



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 13, 2016 – 06:22 PM EDT

PDB ID : 4YAW  
Title : Reduced CYPOR mutant - G141del  
Authors : Xia, C.; Kim, J.J.P.  
Deposited on : 2015-02-17  
Resolution : 2.00 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027790  
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) : rb-20027790

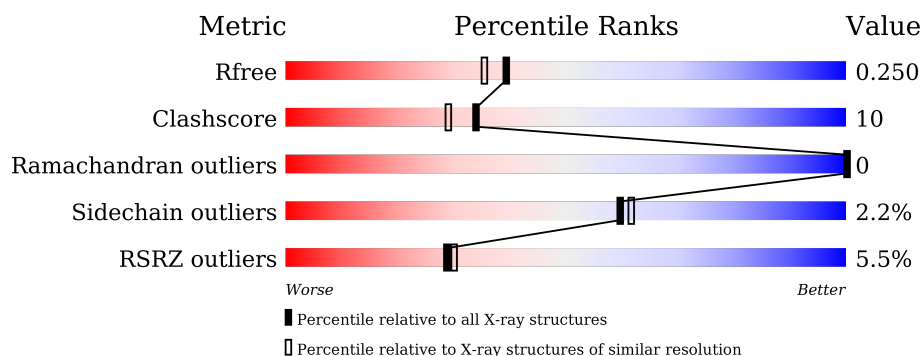
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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  $\geq 3$ , 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	621	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>..</div> </div> </div>
1	B	621	<div> <div>9%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>

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
5	PO4	A	706	-	-	-	X
5	PO4	B	706	-	-	X	X



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.

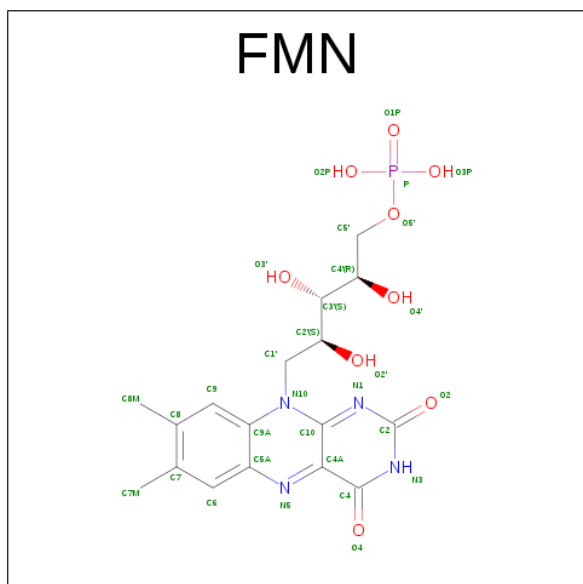
- Molecule 1 is a protein called NADPH-cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	612	Total 4895	C 3102	N 841	O 929	S 23	0	0	0
1	B	601	Total 4787	C 3031	N 828	O 905	S 23	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP P00388
B	?	-	GLY	deletion	UNP P00388

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula:  $C_{17}H_{21}N_4O_9P$ ).



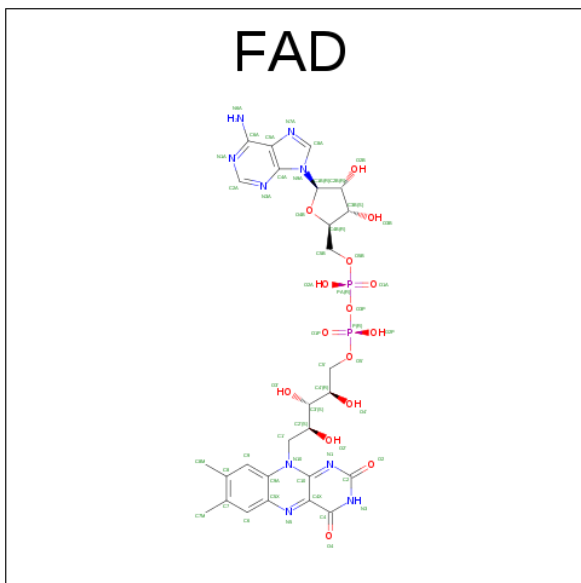
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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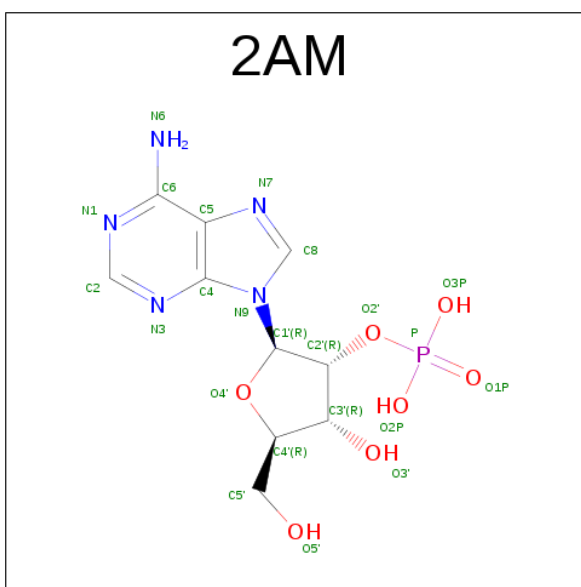
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



