



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 13, 2016 – 05:42 PM EDT

PDB ID : 4YAO  
Title : Reduced CYPOR mutant - G143del  
Authors : Xia, C.; Kim, J.J.P.  
Deposited on : 2015-02-17  
Resolution : 2.50 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

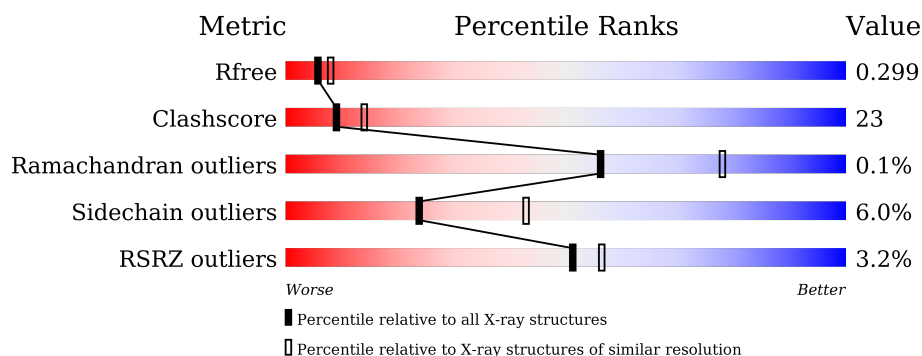
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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></div> <div>56%</div> <div>38%</div> <div>• •</div> </div>
1	B	621	<div> <div>5%</div> <div>51%</div> <div>41%</div> <div>• •</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10066 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.

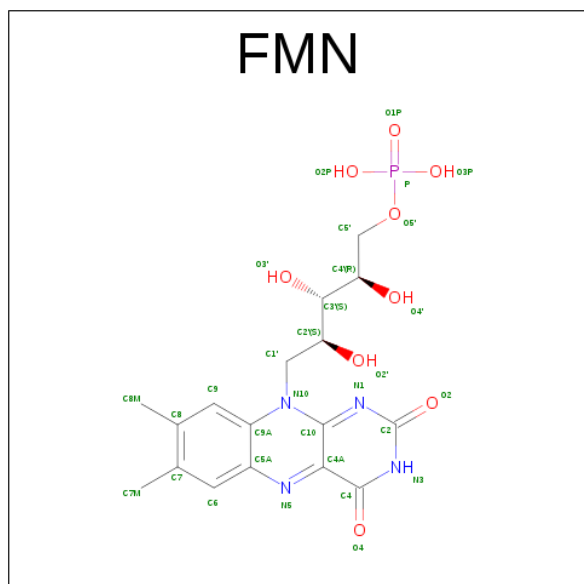
- Molecule 1 is a protein called NADPH–cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	602	Total	C	N	O	S	0	0	0
			4828	3061	834	910	23			
1	B	596	Total	C	N	O	S	0	0	0
			4729	2993	822	891	23			

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

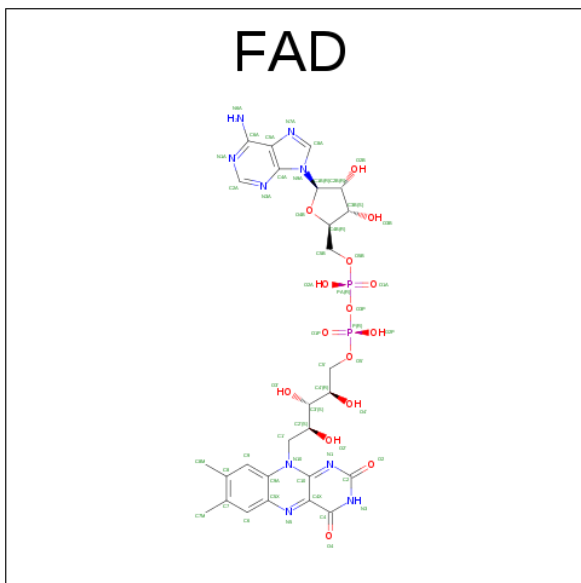
- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



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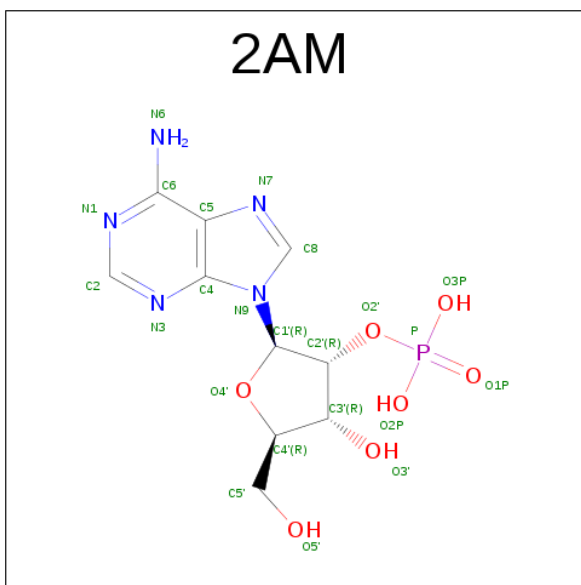
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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



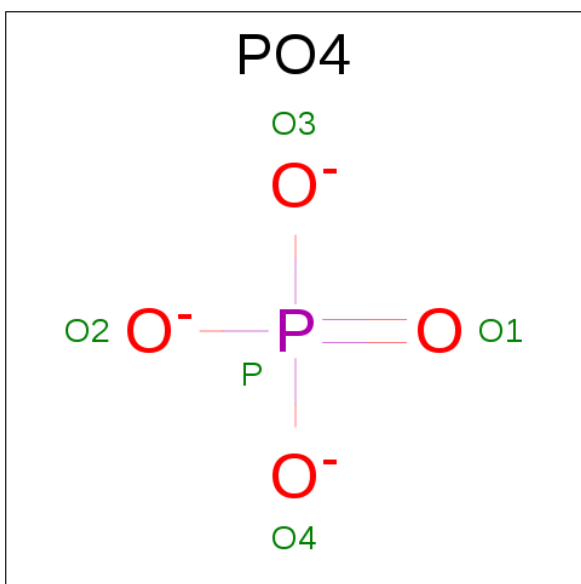
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- 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	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

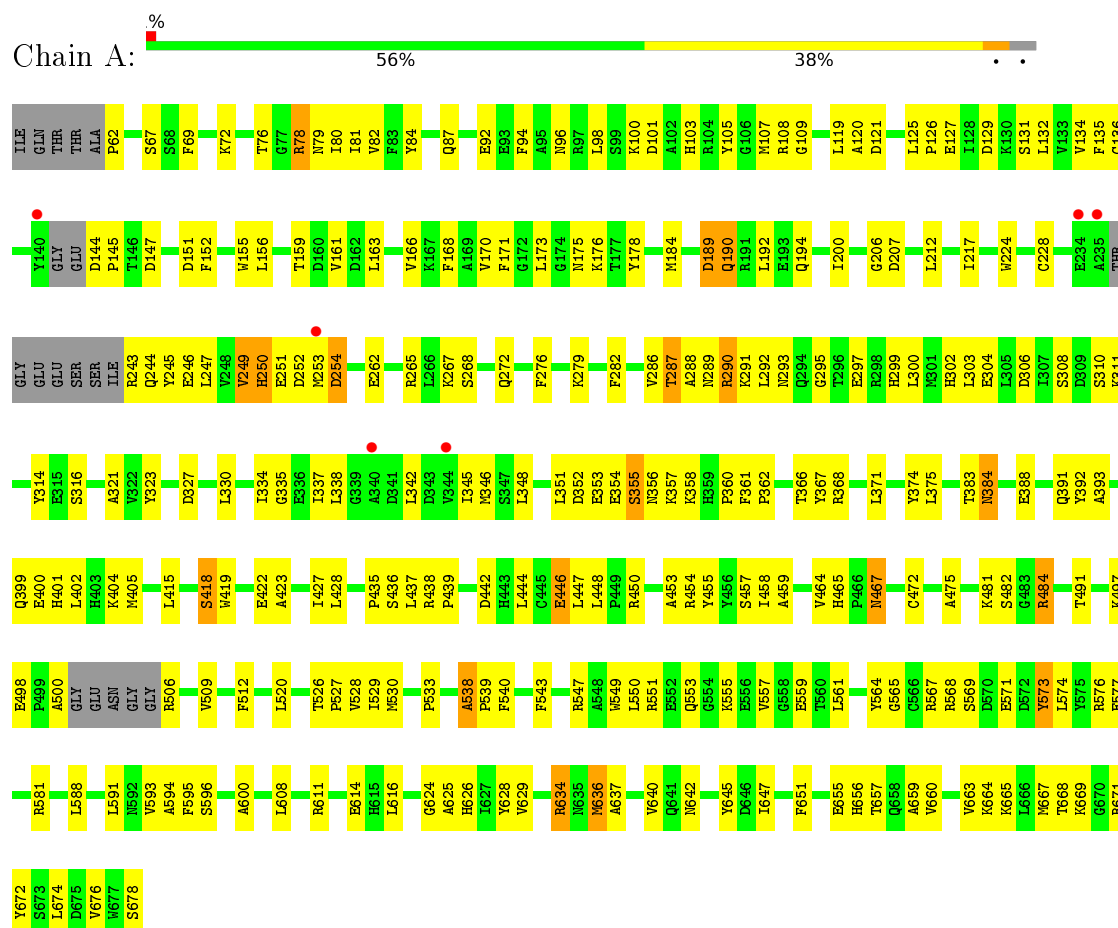
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	155	Total	O	0	0
			155	155		
6	B	120	Total	O	0	0
			120	120		

