



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:50 AM GMT

PDB ID : 1KBO
Title : Complex of Human recombinant NAD(P)H:Quinone Oxide reductase type 1
with 5-methoxy-1,2-dimethyl-3-(phenoxymethyl)indole-4,7-dione(ES1340)
Authors : Faig, M.; Bianchet, M.A.; Amzel, L.M.
Deposited on : 2001-11-06
Resolution : 2.30 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

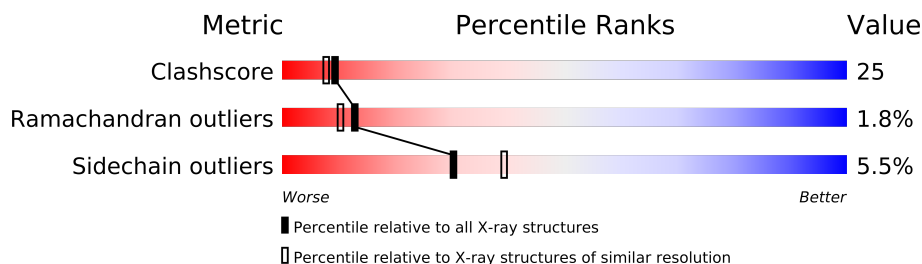
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	

2 Entry composition i

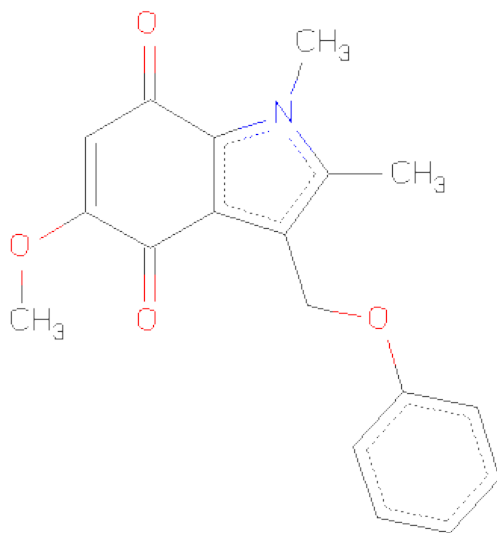
There are 4 unique types of molecules in this entry. The entry contains 9169 atoms, of which 0 are hydrogen and 0 are deuterium.

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 NAD(P)H dehydrogenase [quinone] 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	B	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	C	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	D	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			

- Molecule 2 is 5-METHOXY-1,2-DIMETHYL-3-(PHENOXYMETHYL)INDOLE-4,7-DIONE (three-letter code: 340) (formula: C₁₈H₁₇NO₄).



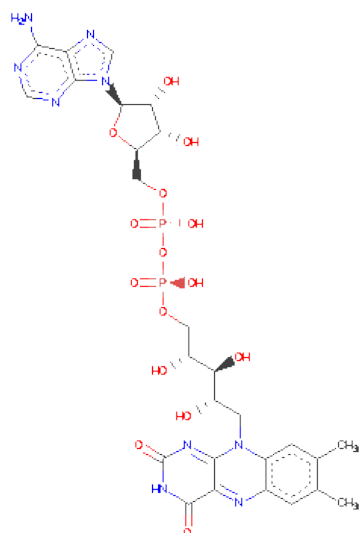
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			23	18	1	4		
2	D	1	Total	C	N	O	0	0
			23	18	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	18	1	4		
2	B	1	Total	C	N	O	0	0
			23	18	1	4		

- 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		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	40	Total	O	0	0
			40	40		
4	B	40	Total	O	0	0
			40	40		
4	C	42	Total	O	0	0
			42	42		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	43	Total	O	0	0
			43	43		

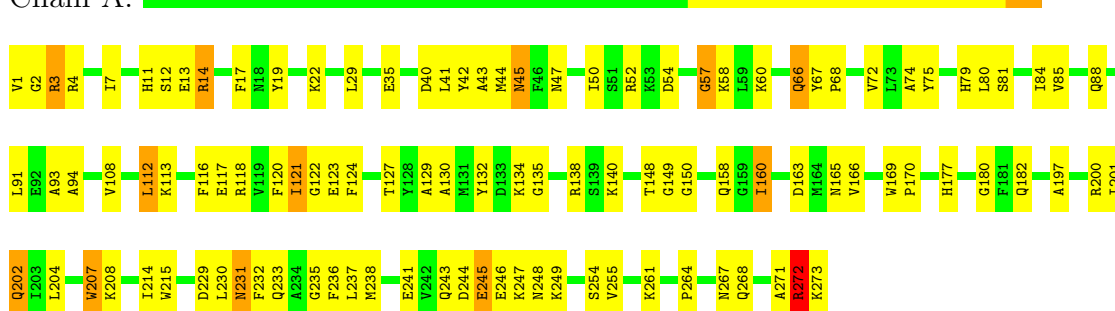
3 Residue-property plots

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.