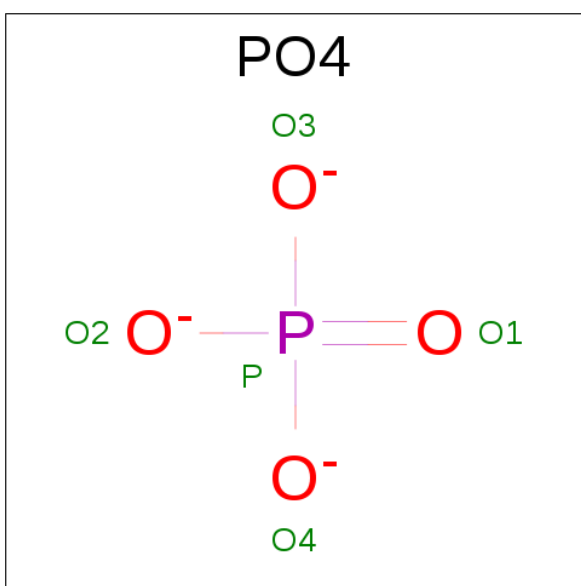
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is ADENOSINE-2'-MONOPHOSPHATE (three-letter code: 2AM) (formula:  $C_{10}H_{14}N_5O_7P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



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

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

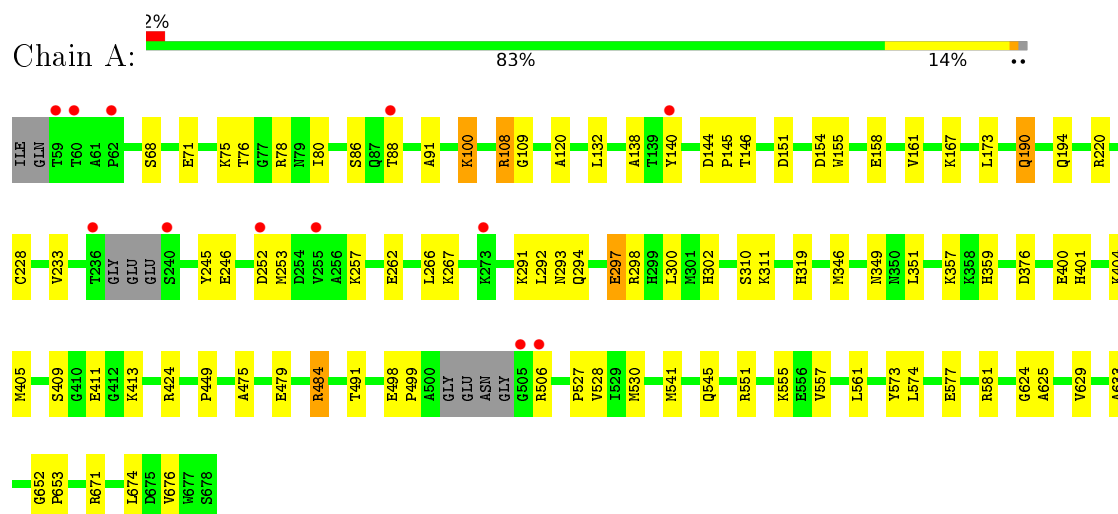
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	638	Total	O	0	0
			638	638		
6	B	529	Total	O	0	0
			529	529		

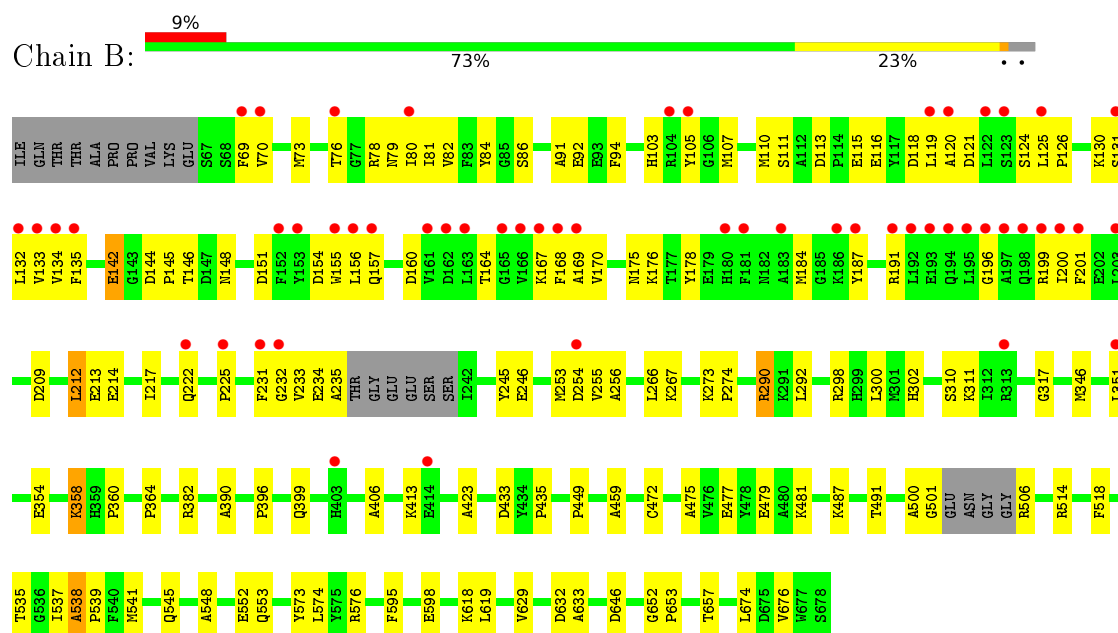
### 3 Residue-property plots [i](#)

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: NADPH-cytochrome P450 reductase