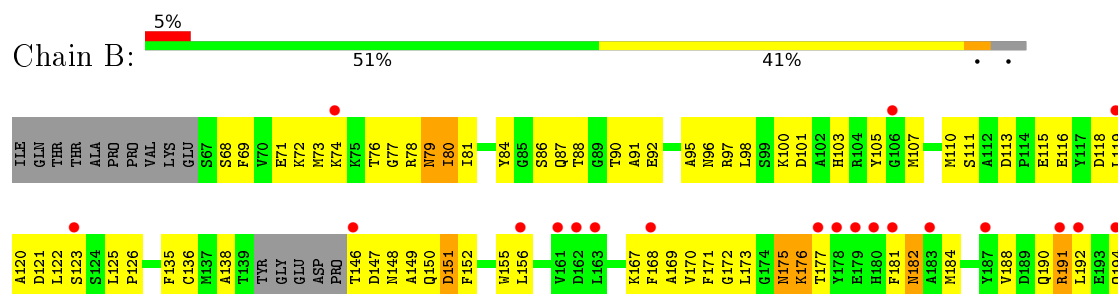
### 3 Residue-property plots

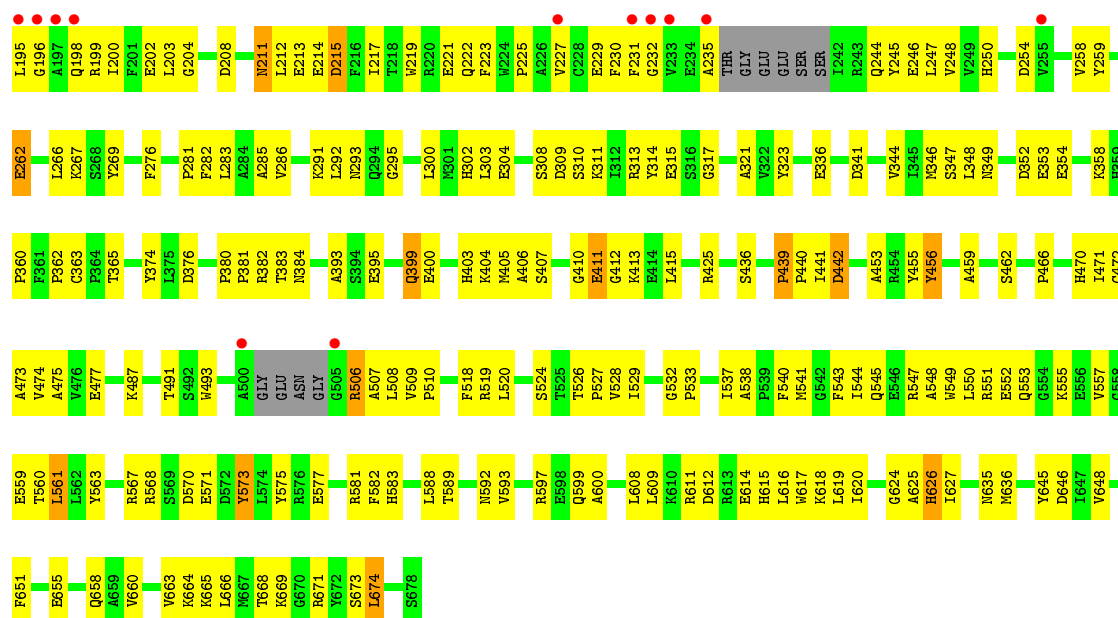
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: 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, $\alpha$ , $\beta$ , $\gamma$	101.48Å 115.52Å 117.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.18 – 2.50 38.18 – 2.50	Depositor EDS
% Data completeness (in resolution range)	89.0 (38.18-2.50) 88.9 (38.18-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.82 (at 2.51Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.234 , 0.298 0.236 , 0.299	Depositor DCC
$R_{free}$ test set	2169 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.7	Xtriage
Anisotropy	0.772	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.023 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10066	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.19 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.0236e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

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	0.44	1/4943 (0.0%)	0.67	5/6687 (0.1%)
1	B	0.40	0/4841	0.68	8/6550 (0.1%)
All	All	0.42	1/9784 (0.0%)	0.68	13/13237 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	539	PRO	N-CD	5.16	1.55	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	506	ARG	N-CA-CB	-7.99	96.21	110.60
1	B	230	PHE	CB-CA-C	7.62	125.64	110.40
1	B	123	SER	CB-CA-C	-7.50	95.84	110.10
1	B	125	LEU	N-CA-C	6.85	129.48	111.00
1	B	232	GLY	N-CA-C	6.61	129.62	113.10
1	B	196	GLY	N-CA-C	6.23	128.66	113.10
1	A	62	PRO	C-N-CD	6.12	141.26	128.40
1	A	249	VAL	CB-CA-C	-6.12	99.78	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	LEU	CB-CA-C	-5.73	99.32	110.20
1	A	538	ALA	C-N-CD	5.70	140.37	128.40
1	B	506	ARG	N-CA-C	-5.57	95.97	111.00
1	B	229	GLU	CB-CA-C	-5.13	100.14	110.40
1	A	355	SER	N-CA-CB	-5.03	102.96	110.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	581	ARG	Sidechain
1	B	456	TYR	Sidechain

## 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	4828	0	4679	207	0
1	B	4729	0	4510	240	0
2	A	31	0	19	0	0
2	B	31	0	19	1	0
3	A	53	0	31	1	0
3	B	53	0	31	2	0
4	A	23	0	12	0	0
4	B	23	0	12	0	0
5	A	10	0	0	1	0
5	B	10	0	0	1	0
6	A	155	0	0	15	0
6	B	120	0	0	13	0
All	All	10066	0	9313	442	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 23.

