0.41
1:A:138:VAL:HG13	1:A:150:VAL:HG23	2.02	0.41
1:A:390:LEU:O	1:A:395:ASP:HB3	2.20	0.41
1:B:304:SER:HA	1:B:305:PRO:HD3	1.96	0.41
1:B:138:VAL:HG13	1:B:150:VAL:HG23	2.03	0.41
1:A:200:HIS:HD2	1:A:202:SER:OG	2.03	0.41
1:B:184:ILE:CG2	1:B:262:LYS:HA	2.51	0.41
1:B:91:ASN:ND2	1:B:92:THR:HG23	2.36	0.41
1:B:129:LEU:N	1:B:130:PRO:HD2	2.36	0.41
1:A:129:LEU:N	1:A:130:PRO:HD2	2.36	0.41
1:A:12:ILE:HD12	1:A:138:VAL:HG21	2.02	0.40
1:B:361:LEU:HD23	1:B:361:LEU:HA	1.96	0.40
1:B:78:PRO:HD2	1:B:155:THR:CG2	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	440/447 (98%)	414 (94%)	24 (6%)	2 (0%)	34	30
1	B	440/447 (98%)	415 (94%)	23 (5%)	2 (0%)	34	30
All	All	880/894 (98%)	829 (94%)	47 (5%)	4 (0%)	34	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	PRO
1	B	4	PRO
1	A	66	LEU
1	B	66	LEU

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	384/385 (100%)	370 (96%)	14 (4%)	42	43
1	B	384/385 (100%)	369 (96%)	15 (4%)	39	39
All	All	768/770 (100%)	739 (96%)	29 (4%)	40	40

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	PRO
1	A	91	ASN
1	A	103	SER
1	A	105	LYS
1	A	150	VAL
1	A	155	THR
1	A	156	LYS
1	A	165	ILE
1	A	226	ASP
1	A	237	HIS
1	A	243	LEU
1	A	251	ASN
1	A	261	THR
1	A	262	LYS
1	B	4	PRO
1	B	91	ASN
1	B	103	SER
1	B	150	VAL
1	B	155	THR
1	B	156	LYS
1	B	165	ILE
1	B	226	ASP
1	B	237	HIS
1	B	243	LEU
1	B	251	ASN
1	B	261	THR
1	B	266	THR

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Mol	Chain	Res	Type
1	B	277	VAL
1	B	297	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	91	ASN
1	A	118	GLN
1	A	121	GLN
1	A	200	HIS
1	A	237	HIS
1	A	373	GLN
1	B	48	ASN
1	B	91	ASN
1	B	118	GLN
1	B	121	GLN
1	B	237	HIS
1	B	373	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](#)

6 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	FAD	A	500	-	48,58,58	2.60	12 (25%)	54,89,89	2.40	9 (16%)
3	NDP	A	501	-	42,52,52	1.47	4 (9%)	55,80,80	1.68	10 (18%)
4	GOL	A	502	-	5,5,5	0.39	0	5,5,5	0.61	0
2	FAD	B	500	-	48,58,58	2.65	16 (33%)	54,89,89	2.43	9 (16%)
3	NDP	B	501	-	42,52,52	1.52	4 (9%)	55,80,80	1.73	9 (16%)
4	GOL	B	502	-	5,5,5	0.39	0	5,5,5	0.58	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
2	FAD	A	500	-	-	0/30/50/50	0/6/6/6
3	NDP	A	501	-	-	0/30/77/77	0/5/5/5
4	GOL	A	502	-	-	0/4/4/4	0/0/0/0
2	FAD	B	500	-	-	0/30/50/50	0/6/6/6
3	NDP	B	501	-	-	0/30/77/77	0/5/5/5
4	GOL	B	502	-	-	0/4/4/4	0/0/0/0