#### • Molecule 1: NADPH-cytochrome P450 reductase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.46Å 116.03Å 118.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.37 – 2.00 38.37 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.0 (38.37-2.00) 93.8 (38.37-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 2.00Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.204 , 0.252 0.204 , 0.250	Depositor DCC
$R_{free}$ test set	4497 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.7	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11093	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, PO4, 2AM, 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	0.33	0/5012	0.57	0/6784
1	B	0.33	1/4902 (0.0%)	0.57	2/6635 (0.0%)
All	All	0.33	1/9914 (0.0%)	0.57	2/13419 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	539	PRO	N-CD	5.19	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	538	ALA	C-N-CD	5.68	140.33	128.40
1	B	232	GLY	N-CA-C	5.59	127.08	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4895	0	4732	78	0
1	B	4787	0	4589	118	0
2	A	31	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	19	1	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0
4	A	23	0	12	0	0
4	B	23	0	12	0	0
5	A	15	0	0	1	0
5	B	15	0	0	2	0
6	A	638	0	0	11	0
6	B	529	0	0	17	0
All	All	11093	0	9445	195	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 (195) 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:253:MET:HE2	1:A:257:LYS:HD3	1.48	0.96
1:B:79:ASN:HB2	1:B:130:LYS:O	1.69	0.92
1:B:86:SER:HB3	1:B:91:ALA:HB3	1.52	0.92
1:A:506:ARG:HG2	1:A:506:ARG:HH11	1.33	0.91
1:A:400:GLU:HG3	1:A:404:LYS:HE2	1.53	0.91
1:A:633:ALA:HB2	1:A:676:VAL:HB	1.54	0.89
1:A:253:MET:CE	1:A:257:LYS:HD3	2.06	0.85
1:B:132:LEU:HD13	1:B:200:ILE:HG13	1.63	0.81
1:B:500:ALA:HA	1:B:506:ARG:HH21	1.48	0.79
1:B:175:ASN:HB3	1:B:178:TYR:HD2	1.49	0.78
1:B:86:SER:HB2	2:B:701:FMN:O3P	1.83	0.77
1:A:297:GLU:HG3	1:A:298:ARG:HG3	1.67	0.76
1:B:472:CYS:HB3	1:B:538:ALA:HB2	1.67	0.74
1:B:134:VAL:HG22	1:B:169:ALA:HB3	1.70	0.73
1:B:506:ARG:HA	6:B:1246:HOH:O	1.88	0.73
1:A:506:ARG:HG2	1:A:506:ARG:NH1	2.02	0.72
1:B:396:PRO:HG2	6:B:823:HOH:O	1.90	0.71
1:A:424:ARG:HD3	6:A:1334:HOH:O	1.92	0.70
1:A:257:LYS:HA	1:A:266:LEU:HD21	1.74	0.69
1:A:246:GLU:HB3	1:A:351:LEU:HD21	1.75	0.68
1:B:167:LYS:HB3	1:B:200:ILE:HD11	1.76	0.67
1:B:175:ASN:HB3	1:B:178:TYR:CD2	2.29	0.66
1:B:595:PHE:HB3	1:B:598:GLU:HG3	1.76	0.66
1:A:297:GLU:HB3	5:A:704:PO4:P	2.38	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:ASP:HB3	1:A:449:PRO:HG2	1.80	0.64
1:A:88:THR:HG22	1:A:88:THR:O	1.97	0.64
1:B:118:ASP:OD2	1:B:120:ALA:HB3	1.98	0.63
1:B:535:THR:HG23	5:B:706:PO4:O2	1.99	0.63
1:B:646:ASP:HB3	6:B:822:HOH:O	1.99	0.63
1:A:86:SER:HB2	1:A:91:ALA:HB3	1.81	0.62
1:B:390:ALA:O	1:B:399:GLN:HG3	1.98	0.62
1:A:253:MET:HE2	1:A:257:LYS:CD	2.28	0.62
1:A:228:CYS:HA	1:A:233:VAL:CG2	2.30	0.62
1:A:319:HIS:HD2	6:A:1089:HOH:O	1.83	0.62
1:A:253:MET:CE	1:A:257:LYS:CD	2.77	0.61
1:B:500:ALA:HA	1:B:506:ARG:NH2	2.14	0.61
1:B:300:LEU:HD13	1:B:574:LEU:HD21	1.81	0.61
1:A:108:ARG:HH11	1:A:108:ARG:HA	1.67	0.60
1:A:100:LYS:HE2	6:A:1150:HOH:O	2.01	0.60
1:B:103:HIS:HA	1:B:107:MET:O	2.03	0.59
1:A:154:ASP:O	1:A:158:GLU:HG2	2.03	0.59
1:A:633:ALA:HB2	1:A:676:VAL:CB	2.31	0.59
1:A:88:THR:HB	2:A:701:FMN:O1P	2.02	0.59
1:A:629:VAL:HB	1:A:674:LEU:HD23	1.85	0.58
1:A:479:GLU:HG2	1:B:479:GLU:OE1	2.04	0.58