All (442) 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:144:ASP:CB	1:A:145:PRO:HD3	1.57	1.31
1:A:144:ASP:CB	1:A:145:PRO:CD	2.29	1.09
1:B:86:SER:HB2	1:B:91:ALA:HB3	1.47	0.93
1:A:82:VAL:HG13	1:A:134:VAL:HB	1.51	0.93
1:A:78:ARG:HE	1:A:108:ARG:HE	1.16	0.92
1:A:352:ASP:OD2	1:A:355:SER:HB2	1.70	0.92
1:B:223:PHE:O	1:B:227:VAL:HG23	1.70	0.91
1:A:472:CYS:HB3	1:A:538:ALA:HB2	1.52	0.91
1:A:337:ILE:HB	1:B:600:ALA:HB1	1.52	0.91
1:A:245:TYR:OH	1:A:357:LYS:HD3	1.73	0.89
1:B:527:PRO:O	1:B:625:ALA:HB1	1.74	0.88
1:A:289:ASN:ND2	1:A:497:LYS:O	2.07	0.87
1:A:527:PRO:HB2	1:A:625:ALA:HB2	1.57	0.86
1:B:167:LYS:CB	1:B:200:ILE:HD11	2.06	0.85
1:B:227:VAL:HG13	1:B:231:PHE:CD2	2.12	0.84
1:B:227:VAL:HG13	1:B:231:PHE:CE2	2.13	0.84
1:A:634:ARG:HH11	1:A:634:ARG:HB3	1.43	0.82
1:B:152:PHE:CZ	1:B:156:LEU:HD11	2.15	0.82
1:B:262:GLU:HG2	1:B:269:TYR:HB2	1.61	0.81
1:B:541:MET:O	1:B:545:GLN:HG3	1.81	0.81
1:A:500:ALA:HB2	1:A:506:ARG:N	1.96	0.81
1:B:292:LEU:HD11	1:B:302:HIS:HB2	1.61	0.81
1:A:678:SER:HB2	6:A:925:HOH:O	1.82	0.79
1:B:529:ILE:HD13	1:B:616:LEU:HD22	1.66	0.78
1:A:384:ASN:O	1:A:388:GLU:HG2	1.83	0.78
1:B:581:ARG:HB2	6:B:898:HOH:O	1.84	0.78
1:B:404:LYS:HE2	1:B:407:SER:OG	1.85	0.77
1:B:188:VAL:O	1:B:192:LEU:HG	1.83	0.77
1:A:159:THR:OG1	1:A:161:VAL:HG13	1.83	0.77
1:A:217:ILE:HD11	1:A:383:THR:OG1	1.85	0.76
1:B:190:GLN:O	1:B:194:GLN:HG3	1.86	0.76
1:B:321:ALA:HB2	1:B:455:TYR:CE1	2.20	0.76
1:B:175:ASN:OD1	1:B:177:THR:HG23	1.87	0.74
1:A:80:ILE:HD12	1:A:132:LEU:O	1.85	0.74
1:A:78:ARG:NE	1:A:108:ARG:HE	1.84	0.74
1:B:175:ASN:O	1:B:181:PHE:CD1	2.41	0.74
1:B:403:HIS:HB3	6:B:903:HOH:O	1.88	0.73
1:A:127:GLU:HB2	6:A:805:HOH:O	1.88	0.73
1:B:120:ALA:HA	1:B:155:TRP:CZ2	2.24	0.73
1:B:615:HIS:O	1:B:619:LEU:HD22	1.89	0.72
1:A:168:PHE:O	1:A:200:ILE:HG22	1.90	0.71
1:B:286:VAL:HG23	1:B:507:ALA:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:ILE:HD11	1:B:107:MET:HB3	1.73	0.69
1:B:533:PRO:HG3	1:B:636:MET:HG3	1.74	0.69
1:A:354:GLU:O	6:A:801:HOH:O	2.09	0.68
1:B:245:TYR:HB3	1:B:348:LEU:HB3	1.75	0.68
1:A:190:GLN:O	1:A:194:GLN:HG3	1.94	0.68
1:A:667:MET:HG2	1:A:672:TYR:HB3	1.74	0.68
1:B:616:LEU:HA	1:B:619:LEU:HD23	1.76	0.68
1:B:352:ASP:OD1	1:B:354:GLU:HB2	1.94	0.68
1:B:537:ILE:HG13	1:B:541:MET:HG2	1.75	0.68
1:B:175:ASN:O	1:B:181:PHE:HB2	1.94	0.67
1:B:213:GLU:O	1:B:217:ILE:HG13	1.95	0.67
1:A:388:GLU:HB2	1:A:447:LEU:HD11	1.76	0.67
1:B:300:LEU:N	1:B:300:LEU:HD12	2.11	0.66
1:A:76:THR:OG1	1:A:78:ARG:HD3	1.96	0.66
1:B:527:PRO:HB2	1:B:625:ALA:HB2	1.78	0.66
1:A:573:TYR:CD2	1:A:576:ARG:HG3	2.31	0.66
1:A:135:PHE:CE2	1:A:192:LEU:HD11	2.32	0.65
1:B:119:LEU:HG	1:B:152:PHE:CD1	2.31	0.65
1:B:382:ARG:HG2	6:B:825:HOH:O	1.95	0.65
1:A:321:ALA:HB2	1:A:455:TYR:CE1	2.30	0.65
1:B:167:LYS:HA	1:B:198:GLN:O	1.95	0.65
1:B:477:GLU:HG3	1:B:487:LYS:HD2	1.79	0.65
1:A:80:ILE:HG23	1:A:109:GLY:HA3	1.79	0.65
1:A:543:PHE:O	1:A:547:ARG:HG2	1.97	0.64
1:B:459:ALA:HA	1:B:538:ALA:O	1.98	0.64
1:A:330:LEU:O	1:A:334:ILE:HG13	1.96	0.64
1:A:527:PRO:HB2	1:A:625:ALA:CB	2.27	0.64
1:B:617:TRP:HZ3	1:B:648:VAL:HG22	1.64	0.63
1:B:527:PRO:HD2	1:B:625:ALA:HB2	1.81	0.63
1:A:400:GLU:HG3	1:A:404:LYS:HE3	1.81	0.63
1:B:247:LEU:HD22	1:B:442:ASP:CG	2.18	0.63
1:A:459:ALA:HB2	1:A:538:ALA:HB1	1.80	0.63
1:A:561:LEU:HD12	1:A:561:LEU:N	2.13	0.63
1:A:655:GLU:O	1:A:657:THR:N	2.31	0.63
1:B:304:GLU:HG2	1:B:470:HIS:CD2	2.34	0.62
1:B:674:LEU:HD12	1:B:674:LEU:N	2.14	0.62
1:A:634:ARG:CB	1:A:634:ARG:HH11	2.10	0.62
1:B:664:LYS:O	1:B:668:THR:HG23	1.99	0.62
1:B:663:VAL:HA	1:B:666:LEU:HD12	1.82	0.62
1:A:262:GLU:HG2	6:A:930:HOH:O	1.98	0.61
1:B:74:LYS:O	1:B:74:LYS:HD3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:GLN:HG3	1:B:146:THR:HB	1.82	0.61
1:A:246:GLU:HB3	1:A:351:LEU:HD21	1.82	0.61
1:A:642:ASN:HA	1:A:645:TYR:CD2	2.36	0.60
1:B:551:ARG:HG3	1:B:557:VAL:HG21	1.83	0.60
1:A:80:ILE:HD11	1:A:134:VAL:HG23	1.82	0.60
1:B:227:VAL:CG1	1:B:231:PHE:HD2	2.15	0.60
1:B:227:VAL:CG1	1:B:231:PHE:CD2	2.85	0.60
1:A:337:ILE:CB	1:B:600:ALA:HB1	2.29	0.60
1:B:527:PRO:HB2	1:B:625:ALA:CB	2.32	0.60
1:A:551:ARG:HG2	1:A:557:VAL:HG21	1.84	0.59
1:A:551:ARG:HG2	1:A:557:VAL:CG2	2.32	0.59
1:B:563:TYR:CE2	1:B:609:LEU:HD23	2.38	0.59
1:A:357:LYS:O	1:A:357:LYS:HG2	2.02	0.59
1:B:69:PHE:CE1	1:B:121:ASP:HB2	2.38	0.59
1:B:472:CYS:HB3	1:B:538:ALA:HB2	1.85	0.58
1:B:666:LEU:HD23	1:B:671:ARG:NH1	2.17	0.58
1:A:600:ALA:HB2	1:B:336:GLU:CG	2.34	0.58
1:A:549:TRP:O	1:A:553:GLN:HG2	2.04	0.58
1:A:300:LEU:HD23	1:A:574:LEU:HD21	1.86	0.58
1:A:291:LYS:HD2	1:A:299:HIS:CE1	2.39	0.57
1:A:593:VAL:O	1:A:608:LEU:HD11	2.04	0.57
1:B:660:VAL:HG12	1:B:664:LYS:HE2	1.85	0.57
1:B:71:GLU:HG3	1:B:72:LYS:N	2.19	0.57
1:A:342:LEU:HA	1:A:367:TYR:HB2	1.86	0.57
1:B:540:PHE:HA	1:B:543:PHE:HB2	1.87	0.57
1:A:163:LEU:HD22	1:A:166:VAL:HG21	1.85	0.57
1:A:576:ARG:HH11	1:A:576:ARG:HB3	1.70	0.57
1:B:79:ASN:H	1:B:79:ASN:ND2	2.02	0.57
1:A:660:VAL:HG12	1:A:664:LYS:HD2	1.85	0.57
1:A:491:THR:HG23	3:A:702:FAD:O1P	2.05	0.56
1:A:276:PHE:CG	1:A:282:PHE:HB2	2.41	0.56
1:A:279:LYS:HE3	6:A:947:HOH:O	2.05	0.56
1:A:105:TYR:CD1	1:A:228:CYS:SG	2.99	0.56
1:A:422:GLU:OE2	1:A:481:LYS:HE3	2.06	0.56
1:A:636:MET:CE	1:A:640:VAL:HG21	2.36	0.56
1:A:655:GLU:O	1:A:656:HIS:C	2.42	0.56
1:A:87:GLN:OE1	1:A:87:GLN:HA	2.06	0.56
1:B:152:PHE:CZ	1:B:156:LEU:CD1	2.88	0.56
1:A:529:ILE:HD13	1:A:616:LEU:HD22	1.87	0.56
1:B:169:ALA:CB	1:B:223:PHE:HE1	2.19	0.56
1:A:472:CYS:HB3	1:A:538:ALA:CB	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:CYS:CB	1:A:538:ALA:HB2	2.31	0.55
1:B:559:GLU:OE1	1:B:619:LEU:HD11	2.06	0.55
1:B:570:ASP:HB3	6:B:880:HOH:O	2.05	0.55
1:A:400:GLU:OE2	1:A:404:LYS:HE3	2.06	0.55
1:A:321:ALA:HB3	1:A:512:PHE:CE1	2.41	0.55
1:A:564:TYR:CG	1:A:565:GLY:N	2.73	0.55
1:A:81:ILE:HG23	1:A:81:ILE:O	2.05	0.55
1:B:404:LYS:HE2	1:B:407:SER:HG	1.69	0.55
1:A:100:LYS:HZ2	1:A:244:GLN:HG2	1.72	0.55
1:A:629:VAL:HB	1:A:674:LEU:HD23	1.87	0.55
1:B:258:VAL:CG1	1:B:365:THR:HA	2.36	0.55
1:A:243:ARG:HH22	1:A:442:ASP:CB	2.20	0.55
1:B:281:PRO:HD2	6:B:870:HOH:O	2.07	0.55
1:B:347:SER:HB3	1:B:363:CYS:HB3	1.89	0.55
1:B:175:ASN:O	1:B:181:PHE:HD1	1.88	0.54
1:B:310:SER:O	1:B:311:LYS:HB2	2.06	0.54
1:B:227:VAL:HG13	1:B:231:PHE:HD2	1.66	0.54
1:A:80:ILE:HG23	1:A:109:GLY:CA	2.36	0.54
1:B:493:TRP:CH2	1:B:509:VAL:HG13	2.42	0.54
1:B:68:SER:O	1:B:71:GLU:HG2	2.07	0.54
3:B:702:FAD:HM81	6:B:869:HOH:O	2.07	0.54
1:A:568:ARG:HD2	1:A:571:GLU:CD	2.27	0.54
1:A:267:LYS:HA	6:A:930:HOH:O	2.06	0.54
1:A:600:ALA:HB2	1:B:336:GLU:HG2	1.88	0.54