Note EDS was not executed.

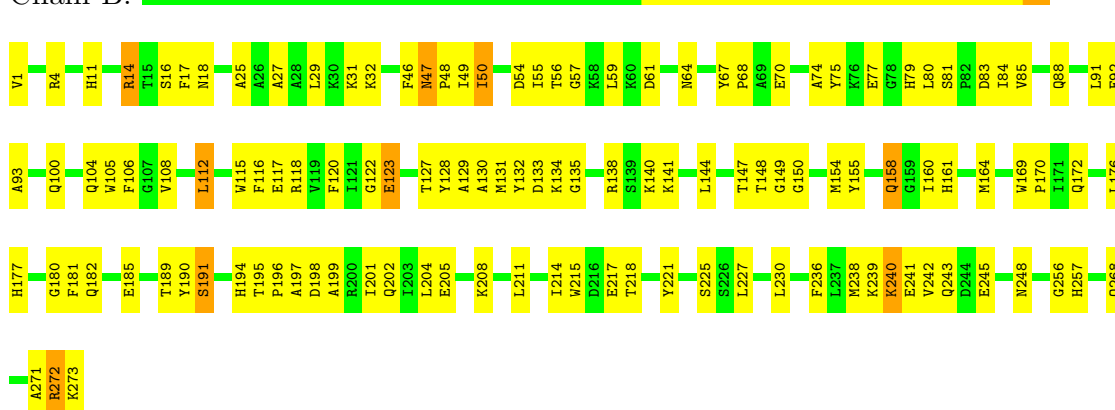
• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain A:



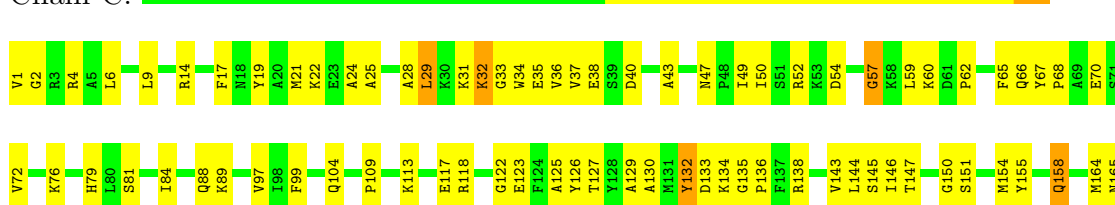
• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain B:



• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

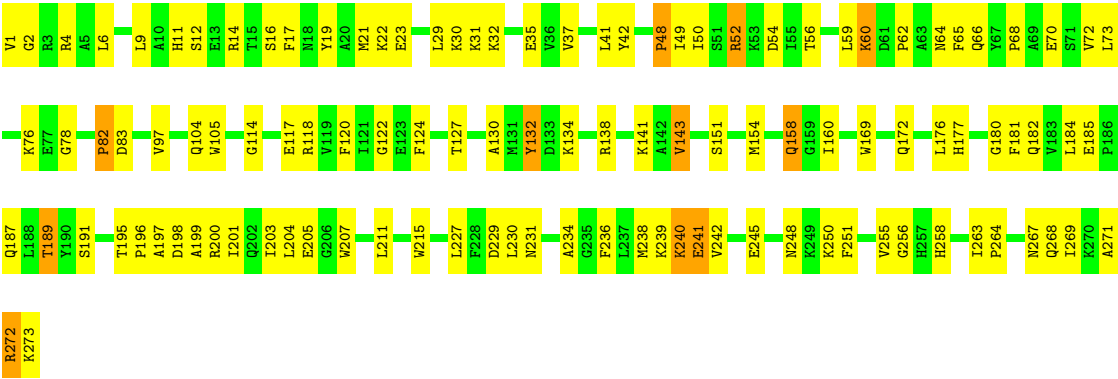
Chain C:





● Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain D:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.64Å 57.03Å 96.88Å 76.80° 76.93° 86.28°	Depositor
Resolution (Å)	35.55 – 2.30	Depositor
% Data completeness (in resolution range)	74.4 (35.55-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.200 , 0.287	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9169	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 340, 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	0.47	0/2233	0.68	0/3015
1	B	0.46	0/2233	0.70	0/3015
1	C	0.47	0/2233	0.65	1/3015 (0.0%)
1	D	0.46	0/2233	0.65	0/3015
All	All	0.46	0/8932	0.67	1/12060 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	182	GLN	N-CA-C	-5.09	97.25	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2175	0	2179	108	0
1	B	2175	0	2179	133	0
1	C	2175	0	2179	119	0
1	D	2175	0	2179	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	23	0	17	0	0
2	B	23	0	17	0	0
2	C	23	0	17	0	0
2	D	23	0	17	1	0
3	A	53	0	31	5	0
3	B	53	0	31	5	0
3	C	53	0	31	4	0
3	D	53	0	31	4	0
4	A	40	0	0	3	0
4	B	40	0	0	3	0
4	C	42	0	0	6	0
4	D	43	0	0	5	0
All	All	9169	0	8908	442	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 25.