1:B:290:ARG:HD3	6:B:867:HOH:O	2.03	0.58
1:B:541:MET:O	1:B:545:GLN:HG3	2.04	0.57
1:B:70:VAL:HG11	1:B:124:SER:O	2.04	0.57
1:B:382:ARG:HG2	6:B:900:HOH:O	2.03	0.57
1:B:115:GLU:OE1	1:B:148:ASN:HA	2.04	0.57
1:B:472:CYS:HB3	1:B:538:ALA:CB	2.34	0.57
1:B:253:MET:SD	1:B:364:PRO:HG3	2.46	0.56
1:B:201:PHE:HZ	1:B:222:GLN:HG3	1.71	0.56
1:B:423:ALA:HA	1:B:481:LYS:HB2	1.87	0.56
1:B:479:GLU:HB3	6:B:1275:HOH:O	2.07	0.55
1:B:459:ALA:HA	1:B:538:ALA:O	2.06	0.55
1:A:294:GLN:HG2	6:A:880:HOH:O	2.06	0.54
1:B:234:GLU:O	1:B:235:ALA:C	2.46	0.54
1:B:298:ARG:HG3	1:B:298:ARG:HH21	1.72	0.54
1:B:657:THR:HG23	6:B:1121:HOH:O	2.08	0.54
1:B:475:ALA:HA	1:B:491:THR:HB	1.90	0.54
1:A:155:TRP:CZ2	1:A:161:VAL:HG11	2.43	0.54
6:A:1066:HOH:O	1:B:479:GLU:HG2	2.06	0.54
1:A:228:CYS:HA	1:A:233:VAL:HG22	1.89	0.53
1:A:551:ARG:NH1	6:A:801:HOH:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:449:PRO:HG3	6:B:1282:HOH:O	2.08	0.53
1:A:551:ARG:HG3	1:A:557:VAL:HG21	1.91	0.53
1:B:142:GLU:OE1	1:B:142:GLU:HA	2.08	0.53
1:B:245:TYR:CD2	1:B:360:PRO:HD3	2.44	0.53
1:B:175:ASN:OD1	1:B:209:ASP:HB2	2.08	0.52
1:B:633:ALA:HB2	1:B:676:VAL:HB	1.91	0.52
1:B:133:VAL:O	1:B:168:PHE:HA	2.08	0.52
1:B:506:ARG:HB2	6:B:1065:HOH:O	2.08	0.52
1:B:187:TYR:HB2	6:B:1153:HOH:O	2.10	0.52
1:A:528:VAL:HG12	1:A:530:MET:HG3	1.92	0.51
1:A:253:MET:HE3	1:A:257:LYS:HD3	1.92	0.51
1:A:78:ARG:NE	1:A:108:ARG:HD2	2.25	0.51
1:B:199:ARG:NH1	1:B:199:ARG:HB2	2.25	0.51
1:B:266:LEU:O	1:B:267:LYS:HB2	2.11	0.51
1:B:477:GLU:HG3	1:B:487:LYS:HD2	1.92	0.50
1:B:82:VAL:O	1:B:111:SER:HA	2.11	0.50
1:B:184:MET:HG2	6:B:851:HOH:O	2.11	0.50
1:B:69:PHE:CE1	1:B:121:ASP:HB2	2.46	0.50
1:A:71:GLU:O	1:A:75:LYS:HG2	2.11	0.50
1:B:130:LYS:CB	1:B:231:PHE:CD1	2.94	0.50
1:B:135:PHE:HB2	1:B:170:VAL:HG22	1.94	0.49
1:A:506:ARG:CG	1:A:506:ARG:NH1	2.73	0.49
1:A:292:LEU:HD11	1:A:302:HIS:HB2	1.94	0.49
1:B:213:GLU:O	1:B:217:ILE:HG13	2.12	0.49
1:B:144:ASP:HB3	1:B:145:PRO:HD2	1.95	0.49
1:B:233:VAL:HG22	1:B:234:GLU:N	2.27	0.49
1:A:76:THR:OG1	1:A:78:ARG:HD3	2.13	0.49
1:A:409:SER:HA	1:A:413:LYS:HD3	1.95	0.49
1:B:406:ALA:HB1	6:B:804:HOH:O	2.12	0.49
1:A:310:SER:O	1:A:311:LYS:HB2	2.12	0.49
1:B:501:GLY:H	1:B:506:ARG:NH2	2.11	0.49
1:B:176:LYS:O	1:B:176:LYS:HD3	2.13	0.48
1:B:81:ILE:HG23	1:B:81:ILE:O	2.12	0.48
1:B:310:SER:O	1:B:311:LYS:HB2	2.13	0.48
1:B:537:ILE:O	1:B:537:ILE:HG13	2.13	0.48
1:A:484:ARG:N	1:A:484:ARG:HD2	2.28	0.48
1:A:652:GLY:N	1:A:653:PRO:HA	2.28	0.48
1:A:78:ARG:CZ	1:A:108:ARG:HD2	2.43	0.48
1:B:130:LYS:HA	1:B:231:PHE:HE1	1.79	0.47
1:B:70:VAL:HA	1:B:73:MET:CE	2.43	0.47
1:A:120:ALA:HA	1:A:155:TRP:CZ2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:LEU:HD12	1:A:300:LEU:N	2.30	0.47
1:A:541:MET:O	1:A:545:GLN:HG3	2.14	0.47
1:B:501:GLY:N	1:B:506:ARG:NH2	2.63	0.47
1:A:577:GLU:CD	1:A:577:GLU:H	2.18	0.47
1:B:81:ILE:HA	1:B:110:MET:O	2.14	0.46
1:B:132:LEU:HD12	1:B:167:LYS:O	2.15	0.46
1:B:199:ARG:HB2	1:B:199:ARG:CZ	2.45	0.46
1:B:246:GLU:HG3	1:B:351:LEU:HD21	1.98	0.46
1:B:70:VAL:HA	1:B:73:MET:HE3	1.97	0.46
1:A:555:LYS:HD2	1:A:555:LYS:N	2.31	0.46
1:B:134:VAL:HA	1:B:169:ALA:O	2.16	0.46
1:B:548:ALA:O	1:B:552:GLU:HG2	2.16	0.46
1:A:144:ASP:HB3	1:A:145:PRO:CD	2.46	0.46
1:A:108:ARG:HH11	1:A:109:GLY:H	1.64	0.46
1:B:201:PHE:CZ	1:B:222:GLN:HG3	2.50	0.45
1:B:292:LEU:HD11	1:B:302:HIS:HB2	1.99	0.45
1:B:576:ARG:HH11	1:B:576:ARG:HG2	1.80	0.45
1:B:433:ASP:C	1:B:435:PRO:HD3	2.37	0.45
1:B:535:THR:CG2	5:B:706:PO4:O2	2.65	0.45