1:A:664:LYS:HA	1:A:667:MET:HE2	1.88	0.54
1:A:159:THR:HG1	1:A:161:VAL:HG13	1.73	0.54
1:A:484:ARG:N	1:A:484:ARG:HD2	2.23	0.54
1:B:258:VAL:HG13	1:B:365:THR:HA	1.90	0.54
1:B:285:ALA:HA	1:B:508:LEU:HD23	1.90	0.54
1:A:475:ALA:HA	1:A:491:THR:HB	1.90	0.53
1:B:120:ALA:HA	1:B:155:TRP:CE2	2.42	0.53
1:B:559:GLU:HB3	1:B:561:LEU:HD21	1.89	0.53
1:A:249:VAL:HG12	1:A:250:HIS:N	2.24	0.53
1:B:441:ILE:HG22	6:B:820:HOH:O	2.08	0.53
1:B:456:TYR:HB3	1:B:471:ILE:HG23	1.90	0.53
1:B:592:ASN:HB3	1:B:608:LEU:HD13	1.91	0.53
1:B:614:GLU:O	1:B:614:GLU:HG3	2.06	0.53
1:A:300:LEU:HD12	1:A:300:LEU:N	2.24	0.53
1:B:175:ASN:C	1:B:181:PHE:CD1	2.81	0.53
1:A:577:GLU:N	1:A:577:GLU:OE1	2.42	0.53
1:B:188:VAL:HG12	1:B:188:VAL:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:358:LYS:HD2	1:B:358:LYS:H	1.73	0.53
1:B:175:ASN:H	1:B:181:PHE:HD1	1.56	0.53
1:A:300:LEU:CD2	1:A:574:LEU:HD21	2.39	0.53
1:A:243:ARG:HH22	1:A:442:ASP:HB3	1.74	0.53
1:B:69:PHE:H	1:B:69:PHE:HD1	1.56	0.53
1:A:152:PHE:CE2	1:A:156:LEU:HD11	2.44	0.53
1:A:345:ILE:HG12	1:A:366:THR:HG22	1.89	0.53
1:B:227:VAL:HG13	1:B:231:PHE:HE2	1.69	0.53
1:B:295:GLY:HA3	5:B:704:PO4:P	2.49	0.53
1:A:438:ARG:HB3	6:A:905:HOH:O	2.09	0.53
1:B:168:PHE:CE1	1:B:199:ARG:HB2	2.43	0.53
1:B:259:TYR:CD2	1:B:362:PRO:HB3	2.45	0.52
1:A:245:TYR:HB2	1:A:446:GLU:HG3	1.91	0.52
1:A:568:ARG:HD2	1:A:571:GLU:OE1	2.10	0.52
1:A:356:ASN:O	1:A:358:LYS:HG2	2.09	0.52
1:A:94:PHE:CD2	1:A:173:LEU:HD21	2.45	0.52
1:A:79:ASN:O	1:A:131:SER:HA	2.10	0.52
1:B:323:TYR:CE1	1:B:453:ALA:HB2	2.44	0.52
1:B:619:LEU:H	1:B:619:LEU:HD22	1.75	0.52
1:B:80:ILE:HD12	1:B:80:ILE:N	2.24	0.52
1:A:464:VAL:HG12	1:A:465:HIS:CE1	2.45	0.51
1:B:493:TRP:CZ3	1:B:509:VAL:HG13	2.46	0.51
1:B:317:GLY:HA3	1:B:518:PHE:O	2.10	0.51
1:A:335:GLY:HA3	1:A:342:LEU:HD21	1.92	0.51
1:B:115:GLU:HB2	1:B:148:ASN:O	2.11	0.51
1:A:528:VAL:HG13	1:A:628:TYR:CE1	2.46	0.51
1:A:568:ARG:NH1	6:A:804:HOH:O	2.39	0.51
1:A:176:LYS:HG3	1:A:207:ASP:CG	2.31	0.51
1:B:191:ARG:HD2	1:B:195:LEU:HD11	1.91	0.51
1:B:302:HIS:HD1	1:B:575:TYR:HE1	1.57	0.51
1:A:393:ALA:HB1	1:A:436:SER:OG	2.11	0.51
1:A:253:MET:CE	1:A:254:ASP:H	2.23	0.51
1:B:91:ALA:HB2	1:B:173:LEU:HD22	1.93	0.51
1:A:173:LEU:N	1:A:173:LEU:HD12	2.26	0.51
1:A:637:ALA:HB2	1:A:676:VAL:HG11	1.94	0.50
1:B:528:VAL:HG23	1:B:528:VAL:O	2.10	0.50
1:A:246:GLU:O	1:A:348:LEU:HA	2.11	0.50
1:A:272:GLN:OE1	1:A:282:PHE:HA	2.11	0.50
1:A:135:PHE:HB2	1:A:170:VAL:HG22	1.93	0.50
1:A:559:GLU:HB3	1:A:561:LEU:HD11	1.93	0.50
1:A:175:ASN:HB3	1:A:178:TYR:HD2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:ALA:HB3	1:B:399:GLN:HB2	1.93	0.50
1:B:395:GLU:H	1:B:436:SER:HB2	1.77	0.50
1:B:211:ASN:O	1:B:215:ASP:HB2	2.11	0.50
1:B:246:GLU:O	1:B:348:LEU:HA	2.11	0.50
1:B:608:LEU:O	1:B:611:ARG:HB3	2.12	0.50
1:B:167:LYS:CB	1:B:200:ILE:CD1	2.86	0.50
1:A:119:LEU:HG	1:A:152:PHE:CD1	2.47	0.50
1:B:583:HIS:HA	1:B:588:LEU:HB3	1.93	0.50
1:A:96:ASN:O	1:A:100:LYS:HG3	2.11	0.49
1:B:95:ALA:HB1	1:B:111:SER:OG	2.11	0.49
1:A:287:THR:HG21	1:A:306:ASP:HB2	1.94	0.49
1:B:620:ILE:HD11	1:B:627:ILE:HD11	1.94	0.49
1:B:69:PHE:HE1	1:B:121:ASP:HB2	1.76	0.49
1:A:135:PHE:HE2	1:A:192:LEU:HD11	1.74	0.49
1:B:374:TYR:HA	6:B:845:HOH:O	2.13	0.49
1:B:527:PRO:CB	1:B:625:ALA:HB2	2.42	0.49
1:B:626:HIS:N	1:B:626:HIS:ND1	2.60	0.49
1:A:573:TYR:CE2	1:A:576:ARG:HG3	2.47	0.49
1:B:308:SER:O	1:B:309:ASP:HB2	2.13	0.49
1:A:550:LEU:O	1:A:555:LYS:HB2	2.13	0.49
1:A:636:MET:CE	1:A:640:VAL:CG2	2.90	0.49
1:B:352:ASP:C	1:B:354:GLU:H	2.13	0.49
1:A:253:MET:HE2	1:A:254:ASP:H	1.77	0.49
1:B:302:HIS:ND1	1:B:575:TYR:HE1	2.11	0.49
1:B:618:LYS:HG2	6:B:872:HOH:O	2.12	0.49
1:B:136:CYS:HA	1:B:171:PHE:O	2.13	0.49
1:B:156:LEU:HD22	1:B:191:ARG:HB3	1.94	0.49
1:B:214:GLU:OE1	1:B:413:LYS:HE3	2.13	0.49
1:A:668:THR:HG22	6:A:937:HOH:O	2.12	0.48
1:A:163:LEU:O	1:A:166:VAL:HG23	2.13	0.48
1:B:168:PHE:CE2	1:B:192:LEU:HB2	2.48	0.48
1:B:291:LYS:HE3	1:B:293:ASN:O	2.13	0.48
1:B:73:MET:O	1:B:77:GLY:N	2.46	0.48
1:B:221:GLU:O	1:B:225:PRO:HG2	2.13	0.48
1:B:425:ARG:HG3	1:B:425:ARG:HH11	1.77	0.48
1:A:415:LEU:HD12	1:A:419:TRP:HB2	1.95	0.48
1:A:569:SER:HB3	1:A:595:PHE:CZ	2.47	0.48
1:B:219:TRP:O	1:B:222:GLN:N	2.44	0.48
1:A:567:ARG:HA	1:A:596:SER:OG	2.13	0.48
1:A:69:PHE:CE1	1:A:121:ASP:HB2	2.49	0.48
1:B:105:TYR:HD1	1:B:235:ALA:HA	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:THR:HG22	1:B:78:ARG:HE	1.79	0.48
1:A:401:HIS:O	1:A:405:MET:HG2	2.13	0.48
1:B:568:ARG:HG3	1:B:571:GLU:HB2	1.96	0.48
1:B:665:LYS:O	1:B:669:LYS:HG3	2.13	0.48
1:B:341:ASP:O	1:B:344:VAL:HG23	2.13	0.48
1:A:100:LYS:HZ2	1:A:244:GLN:CG	2.26	0.48
1:A:588:LEU:HD13	1:A:591:LEU:HD13	1.96	0.48
1:A:147:ASP:HB2	6:A:884:HOH:O	2.13	0.48
1:B:118:ASP:OD2	1:B:120:ALA:HB3	2.14	0.48
1:A:101:ASP:HB3	1:A:224:TRP:CE2	2.49	0.47
1:A:291:LYS:HD2	1:A:299:HIS:ND1	2.28	0.47
1:A:338:LEU:CD2	1:A:439:PRO:HD2	2.44	0.47
1:B:168:PHE:CD1	1:B:168:PHE:C	2.86	0.47
1:A:151:ASP:HB2	6:A:822:HOH:O	2.13	0.47
1:B:135:PHE:HB2	1:B:170:VAL:HG22	1.96	0.47
1:A:262:GLU:CG	6:A:930:HOH:O	2.60	0.47
1:B:247:LEU:HD22	1:B:442:ASP:CB	2.44	0.47
1:B:383:THR:HB	1:B:406:ALA:HA	1.94	0.47
1:B:645:TYR:HD1	1:B:663:VAL:HG21	1.78	0.47
1:A:80:ILE:HD13	1:A:132:LEU:HB3	1.97	0.47
1:A:286:VAL:CG2	1:A:509:VAL:HG23	2.44	0.47
1:B:175:ASN:N	1:B:181:PHE:HD1	2.12	0.47
1:A:588:LEU:CD1	1:A:591:LEU:HD13	2.44	0.47
1:B:175:ASN:O	1:B:181:PHE:CB	2.63	0.47
1:B:666:LEU:CD2	1:B:671:ARG:NH1	2.77	0.47
1:A:423:ALA:O	1:A:482:SER:HB3	2.15	0.47
1:A:457:SER:O	1:A:458:ILE:C	2.53	0.47
1:A:310:SER:O	1:A:311:LYS:HB2	2.14	0.47
1:B:184:MET:HE3	1:B:188:VAL:HG21	1.96	0.47
1:A:393:ALA:HA	1:A:436:SER:O	2.15	0.47
1:B:146:THR:O	1:B:149:ALA:N	2.40	0.46
1:B:462:SER:O	1:B:466:PRO:HD3	2.15	0.46
1:B:199:ARG:HB2	1:B:199:ARG:NH1	2.31	0.46
1:A:418:SER:HA	1:A:422:GLU:HB3	1.97	0.46
1:A:338:LEU:HD22	1:A:439:PRO:HD2	1.96	0.46
1:B:618:LYS:NZ	1:B:618:LYS:HB3	2.31	0.46
1:B:103:HIS:O	1:B:103:HIS:ND1	2.49	0.46
1:B:169:ALA:CB	1:B:223:PHE:CE1	2.98	0.46
1:B:190:GLN:OE1	1:B:190:GLN:HA	2.14	0.46
1:B:276:PHE:CG	1:B:282:PHE:HB2	2.51	0.46
1:B:567:ARG:HD3	1:B:597:ARG:CZ	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:615:HIS:CD2	1:B:619:LEU:HD21	2.51	0.46
1:B:74:LYS:HD3	1:B:74:LYS:C	2.35	0.46
1:B:98:LEU:HA	1:B:101:ASP:HB2	1.98	0.46
1:B:473:ALA:HA	3:B:702:FAD:O2	2.16	0.46
1:B:79:ASN:H	1:B:79:ASN:HD22	1.64	0.46
1:B:103:HIS:HA	1:B:107:MET:O	2.16	0.46
1:A:361:PHE:HB2	1:A:362:PRO:HD2	1.98	0.45
1:B:283:LEU:HD12	1:B:283:LEU:N	2.31	0.45
1:A:120:ALA:HA	1:A:155:TRP:CZ2	2.51	0.45