All (442) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:143:VAL:HG13	1:D:184:LEU:HB2	1.41	0.98
1:A:14:ARG:HE	1:A:14:ARG:N	1.61	0.98
1:A:264:PRO:HG3	1:A:273:LYS:HE3	1.42	0.98
1:B:135:GLY:O	1:B:138:ARG:HG3	1.63	0.97
1:A:14:ARG:H	1:A:14:ARG:NE	1.63	0.95
1:A:202:GLN:HE21	1:A:202:GLN:HA	1.31	0.94
1:A:130:ALA:HB1	1:A:134:LYS:O	1.70	0.90
1:B:240:LYS:HB3	1:B:240:LYS:NZ	1.86	0.89
1:C:233:GLN:HA	1:C:233:GLN:HE21	1.36	0.89
1:D:17:PHE:HB2	3:D:604:FAD:H52A	1.53	0.89
1:C:240:LYS:HD2	1:C:240:LYS:H	1.37	0.87
1:A:66:GLN:HA	1:A:66:GLN:HE21	1.37	0.87
1:A:68:PRO:O	1:A:72:VAL:HG23	1.75	0.86
1:A:127:THR:HG22	1:A:129:ALA:H	1.42	0.85
1:C:204:LEU:O	1:C:208:LYS:HG3	1.77	0.84
1:D:138:ARG:HA	1:D:180:GLY:O	1.77	0.83
1:C:209:LYS:HD3	1:C:210:ARG:N	1.94	0.82
1:C:151:SER:H	1:C:154:MET:HE3	1.43	0.81
1:A:163:ASP:OD2	1:A:165:ASN:HB2	1.80	0.81
1:A:17:PHE:HB2	3:A:601:FAD:H52A	1.62	0.81
1:B:17:PHE:HB2	3:B:602:FAD:H52A	1.65	0.78
1:A:14:ARG:HE	1:A:14:ARG:H	0.83	0.77
1:B:176:LEU:O	1:B:181:PHE:HB2	1.84	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:1:VAL:HB	1:D:215:TRP:CD1	2.20	0.76
1:C:1:VAL:HG12	1:C:2:GLY:H	1.49	0.76
1:A:50:ILE:CD1	1:A:117:GLU:HB3	2.16	0.75
1:C:197:ALA:O	1:C:201:ILE:HG13	1.87	0.75
1:A:40:ASP:HB3	1:A:43:ALA:HB3	1.70	0.74
1:A:118:ARG:O	1:A:121:ILE:HD12	1.88	0.73
1:A:241:GLU:O	1:A:245:GLU:HG3	1.88	0.73
1:C:76:LYS:HE3	1:C:123:GLU:HG3	1.71	0.73
1:B:48:PRO:HG3	1:D:49:ILE:HD11	1.70	0.73
1:C:169:TRP:HB3	1:C:170:PRO:HD3	1.72	0.72
1:B:88:GLN:O	1:B:92:GLU:HG3	1.89	0.72
1:A:255:VAL:HG23	1:A:267:ASN:HD22	1.54	0.72
1:A:271:ALA:O	1:A:272:ARG:HB3	1.91	0.71
1:D:201:ILE:O	1:D:205:GLU:HG2	1.91	0.71
1:A:202:GLN:NE2	1:A:202:GLN:HA	2.05	0.71
1:B:1:VAL:HA	1:B:215:TRP:CD1	2.27	0.70
1:D:199:ALA:O	1:D:203:ILE:HG13	1.90	0.70
1:B:240:LYS:HB3	1:B:240:LYS:HZ3	1.55	0.69
1:C:233:GLN:HA	1:C:233:GLN:NE2	2.06	0.69
1:D:132:TYR:O	1:D:180:GLY:HA2	1.93	0.69
1:B:1:VAL:HA	1:B:215:TRP:NE1	2.07	0.69
1:B:169:TRP:HB3	1:B:170:PRO:HD3	1.72	0.69
1:C:9:LEU:HD22	1:C:22:LYS:HD3	1.75	0.69
1:D:9:LEU:HD22	1:D:22:LYS:HD3	1.73	0.69
1:C:1:VAL:HA	1:C:215:TRP:NE1	2.07	0.69
1:B:236:PHE:HD2	1:D:160:ILE:HD12	1.57	0.69
1:C:143:VAL:HG22	1:C:184:LEU:HB2	1.73	0.69
1:D:127:THR:CG2	1:D:130:ALA:HB3	2.23	0.68
1:A:50:ILE:HD11	1:A:117:GLU:HB3	1.74	0.68