1:B:84:TYR:CD1	1:B:84:TYR:O	2.70	0.45
1:A:633:ALA:CB	1:A:676:VAL:HB	2.37	0.44
1:A:291:LYS:HE3	1:A:293:ASN:O	2.16	0.44
1:B:164:THR:HA	1:B:196:GLY:O	2.17	0.44
1:A:253:MET:HG3	1:A:257:LYS:HD2	1.98	0.44
1:B:79:ASN:O	1:B:131:SER:HA	2.17	0.44
1:A:561:LEU:HD12	1:A:561:LEU:N	2.32	0.44
1:B:133:VAL:HG13	1:B:133:VAL:O	2.18	0.44
1:B:119:LEU:N	1:B:119:LEU:HD22	2.33	0.44
1:A:581:ARG:HG2	1:A:581:ARG:HH11	1.83	0.44
1:B:506:ARG:NH1	6:B:811:HOH:O	2.51	0.44
1:B:84:TYR:CG	1:B:92:GLU:HA	2.53	0.44
1:A:349:ASN:HB3	6:A:1132:HOH:O	2.17	0.44
1:B:618:LYS:NZ	6:B:807:HOH:O	2.50	0.44
1:A:253:MET:HE3	1:A:257:LYS:CD	2.47	0.43
1:A:140:TYR:CD1	1:A:146:THR:HG22	2.53	0.43
1:B:358:LYS:N	1:B:358:LYS:HD2	2.33	0.43
1:A:267:LYS:HA	6:A:1181:HOH:O	2.18	0.43
1:B:130:LYS:CA	1:B:231:PHE:CE1	3.01	0.43
1:A:155:TRP:HZ2	1:A:161:VAL:HG11	1.84	0.43
1:A:262:GLU:HG3	6:A:1154:HOH:O	2.18	0.43
1:B:222:GLN:C	1:B:225:PRO:HD2	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:629:VAL:HB	1:B:674:LEU:HD23	1.99	0.43
1:A:138:ALA:HA	1:A:173:LEU:HB2	2.01	0.43
1:B:481:LYS:HG2	6:B:1013:HOH:O	2.18	0.43
1:B:105:TYR:C	1:B:107:MET:H	2.22	0.43
1:A:300:LEU:HD22	1:A:574:LEU:HD21	2.01	0.42
1:B:160:ASP:O	1:B:160:ASP:OD1	2.37	0.42
1:B:78:ARG:HH11	1:B:78:ARG:HG2	1.84	0.42
1:A:245:TYR:OH	1:A:357:LYS:HE2	2.19	0.42
1:A:624:GLY:HA2	1:A:671:ARG:NH2	2.35	0.42
1:B:156:LEU:O	1:B:191:ARG:NH1	2.47	0.42
1:B:130:LYS:HA	1:B:231:PHE:CE1	2.54	0.42
1:B:145:PRO:HB3	1:B:184:MET:SD	2.60	0.42
1:B:79:ASN:CB	1:B:130:LYS:O	2.56	0.42
1:B:86:SER:HA	1:B:146:THR:HG21	2.00	0.42
1:B:131:SER:O	1:B:231:PHE:HZ	2.02	0.42
1:A:220:ARG:NH1	6:A:818:HOH:O	2.52	0.42
1:B:632:ASP:HB2	6:B:1209:HOH:O	2.19	0.42
1:A:349:ASN:OD1	1:A:359:HIS:CE1	2.73	0.41
1:B:94:PHE:CE2	1:B:212:LEU:HD22	2.55	0.41
1:A:262:GLU:HG2	6:A:1181:HOH:O	2.19	0.41
1:A:475:ALA:HA	1:A:491:THR:HB	2.01	0.41
1:B:103:HIS:HB2	6:B:1254:HOH:O	2.20	0.41
1:B:130:LYS:CB	1:B:231:PHE:HD1	2.33	0.41
1:B:125:LEU:N	1:B:126:PRO:CD	2.83	0.41
1:A:527:PRO:HB2	1:A:625:ALA:HB2	2.02	0.41
1:A:108:ARG:NH1	1:A:109:GLY:H	2.19	0.41
1:A:138:ALA:HA	1:A:173:LEU:O	2.21	0.41
1:A:190:GLN:O	1:A:194:GLN:HG3	2.20	0.41
1:B:154:ASP:O	1:B:157:GLN:HB2	2.20	0.41
1:B:317:GLY:HA3	1:B:518:PHE:O	2.20	0.41
1:A:80:ILE:HG23	1:A:109:GLY:HA3	2.01	0.41
1:B:113:ASP:HB3	1:B:116:GLU:HG3	2.02	0.41
1:B:80:ILE:HD11	1:B:107:MET:SD	2.61	0.41
1:B:176:LYS:HD3	1:B:176:LYS:C	2.41	0.41
1:B:255:VAL:HG23	1:B:256:ALA:N	2.36	0.41
1:B:76:THR:HG23	1:B:354:GLU:HG3	2.01	0.41
1:B:73:MET:HB3	1:B:78:ARG:O	2.20	0.41
1:A:80:ILE:HG23	1:A:109:GLY:CA	2.51	0.41
1:B:652:GLY:N	1:B:653:PRO:HA	2.36	0.41
1:A:132:LEU:HD12	1:A:167:LYS:O	2.21	0.40
1:B:233:VAL:CG2	1:B:234:GLU:N	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:HIS:O	1:A:405:MET:HG2	2.21	0.40
1:A:581:ARG:HG2	1:A:581:ARG:NH1	2.36	0.40
1:B:118:ASP:C	1:B:120:ALA:H	2.25	0.40
1:B:120:ALA:HA	1:B:155:TRP:CZ2	2.57	0.40
1:A:498:GLU:HA	1:A:499:PRO:HD3	1.97	0.40
1:B:273:LYS:HA	1:B:274:PRO:HD3	1.95	0.40
1:B:214:GLU:OE1	1:B:413:LYS:HE3	2.21	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	606/621 (98%)	589 (97%)	17 (3%)	0	100	100
1	B	595/621 (96%)	566 (95%)	29 (5%)	0	100	100
All	All	1201/1242 (97%)	1155 (96%)	46 (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	521/531 (98%)	510 (98%)	11 (2%)	61	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	502/531 (94%)	491 (98%)	11 (2%)	60	62
All	All	1023/1062 (96%)	1001 (98%)	22 (2%)	60	62