1:A:246:GLU:HB3	1:A:351:LEU:CD2	2.45	0.45
1:A:295:GLY:HA3	5:A:704:PO4:P	2.56	0.45
1:B:79:ASN:OD1	1:B:107:MET:HB3	2.16	0.45
1:A:342:LEU:HD12	1:A:368:ARG:CZ	2.46	0.45
1:B:624:GLY:HA2	1:B:671:ARG:NH2	2.31	0.45
1:A:361:PHE:HB2	1:A:362:PRO:CD	2.46	0.45
1:A:533:PRO:HG3	1:A:636:MET:HG3	1.99	0.45
1:B:526:THR:HA	1:B:527:PRO:HD3	1.83	0.45
1:B:527:PRO:CD	1:B:625:ALA:HB2	2.46	0.45
1:A:105:TYR:HD1	1:A:228:CYS:SG	2.39	0.45
1:A:288:ALA:HB3	1:A:304:GLU:HB2	1.97	0.45
1:A:98:LEU:O	1:A:101:ASP:HB2	2.16	0.45
1:A:253:MET:HE2	1:A:254:ASP:N	2.32	0.45
1:B:315:GLU:HB2	1:B:519:ARG:NE	2.31	0.45
1:A:287:THR:CG2	1:A:306:ASP:HB2	2.47	0.45
1:A:391:GLN:HA	1:A:399:GLN:HE21	1.82	0.45
1:B:168:PHE:CE1	1:B:199:ARG:HG3	2.52	0.45
1:A:402:LEU:HD11	1:A:437:LEU:HD22	1.99	0.45
1:B:673:SER:C	1:B:674:LEU:HD12	2.37	0.45
1:B:348:LEU:HD12	1:B:360:PRO:HG3	1.99	0.44
1:B:84:TYR:CD1	1:B:84:TYR:O	2.70	0.44
1:A:101:ASP:HB3	1:A:224:TRP:CZ2	2.53	0.44
1:A:84:TYR:O	1:A:84:TYR:CD1	2.70	0.44
1:B:552:GLU:HG3	6:B:882:HOH:O	2.16	0.44
1:A:206:GLY:HA3	1:A:212:LEU:CD1	2.48	0.44
1:A:245:TYR:CD2	1:A:360:PRO:HD3	2.52	0.44
1:B:247:LEU:HD12	1:B:248:VAL:N	2.32	0.44
1:A:119:LEU:HD22	1:A:119:LEU:N	2.33	0.44
1:A:125:LEU:N	1:A:126:PRO:CD	2.80	0.44
1:A:265:ARG:O	1:A:268:SER:HB3	2.17	0.44
1:B:122:LEU:HD23	1:B:122:LEU:O	2.17	0.44
1:B:168:PHE:CE1	1:B:199:ARG:CB	3.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:532:GLY:HA3	1:B:540:PHE:HE2	1.82	0.44
1:A:103:HIS:HA	1:A:107:MET:O	2.18	0.44
1:A:637:ALA:CB	1:A:676:VAL:HG11	2.48	0.44
1:A:444:LEU:O	1:A:448:LEU:HG	2.18	0.44
1:A:600:ALA:CB	1:B:336:GLU:HG2	2.48	0.44
1:B:245:TYR:CB	1:B:348:LEU:HB3	2.46	0.44
1:B:84:TYR:CZ	1:B:92:GLU:HG3	2.53	0.44
1:B:222:GLN:C	1:B:225:PRO:HD2	2.37	0.44
1:B:405:MET:HE2	1:B:415:LEU:HD23	1.99	0.44
1:A:659:ALA:O	1:A:663:VAL:HG23	2.17	0.43
1:B:283:LEU:HG	1:B:510:PRO:HG3	2.00	0.43
1:B:314:TYR:O	1:B:462:SER:HB3	2.18	0.43
1:A:243:ARG:HH12	1:A:442:ASP:HB2	1.84	0.43
1:A:371:LEU:HD23	1:A:375:LEU:HD12	1.99	0.43
1:B:172:GLY:C	1:B:182:ASN:HD21	2.21	0.43
1:B:303:LEU:HD12	1:B:303:LEU:N	2.34	0.43
1:A:530:MET:HB3	1:A:540:PHE:CD1	2.54	0.43
1:B:96:ASN:O	1:B:100:LYS:HD3	2.18	0.43
1:B:245:TYR:HA	1:B:349:ASN:O	2.19	0.43
1:A:292:LEU:HD21	1:A:302:HIS:HB2	2.01	0.43
1:A:348:LEU:HD12	1:A:360:PRO:HG3	2.01	0.43
1:A:665:LYS:HE2	1:A:669:LYS:HE3	2.01	0.43
1:B:520:LEU:HD21	1:B:543:PHE:CG	2.53	0.43
1:A:392:TYR:CD2	1:A:439:PRO:HB3	2.53	0.43
1:B:98:LEU:C	1:B:100:LYS:H	2.22	0.43
1:B:138:ALA:HB3	1:B:146:THR:HG21	2.00	0.43
1:B:151:ASP:O	1:B:152:PHE:C	2.55	0.43
1:A:520:LEU:HD11	1:A:543:PHE:HA	2.00	0.43
1:B:97:ARG:NE	1:B:384:ASN:HB3	2.34	0.43
1:B:524:SER:HB2	1:B:550:LEU:HD13	2.00	0.43
1:B:549:TRP:HA	1:B:552:GLU:OE1	2.18	0.43
1:A:152:PHE:CE1	1:A:156:LEU:HD21	2.54	0.43
1:A:145:PRO:HG3	1:A:184:MET:SD	2.59	0.43
1:A:435:PRO:HA	1:A:438:ARG:HH12	1.83	0.43
1:B:203:LEU:HD12	1:B:204:GLY:H	1.84	0.43
1:B:69:PHE:O	1:B:73:MET:HG3	2.18	0.43
1:A:374:TYR:O	1:A:450:ARG:HD2	2.18	0.42
1:A:608:LEU:O	1:A:611:ARG:HB3	2.18	0.42
1:A:593:VAL:HG12	1:A:594:ALA:N	2.34	0.42
1:B:266:LEU:O	1:B:267:LYS:HB2	2.17	0.42
1:A:600:ALA:HB2	1:B:336:GLU:CD	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:VAL:HG12	1:B:250:HIS:CE1	2.54	0.42
1:B:259:TYR:CE2	1:B:362:PRO:HB3	2.54	0.42
1:A:624:GLY:HA2	1:A:671:ARG:NH2	2.35	0.42
1:B:254:ASP:OD1	1:B:254:ASP:O	2.37	0.42
1:B:376:ASP:HA	6:B:830:HOH:O	2.19	0.42
1:B:674:LEU:N	1:B:674:LEU:CD1	2.82	0.42
1:B:212:LEU:HD12	1:B:212:LEU:HA	1.85	0.42
1:B:212:LEU:HD21	2:B:701:FMN:O4'	2.20	0.42
1:B:475:ALA:HA	1:B:491:THR:HB	2.01	0.42
1:B:550:LEU:O	1:B:555:LYS:HB2	2.19	0.42
1:B:71:GLU:HG3	1:B:72:LYS:H	1.85	0.42
1:A:189:ASP:C	1:A:189:ASP:OD1	2.58	0.42
1:A:308:SER:HA	1:A:467:ASN:OD1	2.19	0.42
1:A:526:THR:HA	1:A:527:PRO:HD3	1.91	0.42
1:A:647:ILE:O	1:A:651:PHE:HD1	2.03	0.42
1:B:176:LYS:O	1:B:177:THR:C	2.58	0.42
1:B:208:ASP:HB2	1:B:212:LEU:HD22	2.02	0.42
1:B:410:GLY:O	1:B:411:GLU:C	2.57	0.42
1:B:582:PHE:HB3	1:B:588:LEU:HB2	2.01	0.42
1:A:530:MET:HB3	1:A:540:PHE:CE1	2.54	0.42
1:B:76:THR:HG21	1:B:78:ARG:NH2	2.35	0.42
1:A:564:TYR:OH	1:A:574:LEU:HG	2.19	0.42
1:B:669:LYS:HE2	1:B:669:LYS:HB3	1.83	0.42
1:A:314:TYR:CD1	1:A:314:TYR:C	2.93	0.41
1:A:175:ASN:HB3	1:A:178:TYR:CD2	2.55	0.41
1:A:176:LYS:HB3	6:A:847:HOH:O	2.18	0.41
1:B:173:LEU:N	1:B:173:LEU:HD12	2.35	0.41
1:B:548:ALA:O	1:B:552:GLU:HG2	2.20	0.41
1:A:291:LYS:NZ	1:A:293:ASN:ND2	2.69	0.41
1:B:551:ARG:C	1:B:553:GLN:H	2.23	0.41
1:B:651:PHE:CD1	1:B:651:PHE:N	2.88	0.41
1:A:84:TYR:CE2	1:A:92:GLU:HG3	2.56	0.41
1:B:81:ILE:HG13	1:B:110:MET:HG3	2.02	0.41
1:B:321:ALA:HB2	1:B:455:TYR:HE1	1.77	0.41
1:A:288:ALA:O	1:A:303:LEU:HA	2.20	0.41
1:B:169:ALA:HB2	1:B:223:PHE:HE1	1.85	0.41
1:B:352:ASP:C	1:B:354:GLU:N	2.74	0.41
1:B:84:TYR:CE2	1:B:92:GLU:HG3	2.55	0.41
1:A:136:CYS:HA	1:A:171:PHE:O	2.21	0.41
1:A:464:VAL:HG12	1:A:465:HIS:ND1	2.35	0.41
1:B:380:PRO:HA	1:B:381:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:474:VAL:O	1:B:474:VAL:HG13	2.21	0.41
1:B:168:PHE:CZ	1:B:199:ARG:HB2	2.55	0.41
1:B:313:ARG:HG2	1:B:313:ARG:HH11	1.86	0.41
1:B:71:GLU:CG	1:B:72:LYS:N	2.82	0.41
1:A:400:GLU:CG	1:A:404:LYS:HE3	2.49	0.41
1:A:569:SER:HB3	1:A:595:PHE:CE1	2.55	0.41
1:B:199:ARG:CB	1:B:199:ARG:HH11	2.33	0.41
1:B:244:GLN:O	1:B:244:GLN:HG3	2.21	0.41
1:A:356:ASN:O	1:A:358:LYS:N	2.53	0.41
1:B:116:GLU:HA	6:B:907:HOH:O	2.20	0.41
1:B:113:ASP:HB3	1:B:116:GLU:HG2	2.03	0.41
1:B:300:LEU:CD1	1:B:300:LEU:N	2.82	0.41
1:B:410:GLY:O	1:B:412:GLY:N	2.54	0.41
1:B:665:LYS:HE2	1:B:665:LYS:HB3	1.85	0.41
1:A:290:ARG:HG2	1:A:302:HIS:HB3	2.03	0.41
1:B:98:LEU:C	1:B:100:LYS:N	2.74	0.41
1:A:316:SER:HB3	6:A:857:HOH:O	2.20	0.40
1:A:323:TYR:CE1	1:A:453:ALA:HB2	2.56	0.40
1:B:573:TYR:OH	1:B:593:VAL:HG21	2.21	0.40
1:B:635:ASN:HB2	6:B:822:HOH:O	2.20	0.40
1:A:528:VAL:HG13	1:A:628:TYR:HE1	1.85	0.40
1:B:439:PRO:HA	1:B:440:PRO:HD3	1.91	0.40
1:A:454:ARG:HA	6:A:886:HOH:O	2.19	0.40
1:A:576:ARG:NH1	1:A:576:ARG:HB3	2.35	0.40
1:B:411:GLU:H	1:B:411:GLU:HG2	1.53	0.40
1:A:250:HIS:HB2	1:A:345:ILE:O	2.21	0.40
1:A:67:SER:O	1:A:72:LYS:HE3	2.21	0.40
1:B:528:VAL:CG2	1:B:560:THR:HA	2.52	0.40
1:B:544:ILE:HG21	1:B:582:PHE:CD2	2.56	0.40
1:B:79:ASN:C	1:B:80:ILE:HG13	2.42	0.40
1:A:427:ILE:HG23	1:A:428:LEU:N	2.37	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	594/621 (96%)	546 (92%)	47 (8%)	1 (0%)	52	75
1	B	588/621 (95%)	532 (90%)	56 (10%)	0	100	100
All	All	1182/1242 (95%)	1078 (91%)	103 (9%)	1 (0%)	56	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	GLU