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	FAD	C1'-N10	-5.32	1.42	1.48
2	A	500	FAD	C1'-N10	-5.12	1.43	1.48
3	B	501	NDP	C4N-C5N	-5.06	1.38	1.49
3	A	501	NDP	C4N-C5N	-4.74	1.38	1.49
2	B	500	FAD	C5A-C4A	-3.68	1.32	1.40
2	A	500	FAD	C5A-C4A	-3.64	1.32	1.40
2	B	500	FAD	C2B-C3B	-2.52	1.46	1.53
2	A	500	FAD	C2B-C3B	-2.40	1.46	1.53
2	B	500	FAD	C5'-C4'	-2.39	1.48	1.51
2	B	500	FAD	C8A-N7A	-2.10	1.30	1.34
3	A	501	NDP	PA-O1A	-2.01	1.43	1.51
2	B	500	FAD	C10-N1	2.00	1.39	1.35
2	B	500	FAD	C6-C7	2.09	1.43	1.37
2	A	500	FAD	C10-N1	2.13	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	NDP	C4A-N3A	2.33	1.39	1.35
2	B	500	FAD	O4B-C1B	2.39	1.44	1.41
2	A	500	FAD	C9A-C5X	2.47	1.47	1.42
2	B	500	FAD	C9A-C5X	2.49	1.47	1.42
3	A	501	NDP	C2N-C3N	3.07	1.42	1.34
3	B	501	NDP	C2N-C3N	3.12	1.42	1.34
3	B	501	NDP	C6N-C5N	3.51	1.40	1.33
3	A	501	NDP	C6N-C5N	3.56	1.40	1.33
2	B	500	FAD	C4-N3	4.57	1.41	1.33
2	B	500	FAD	P-O5'	4.58	1.80	1.59
2	A	500	FAD	P-O5'	4.79	1.81	1.59
2	A	500	FAD	C5X-N5	4.91	1.43	1.35
2	B	500	FAD	C5X-N5	4.94	1.43	1.35
2	A	500	FAD	C4-N3	5.02	1.42	1.33
2	A	500	FAD	C2A-N3A	5.11	1.41	1.32
2	B	500	FAD	C2A-N3A	5.38	1.41	1.32
2	A	500	FAD	C4A-N3A	5.53	1.43	1.35
2	B	500	FAD	C4A-N3A	5.57	1.43	1.35
2	A	500	FAD	C4X-N5	6.65	1.43	1.33
2	B	500	FAD	C4X-N5	7.00	1.44	1.33
2	A	500	FAD	C9A-N10	7.20	1.48	1.38
2	B	500	FAD	C9A-N10	7.29	1.48	1.38