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	SER
1	A	100	LYS
1	A	108	ARG
1	A	151	ASP
1	A	190	GLN
1	A	252	ASP
1	A	297	GLU
1	A	346	MET
1	A	411	GLU
1	A	484	ARG
1	A	573	TYR
1	B	142	GLU
1	B	151	ASP
1	B	212	LEU
1	B	254	ASP
1	B	290	ARG
1	B	346	MET
1	B	358	LYS
1	B	514	ARG
1	B	553	GLN
1	B	573	TYR
1	B	619	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	HIS
1	A	465	HIS
1	A	583	HIS
1	B	87	GLN
1	B	96	ASN
1	B	222	GLN
1	B	333	GLN
1	B	359	HIS
1	B	641	GLN

### 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 ⓘ

12 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	FMN	A	701	-	32,33,33	2.92	12 (37%)	34,50,50	3.65	13 (38%)
3	FAD	A	702	-	52,58,58	2.14	11 (21%)	52,89,89	2.55	10 (19%)
4	2AM	A	703	-	21,25,25	1.70	3 (14%)	25,38,38	3.23	4 (16%)
5	PO4	A	704	-	4,4,4	1.45	0	6,6,6	0.23	0
5	PO4	A	705	-	4,4,4	1.43	0	6,6,6	0.23	0
5	PO4	A	706	-	4,4,4	0.75	0	6,6,6	0.23	0
2	FMN	B	701	-	32,33,33	2.94	13 (40%)	34,50,50	3.70	13 (38%)
3	FAD	B	702	-	52,58,58	2.14	11 (21%)	52,89,89	2.57	9 (17%)
4	2AM	B	703	-	21,25,25	1.71	3 (14%)	25,38,38	3.14	4 (16%)
5	PO4	B	704	-	4,4,4	1.38	0	6,6,6	0.23	0
5	PO4	B	705	-	4,4,4	1.43	0	6,6,6	0.23	0
5	PO4	B	706	-	4,4,4	0.75	0	6,6,6	0.23	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	FMN	A	701	-	-	0/18/18/18	0/3/3/3
3	FAD	A	702	-	-	0/30/50/50	0/6/6/6
4	2AM	A	703	-	-	0/7/27/27	0/3/3/3
5	PO4	A	704	-	-	0/0/0/0	0/0/0/0
5	PO4	A	705	-	-	0/0/0/0	0/0/0/0
5	PO4	A	706	-	-	0/0/0/0	0/0/0/0
2	FMN	B	701	-	-	0/18/18/18	0/3/3/3
3	FAD	B	702	-	-	0/30/50/50	0/6/6/6
4	2AM	B	703	-	-	0/7/27/27	0/3/3/3
5	PO4	B	704	-	-	0/0/0/0	0/0/0/0
5	PO4	B	705	-	-	0/0/0/0	0/0/0/0
5	PO4	B	706	-	-	0/0/0/0	0/0/0/0