### 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	514/531 (97%)	490 (95%)	24 (5%)	32	56
1	B	490/531 (92%)	454 (93%)	36 (7%)	17	32
All	All	1004/1062 (94%)	944 (94%)	60 (6%)	24	43

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ARG
1	A	129	ASP
1	A	189	ASP
1	A	190	GLN
1	A	250	HIS
1	A	251	GLU
1	A	252	ASP
1	A	254	ASP
1	A	287	THR
1	A	290	ARG
1	A	297	GLU
1	A	327	ASP

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Mol	Chain	Res	Type
1	A	346	MET
1	A	384	ASN
1	A	418	SER
1	A	446	GLU
1	A	467	ASN
1	A	484	ARG
1	A	498	GLU
1	A	573	TYR
1	A	614	GLU
1	A	626	HIS
1	A	634	ARG
1	A	636	MET
1	B	79	ASN
1	B	80	ILE
1	B	88	THR
1	B	90	THR
1	B	126	PRO
1	B	147	ASP
1	B	150	GLN
1	B	151	ASP
1	B	175	ASN
1	B	176	LYS
1	B	182	ASN
1	B	191	ARG
1	B	202	GLU
1	B	211	ASN
1	B	215	ASP
1	B	262	GLU
1	B	346	MET
1	B	353	GLU
1	B	399	GLN
1	B	400	GLU
1	B	411	GLU
1	B	439	PRO
1	B	442	ASP
1	B	506	ARG
1	B	547	ARG
1	B	561	LEU
1	B	573	TYR
1	B	577	GLU
1	B	589	THR
1	B	599	GLN