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	FAD	O3P-P-O5'	-6.28	86.28	102.94
2	A	500	FAD	O3P-P-O5'	-6.18	86.54	102.94
2	A	500	FAD	C4X-C4-N3	-6.04	115.33	123.59
2	B	500	FAD	C4X-C4-N3	-5.94	115.47	123.59
2	B	500	FAD	N3A-C2A-N1A	-5.14	124.95	128.89
3	B	501	NDP	N3A-C2A-N1A	-4.77	125.24	128.89
2	A	500	FAD	N3A-C2A-N1A	-4.76	125.25	128.89
3	A	501	NDP	N3A-C2A-N1A	-4.31	125.60	128.89
3	A	501	NDP	C1D-N1N-C2N	-4.12	113.72	120.91
3	B	501	NDP	C1D-N1N-C2N	-4.12	113.72	120.91
3	B	501	NDP	C3N-C2N-N1N	-4.11	117.25	123.14
2	B	500	FAD	C5X-C9A-N10	-4.02	114.57	117.62
2	A	500	FAD	C5X-C9A-N10	-4.01	114.57	117.62
3	A	501	NDP	C3N-C2N-N1N	-3.98	117.44	123.14
3	A	501	NDP	C4B-O4B-C1B	-3.89	105.44	109.72
3	B	501	NDP	C4B-O4B-C1B	-3.82	105.52	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	NDP	C4N-C5N-C6N	-2.80	117.96	122.58
3	B	501	NDP	C4N-C5N-C6N	-2.76	118.02	122.58
2	B	500	FAD	O3'-C3'-C4'	-2.72	101.89	108.75
2	A	500	FAD	O3'-C3'-C4'	-2.67	102.03	108.75
2	A	500	FAD	O2'-C2'-C1'	-2.62	103.51	109.94
2	B	500	FAD	O2'-C2'-C1'	-2.60	103.55	109.94
3	B	501	NDP	O7N-C7N-N7N	-2.36	116.90	122.76
3	B	501	NDP	O5B-C5B-C4B	-2.29	100.66	109.12
3	A	501	NDP	O5B-C5B-C4B	-2.22	100.95	109.12
3	A	501	NDP	O7N-C7N-N7N	-2.21	117.27	122.76
3	A	501	NDP	O2B-P2B-O1X	-2.09	101.89	107.11
3	B	501	NDP	PN-O3-PA	2.17	138.81	132.73
3	A	501	NDP	PN-O3-PA	2.17	138.83	132.73
2	B	500	FAD	O2B-C2B-C3B	2.52	120.01	111.83
2	A	500	FAD	O2B-C2B-C3B	2.56	120.16	111.83
2	B	500	FAD	O5'-P-O1P	2.82	120.56	109.62
2	A	500	FAD	O5'-P-O1P	2.83	120.59	109.62
3	A	501	NDP	C5N-C4N-C3N	3.84	123.09	112.52
3	B	501	NDP	C5N-C4N-C3N	3.87	123.19	112.52
2	A	500	FAD	C4-N3-C2	11.56	125.24	115.25
2	B	500	FAD	C4-N3-C2	11.74	125.40	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	FAD	5	0
3	A	501	NDP	4	0
2	B	500	FAD	5	0
3	B	501	NDP	4	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	438/447 (97%)	0.16	7 (1%) 74 79	11, 28, 42, 51	0
1	B	438/447 (97%)	0.49	39 (8%) 12 16	11, 30, 44, 52	0
All	All	876/894 (97%)	0.32	46 (5%) 30 39	11, 29, 43, 52	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	LEU	7.1
1	B	271	TYR	5.8
1	B	266	THR	5.6
1	A	3	LEU	5.0
1	B	4	PRO	4.7
1	B	444	GLU	4.3
1	A	4	PRO	4.2
1	B	251	ASN	3.9
1	B	249	ILE	3.9
1	B	272	LEU	3.5
1	B	263	PHE	3.5
1	B	277	VAL	3.5
1	B	238	PRO	3.4
1	B	240	TYR	3.3
1	A	157	ALA	3.3
1	B	264	ASP	3.2
1	B	252	GLU	3.1
1	B	275	GLY	3.1
1	B	443	ILE	3.1
1	B	267	THR	3.1
1	B	262	LYS	3.1
1	B	274	GLY	3.0
1	B	261	THR	3.0
1	B	253	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	279	SER	2.9
1	B	273	LYS	2.9
1	B	158	GLY	2.9
1	B	189	GLU	2.8
1	A	251	ASN	2.6
1	B	367	GLU	2.5
1	B	265	PRO	2.5
1	B	237	HIS	2.5
1	B	280	ASN	2.5
1	B	438	ALA	2.4
1	B	65	ILE	2.4
1	A	248	ASP	2.3
1	B	236	LYS	2.3
1	A	158	GLY	2.2
1	B	414	GLU	2.2
1	B	371	LYS	2.2
1	A	408	GLN	2.1
1	B	250	GLN	2.1
1	B	281	ILE	2.1
1	B	185	LYS	2.0
1	B	442	GLY	2.0
1	B	248	ASP	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. 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
2	FAD	B	500	53/53	0.94	0.20	1.70	14,20,23,25	0
2	FAD	A	500	53/53	0.95	0.18	1.24	15,18,24,24	0
4	GOL	A	502	6/6	0.94	0.18	1.19	15,18,19,20	0
3	NDP	A	501	48/48	0.89	0.16	0.86	24,27,43,45	0
4	GOL	B	502	6/6	0.95	0.17	0.82	16,18,20,21	0
3	NDP	B	501	48/48	0.89	0.14	0.15	27,32,47,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.