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	FMN	C8M-C8	-6.46	1.38	1.51
2	A	701	FMN	C8M-C8	-6.30	1.38	1.51
3	B	702	FAD	C7M-C7	-5.79	1.39	1.51
3	B	702	FAD	C8M-C8	-5.78	1.39	1.51
3	A	702	FAD	C8M-C8	-5.76	1.39	1.51
3	A	702	FAD	C7M-C7	-5.76	1.39	1.51
3	B	702	FAD	C10-N10	-4.08	1.34	1.39
3	A	702	FAD	C10-N10	-4.05	1.34	1.39
2	A	701	FMN	C1'-N10	-3.09	1.45	1.48
4	B	703	2AM	C5-C4	-3.08	1.33	1.40
4	A	703	2AM	C5-C4	-3.06	1.33	1.40
3	A	702	FAD	C9A-N10	-3.02	1.34	1.38
3	B	702	FAD	C9A-N10	-2.98	1.34	1.38
3	A	702	FAD	C5A-C4A	-2.93	1.33	1.40
3	B	702	FAD	C5A-C4A	-2.89	1.34	1.40
2	B	701	FMN	C1'-N10	-2.67	1.45	1.48
3	A	702	FAD	O4B-C1B	2.09	1.44	1.41
3	B	702	FAD	O4B-C1B	2.13	1.44	1.41
2	B	701	FMN	C4'-C3'	2.16	1.57	1.53
2	A	701	FMN	O2'-C2'	2.35	1.48	1.43
2	A	701	FMN	C10-N1	2.37	1.39	1.35
2	B	701	FMN	C9A-C5A	2.38	1.47	1.42
2	B	701	FMN	O2'-C2'	2.41	1.48	1.43
2	B	701	FMN	C10-N1	2.47	1.39	1.35
2	A	701	FMN	C9A-C5A	2.51	1.47	1.42
3	A	702	FAD	C10-N1	2.79	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	702	FAD	C10-N1	2.87	1.40	1.35
2	A	701	FMN	C9-C9A	2.96	1.47	1.40
2	A	701	FMN	C5A-N5	2.98	1.40	1.35
2	B	701	FMN	C9-C9A	3.00	1.47	1.40
2	B	701	FMN	C5A-N5	3.22	1.40	1.35
3	B	702	FAD	C2A-N1A	3.29	1.40	1.33
2	B	701	FMN	C8-C7	3.33	1.49	1.41
3	A	702	FAD	C2A-N1A	3.35	1.40	1.33
4	B	703	2AM	C2-N1	3.36	1.40	1.33
4	A	703	2AM	C2-N1	3.38	1.40	1.33
2	A	701	FMN	C8-C7	3.55	1.50	1.41
2	B	701	FMN	C4-N3	4.05	1.40	1.33
3	A	702	FAD	C4-N3	4.13	1.40	1.33
3	B	702	FAD	C4-N3	4.14	1.40	1.33
2	A	701	FMN	C4-N3	4.18	1.40	1.33
4	A	703	2AM	C2-N3	4.59	1.40	1.32
4	B	703	2AM	C2-N3	4.63	1.40	1.32
3	A	702	FAD	C2A-N3A	4.63	1.40	1.32
3	B	702	FAD	C2A-N3A	4.65	1.40	1.32
2	B	701	FMN	C4A-N5	5.65	1.42	1.33
2	A	701	FMN	C4A-N5	5.88	1.42	1.33
2	A	701	FMN	C9A-N10	6.65	1.48	1.38
2	B	701	FMN	C9A-N10	6.71	1.48	1.38
3	B	702	FAD	C8A-N7A	6.94	1.48	1.34
3	A	702	FAD	C8A-N7A	7.02	1.48	1.34
2	A	701	FMN	C10-N10	7.33	1.47	1.39
2	B	701	FMN	C10-N10	7.68	1.48	1.39