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Mol	Chain	Res	Type
1	B	612	ASP
1	B	626	HIS
1	B	646	ASP
1	B	655	GLU
1	B	658	GLN
1	B	674	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	190	GLN
1	A	399	GLN
1	A	601	HIS
1	B	150	GLN
1	B	250	HIS
1	B	642	ASN

### 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](#)

10 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	2.83	12 (37%)	34,50,50	3.66	13 (38%)
3	FAD	A	702	-	52,58,58	2.14	11 (21%)	52,89,89	2.57	8 (15%)
4	2AM	A	703	-	21,25,25	1.70	3 (14%)	25,38,38	3.18	5 (20%)
5	PO4	A	704	-	4,4,4	1.48	0	6,6,6	0.23	0
5	PO4	A	705	-	4,4,4	1.39	0	6,6,6	0.23	0
2	FMN	B	701	-	32,33,33	3.02	12 (37%)	34,50,50	3.73	14 (41%)
3	FAD	B	702	-	52,58,58	2.14	11 (21%)	52,89,89	2.50	8 (15%)
4	2AM	B	703	-	21,25,25	1.72	4 (19%)	25,38,38	3.01	3 (12%)
5	PO4	B	704	-	4,4,4	1.46	0	6,6,6	0.23	0
5	PO4	B	705	-	4,4,4	1.43	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
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

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	FMN	C8M-C8	-6.50	1.38	1.51
2	B	701	FMN	C8M-C8	-6.36	1.38	1.51
3	B	702	FAD	C7M-C7	-5.81	1.39	1.51
3	A	702	FAD	C7M-C7	-5.78	1.39	1.51
3	B	702	FAD	C8M-C8	-5.77	1.39	1.51
3	A	702	FAD	C8M-C8	-5.75	1.39	1.51
3	B	702	FAD	C10-N10	-3.95	1.34	1.39
3	A	702	FAD	C10-N10	-3.89	1.34	1.39
4	A	703	2AM	C5-C4	-3.09	1.33	1.40
4	B	703	2AM	C5-C4	-3.06	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	FAD	C9A-N10	-3.05	1.34	1.38
3	B	702	FAD	C9A-N10	-2.99	1.34	1.38
3	B	702	FAD	C5A-C4A	-2.95	1.33	1.40
3	A	702	FAD	C5A-C4A	-2.90	1.34	1.40
2	A	701	FMN	C10-N1	2.01	1.39	1.35
4	B	703	2AM	O4'-C1'	2.04	1.44	1.41
2	A	701	FMN	C7M-C7	2.06	1.55	1.51
3	B	702	FAD	O4B-C1B	2.16	1.44	1.41
3	A	702	FAD	O4B-C1B	2.18	1.44	1.41
2	B	701	FMN	C4'-C3'	2.33	1.58	1.53
2	B	701	FMN	O2'-C2'	2.43	1.48	1.43
2	A	701	FMN	C4'-C3'	2.47	1.58	1.53
2	A	701	FMN	C5A-N5	2.49	1.39	1.35
2	B	701	FMN	C9A-C5A	2.50	1.47	1.42
2	A	701	FMN	C9A-C5A	2.63	1.48	1.42
2	A	701	FMN	C9-C9A	2.74	1.46	1.40
2	B	701	FMN	C10-N1	2.74	1.40	1.35
3	B	702	FAD	C10-N1	2.87	1.40	1.35
3	A	702	FAD	C10-N1	2.87	1.40	1.35
3	B	702	FAD	C2A-N1A	3.29	1.40	1.33
2	B	701	FMN	C9-C9A	3.30	1.48	1.40
4	A	703	2AM	C2-N1	3.33	1.40	1.33
4	B	703	2AM	C2-N1	3.35	1.40	1.33
3	A	702	FAD	C2A-N1A	3.36	1.40	1.33
2	B	701	FMN	C5A-N5	3.39	1.40	1.35
2	B	701	FMN	C8-C7	3.40	1.50	1.41
2	A	701	FMN	C8-C7	3.51	1.50	1.41
2	A	701	FMN	C4-N3	3.64	1.39	1.33
3	B	702	FAD	C4-N3	4.08	1.40	1.33
3	A	702	FAD	C4-N3	4.12	1.40	1.33
2	B	701	FMN	C4-N3	4.25	1.40	1.33
4	A	703	2AM	C2-N3	4.61	1.40	1.32
3	B	702	FAD	C2A-N3A	4.62	1.40	1.32
3	A	702	FAD	C2A-N3A	4.64	1.40	1.32
4	B	703	2AM	C2-N3	4.65	1.40	1.32
2	A	701	FMN	C4A-N5	5.23	1.41	1.33
2	B	701	FMN	C4A-N5	5.83	1.42	1.33
2	A	701	FMN	C9A-N10	6.65	1.48	1.38
2	B	701	FMN	C9A-N10	6.88	1.48	1.38
3	B	702	FAD	C8A-N7A	6.96	1.48	1.34
3	A	702	FAD	C8A-N7A	7.05	1.48	1.34
2	A	701	FMN	C10-N10	7.73	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	FMN	C10-N10	8.08	1.48	1.39