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	FAD	N3A-C2A-N1A	-14.63	117.38	128.87
3	B	702	FAD	N3A-C2A-N1A	-14.48	117.50	128.87
4	A	703	2AM	N3-C2-N1	-14.40	117.56	128.87
4	B	703	2AM	N3-C2-N1	-14.23	117.69	128.87
2	B	701	FMN	C4-C4A-C10	-7.95	114.85	119.94
2	A	701	FMN	C4-C4A-C10	-7.80	114.95	119.94
2	B	701	FMN	N3-C2-N1	-6.59	116.60	127.69
2	A	701	FMN	N3-C2-N1	-6.47	116.80	127.69
2	B	701	FMN	C4A-C10-N10	-5.66	116.41	120.52
2	A	701	FMN	C4A-C10-N10	-5.62	116.44	120.52
2	A	701	FMN	C4A-C4-N3	-5.34	116.54	123.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	FMN	C4A-C4-N3	-5.23	116.68	123.52
3	B	702	FAD	N3-C2-N1	-4.90	119.44	127.69
3	A	702	FAD	N3-C2-N1	-4.69	119.79	127.69
4	A	703	2AM	C4'-O4'-C1'	-3.90	105.51	109.64
3	B	702	FAD	C4B-O4B-C1B	-3.27	106.18	109.64
4	B	703	2AM	C4'-O4'-C1'	-3.21	106.24	109.64
2	B	701	FMN	O4'-C4'-C3'	-3.17	100.81	108.96
2	A	701	FMN	O4'-C4'-C3'	-3.16	100.82	108.96
3	A	702	FAD	C4B-O4B-C1B	-2.93	106.54	109.64
2	A	701	FMN	C6-C5A-N5	-2.88	115.33	118.92
2	B	701	FMN	C6-C5A-N5	-2.85	115.36	118.92
2	B	701	FMN	C5A-C9A-N10	-2.82	115.46	117.58
4	A	703	2AM	O4'-C1'-C2'	-2.80	101.56	106.60
3	A	702	FAD	C4X-C4-N3	-2.78	119.89	123.52
2	B	701	FMN	O3P-P-O5'	-2.76	98.66	106.72
3	B	702	FAD	C4X-C4-N3	-2.73	119.95	123.52
2	A	701	FMN	C5A-C9A-N10	-2.69	115.56	117.58
4	A	703	2AM	C1'-N9-C4	-2.54	123.97	126.81
3	B	702	FAD	C2B-C3B-C4B	-2.46	97.60	102.64
2	A	701	FMN	C4A-N5-C5A	-2.36	113.94	116.72
2	A	701	FMN	O3P-P-O5'	-2.28	100.08	106.72
2	B	701	FMN	C4A-N5-C5A	-2.17	114.17	116.72
3	A	702	FAD	C2B-C3B-C4B	-2.16	98.21	102.64
4	B	703	2AM	C3'-C2'-C1'	-2.09	98.64	102.63
3	A	702	FAD	C1B-N9A-C4A	-2.07	124.49	126.81
3	B	702	FAD	C4X-C10-N10	-2.01	119.06	120.52
4	B	703	2AM	O4'-C1'-N9	2.17	112.21	108.11
3	A	702	FAD	C1'-N10-C9A	2.33	121.53	118.83
2	B	701	FMN	C8M-C8-C7	2.44	125.98	120.73
2	A	701	FMN	C8M-C8-C7	2.57	126.25	120.73
3	A	702	FAD	C4X-N5-C5X	2.60	119.78	116.72
3	B	702	FAD	C5X-C9A-N10	2.69	119.59	117.58
3	B	702	FAD	C4X-N5-C5X	2.73	119.94	116.72
2	B	701	FMN	C9A-C5A-N5	2.74	126.64	122.18
2	A	701	FMN	C9A-C5A-N5	2.74	126.64	122.18
2	A	701	FMN	O2P-P-O1P	2.79	119.74	110.63
3	A	702	FAD	C5X-C9A-N10	2.86	119.72	117.58
2	B	701	FMN	O2P-P-O1P	2.90	120.08	110.63
3	A	702	FAD	C4-N3-C2	5.88	120.06	115.16
3	B	702	FAD	C4-N3-C2	6.16	120.30	115.16
2	A	701	FMN	C4-N3-C2	14.53	127.28	115.16
2	B	701	FMN	C4-N3-C2	14.72	127.44	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	FMN	1	0
5	A	704	PO4	1	0
2	B	701	FMN	1	0
5	B	706	PO4	2	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	612/621 (98%)	-0.20	12 (1%) 68 69	23, 33, 50, 82	2 (0%)
1	B	601/621 (96%)	0.37	55 (9%) 11 12	22, 38, 86, 98	0
All	All	1213/1242 (97%)	0.08	67 (5%) 29 30	22, 35, 77, 98	2 (0%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	TYR	9.3
1	B	119	LEU	6.4
1	B	181	PHE	5.8
1	B	156	LEU	5.8
1	B	162	ASP	5.7
1	B	163	LEU	5.6
1	B	200	ILE	5.6
1	B	125	LEU	5.3
1	B	165	GLY	5.1
1	B	161	VAL	5.0
1	B	197	ALA	4.8
1	B	187	TYR	4.7
1	B	120	ALA	4.5
1	A	505	GLY	4.3
1	B	166	VAL	4.0
1	B	155	TRP	4.0
1	A	252	ASP	4.0
1	B	168	PHE	3.9
1	B	152	PHE	3.8
1	B	135	PHE	3.8
1	A	240	SER	3.5
1	B	196	GLY	3.5
1	B	195	LEU	3.3
1	B	69	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	80	ILE	3.2
1	B	232	GLY	3.1
1	B	231	PHE	3.1
1	B	133	VAL	3.1
1	B	198	GLN	3.0
1	B	169	ALA	3.0
1	B	201	PHE	2.9
1	B	70	VAL	2.9
1	B	183	ALA	2.8
1	B	186	LYS	2.8
1	A	60	THR	2.8
1	A	506	ARG	2.8
1	B	134	VAL	2.7
1	A	62	PRO	2.7
1	B	225	PRO	2.7
1	A	59	THR	2.6
1	B	192	LEU	2.6
1	B	180	HIS	2.5
1	B	203	LEU	2.5
1	A	255	VAL	2.5
1	B	157	GLN	2.5
1	A	236	THR	2.4
1	A	88	THR	2.4
1	B	131	SER	2.4
1	B	153	TYR	2.4
1	A	273	LYS	2.4
1	B	167	LYS	2.4
1	B	132	LEU	2.3
1	B	193	GLU	2.3
1	B	199	ARG	2.3
1	B	76	THR	2.3
1	B	222	GLN	2.2
1	B	191	ARG	2.2
1	B	351	LEU	2.2
1	B	403	HIS	2.2
1	B	104	ARG	2.1
1	B	123	SER	2.1
1	B	194	GLN	2.1
1	B	313	ARG	2.1
1	B	414	GLU	2.1
1	B	254	ASP	2.0
1	B	122	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	105	TYR	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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
5	PO4	B	706	5/5	0.85	0.26	4.60	105,105,105,106	0
5	PO4	A	706	5/5	0.87	0.18	2.97	86,86,86,86	0
5	PO4	B	705	5/5	0.92	0.12	0.98	55,58,59,61	0
5	PO4	A	704	5/5	0.92	0.15	0.02	50,55,55,55	0
4	2AM	A	703	23/23	0.97	0.10	-0.02	24,29,32,37	0
3	FAD	B	702	53/53	0.97	0.14	-0.17	21,27,35,38	0
3	FAD	A	702	53/53	0.97	0.12	-0.18	21,26,31,32	0
2	FMN	A	701	31/31	0.96	0.14	-0.22	32,36,39,40	0
2	FMN	B	701	31/31	0.93	0.12	-0.66	47,57,59,60	0
4	2AM	B	703	23/23	0.98	0.09	-0.80	26,28,29,34	0
5	PO4	B	704	5/5	0.94	0.09	-1.22	48,50,52,53	0
5	PO4	A	705	5/5	0.66	0.33	-	117,117,118,118	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.