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	702	FAD	N3A-C2A-N1A	-14.64	117.37	128.87
3	A	702	FAD	N3A-C2A-N1A	-14.63	117.38	128.87
4	B	703	2AM	N3-C2-N1	-14.02	117.86	128.87
4	A	703	2AM	N3-C2-N1	-13.84	118.00	128.87
2	B	701	FMN	C4-C4A-C10	-8.21	114.68	119.94
2	A	701	FMN	C4-C4A-C10	-7.89	114.89	119.94
2	B	701	FMN	N3-C2-N1	-6.70	116.40	127.69
2	A	701	FMN	N3-C2-N1	-6.29	117.10	127.69
2	B	701	FMN	C4A-C10-N10	-5.59	116.46	120.52
2	A	701	FMN	C4A-C4-N3	-5.45	116.39	123.52
2	B	701	FMN	C4A-C4-N3	-5.23	116.68	123.52
2	A	701	FMN	C4A-C10-N10	-5.19	116.75	120.52
4	A	703	2AM	C4'-O4'-C1'	-4.85	104.50	109.64
3	A	702	FAD	N3-C2-N1	-4.78	119.63	127.69
3	B	702	FAD	N3-C2-N1	-4.64	119.89	127.69
3	A	702	FAD	C4B-O4B-C1B	-3.50	105.94	109.64
2	A	701	FMN	C6-C5A-N5	-3.36	114.72	118.92
4	A	703	2AM	O4'-C1'-C2'	-3.16	100.92	106.60
2	B	701	FMN	O4'-C4'-C3'	-3.08	101.04	108.96
2	B	701	FMN	C5A-C9A-N10	-3.01	115.32	117.58
3	A	702	FAD	C4X-C4-N3	-2.93	119.69	123.52
2	A	701	FMN	O4'-C4'-C3'	-2.86	101.59	108.96
3	A	702	FAD	C2B-C3B-C4B	-2.80	96.90	102.64
3	B	702	FAD	C4X-C4-N3	-2.78	119.89	123.52
2	A	701	FMN	C5A-C9A-N10	-2.76	115.51	117.58
2	B	701	FMN	C6-C5A-N5	-2.75	115.49	118.92
2	B	701	FMN	O3P-P-O5'	-2.59	99.15	106.72
4	A	703	2AM	C1'-N9-C4	-2.28	124.26	126.81
3	B	702	FAD	C4B-O4B-C1B	-2.25	107.26	109.64
3	B	702	FAD	C2B-C3B-C4B	-2.15	98.24	102.64
4	A	703	2AM	C3'-C2'-C1'	-2.14	98.53	102.63
2	A	701	FMN	C4A-N5-C5A	-2.13	114.21	116.72
2	B	701	FMN	C4A-N5-C5A	-2.09	114.26	116.72
4	B	703	2AM	C3'-C2'-C1'	-2.09	98.63	102.63
2	B	701	FMN	O4'-C4'-C5'	-2.06	105.60	110.09
4	B	703	2AM	C4'-O4'-C1'	-2.03	107.49	109.64
2	A	701	FMN	C1'-N10-C9A	2.27	121.46	118.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	FMN	C8M-C8-C7	2.32	125.72	120.73
2	B	701	FMN	C8M-C8-C7	2.39	125.86	120.73
3	A	702	FAD	C5X-C9A-N10	2.51	119.46	117.58
3	B	702	FAD	C4X-N5-C5X	2.58	119.76	116.72
3	A	702	FAD	C4X-N5-C5X	2.61	119.80	116.72
2	B	701	FMN	C9A-C5A-N5	2.73	126.62	122.18
2	A	701	FMN	C9A-C5A-N5	2.84	126.81	122.18
2	B	701	FMN	O2P-P-O1P	2.87	119.99	110.63
3	B	702	FAD	C5X-C9A-N10	3.00	119.82	117.58
2	A	701	FMN	O2P-P-O1P	3.08	120.67	110.63
3	B	702	FAD	C4-N3-C2	5.68	119.89	115.16
3	A	702	FAD	C4-N3-C2	6.17	120.30	115.16
2	A	701	FMN	C4-N3-C2	14.56	127.30	115.16
2	B	701	FMN	C4-N3-C2	14.80	127.50	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	FAD	1	0
5	A	704	PO4	1	0
2	B	701	FMN	1	0
3	B	702	FAD	2	0
5	B	704	PO4	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, 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	602/621 (96%)	-0.04	6 (0%) 84 86	26, 55, 78, 102	0
1	B	596/621 (95%)	0.24	32 (5%) 29 33	26, 61, 108, 133	0
All	All	1198/1242 (96%)	0.10	38 (3%) 51 56	26, 57, 103, 133	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	505	GLY	5.5
1	B	196	GLY	4.5
1	B	156	LEU	4.4
1	B	198	GLN	4.3
1	B	183	ALA	4.2
1	B	180	HIS	4.2
1	B	162	ASP	4.1
1	B	195	LEU	4.0
1	B	194	GLN	3.9
1	B	177	THR	3.8
1	B	187	TYR	3.6
1	B	231	PHE	3.5
1	A	344	VAL	3.4
1	B	197	ALA	3.4
1	A	140	TYR	3.3
1	B	192	LEU	3.2
1	B	179	GLU	3.0
1	B	232	GLY	3.0
1	A	235	ALA	2.8
1	B	119	LEU	2.8
1	A	234	GLU	2.7
1	B	181	PHE	2.7
1	B	191	ARG	2.7
1	B	146	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	235	ALA	2.6
1	B	161	VAL	2.5
1	B	233	VAL	2.5
1	B	168	PHE	2.4
1	B	123	SER	2.4
1	B	500	ALA	2.4
1	B	178	TYR	2.3
1	A	340	ALA	2.3
1	B	227	VAL	2.3
1	A	253	MET	2.3
1	B	255	VAL	2.2
1	B	163	LEU	2.2
1	B	106	GLY	2.2
1	B	74	LYS	2.1

## 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( $\text{\AA}^2$ )	Q<0.9
3	FAD	B	702	53/53	0.97	0.16	0.28	29,43,52,53	0
3	FAD	A	702	53/53	0.97	0.15	0.01	32,38,47,47	0
2	FMN	A	701	31/31	0.96	0.17	-0.10	44,52,58,60	0
5	PO4	A	704	5/5	0.96	0.15	-0.12	49,50,54,57	0
4	2AM	B	703	23/23	0.96	0.13	-0.20	43,46,49,51	0
4	2AM	A	703	23/23	0.98	0.12	-0.23	29,40,45,46	0
5	PO4	A	705	5/5	0.90	0.13	-0.82	103,103,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PO4	B	704	5/5	0.98	0.12	-0.96	43,44,48,51	0
2	FMN	B	701	31/31	0.91	0.17	-1.02	77,79,80,81	0
5	PO4	B	705	5/5	0.92	0.16	-	97,97,98,99	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.