1:D:64:ASN:HD21	1:D:66:GLN:HE21	1.42	0.68
1:C:1:VAL:HA	1:C:215:TRP:CD1	2.29	0.68
1:A:148:THR:HG23	3:A:601:FAD:O2	1.93	0.68
1:D:1:VAL:HG23	1:D:2:GLY:N	2.10	0.67
1:D:132:TYR:HA	1:D:177:HIS:O	1.95	0.66
1:A:4:ARG:HG2	1:A:35:GLU:OE2	1.95	0.66
1:A:169:TRP:HB3	1:A:170:PRO:HD3	1.78	0.66
1:A:246:GLU:HA	1:A:249:LYS:HG3	1.77	0.66
1:B:160:ILE:HG12	1:D:236:PHE:HB3	1.77	0.65
1:A:108:VAL:HG13	1:A:112:LEU:HB3	1.77	0.65
1:C:29:LEU:O	1:C:34:TRP:HB2	1.97	0.65
1:C:138:ARG:HA	1:C:180:GLY:O	1.97	0.64
1:B:108:VAL:CG1	1:B:112:LEU:HB3	2.27	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:50:ILE:HD12	1:B:117:GLU:HB3	1.80	0.64
1:D:151:SER:H	1:D:154:MET:HE3	1.62	0.63
1:C:14:ARG:HB2	1:C:14:ARG:HH11	1.63	0.63
1:C:271:ALA:O	1:C:272:ARG:HB2	1.96	0.63
1:C:57:GLY:H	1:C:79:HIS:HB3	1.63	0.63
1:A:58:LYS:N	1:A:58:LYS:HD2	2.13	0.63
1:B:185:GLU:HG3	4:B:707:HOH:O	1.98	0.63
1:B:83:ASP:OD2	1:B:118:ARG:NH2	2.31	0.62
1:B:214:ILE:HG23	1:B:215:TRP:N	2.14	0.62
1:C:1:VAL:HG12	1:C:2:GLY:N	2.14	0.62
1:D:1:VAL:HG23	1:D:2:GLY:H	1.63	0.62
1:C:14:ARG:HB2	1:C:14:ARG:NH1	2.14	0.62
1:B:221:TYR:CB	1:B:273:LYS:HA	2.30	0.62
1:C:231:ASN:OD1	1:C:233:GLN:HB3	2.00	0.62
1:D:1:VAL:HB	1:D:215:TRP:NE1	2.15	0.62
1:B:214:ILE:O	1:B:217:GLU:HG3	2.00	0.61
1:B:154:MET:HE3	1:B:160:ILE:HD11	1.81	0.61
1:B:112:LEU:HD22	1:B:116:PHE:CE2	2.35	0.61
1:B:135:GLY:O	1:B:138:ARG:CG	2.45	0.61
1:D:197:ALA:O	1:D:201:ILE:HG13	2.00	0.61
1:D:52:ARG:HG2	4:D:712:HOH:O	2.00	0.61
1:B:84:ILE:O	1:B:88:GLN:HG3	2.00	0.61
1:C:50:ILE:HG22	1:C:118:ARG:HG2	1.82	0.60
1:C:122:GLY:O	1:C:123:GLU:HB2	2.01	0.60
1:C:240:LYS:HD2	1:C:240:LYS:N	2.13	0.60
1:D:127:THR:HG23	1:D:130:ALA:H	1.66	0.60
1:A:1:VAL:HG12	1:A:2:GLY:H	1.65	0.60
1:C:130:ALA:HB1	1:C:134:LYS:O	2.01	0.60
1:B:54:ASP:OD1	1:B:118:ARG:NH1	2.34	0.60
1:A:272:ARG:HG2	1:A:272:ARG:O	2.00	0.60
1:A:50:ILE:HD12	1:A:117:GLU:HB3	1.83	0.60
1:D:50:ILE:HG22	1:D:118:ARG:HG2	1.83	0.59
1:B:47:ASN:ND2	1:B:49:ILE:H	2.00	0.59
1:B:198:ASP:O	1:B:202:GLN:HG2	2.02	0.59
1:B:127:THR:HG22	1:B:129:ALA:H	1.66	0.59
1:D:241:GLU:O	1:D:245:GLU:HG3	2.02	0.59
1:B:134:LYS:HB2	1:B:134:LYS:NZ	2.17	0.59
1:C:240:LYS:CD	1:C:240:LYS:H	2.15	0.59
1:A:138:ARG:HA	1:A:180:GLY:O	2.02	0.59
1:D:60:LYS:HD2	1:D:73:LEU:HD22	1.85	0.59
1:D:17:PHE:HB2	3:D:604:FAD:C5B	2.31	0.59
1:A:41:LEU:HD23	1:A:44:MET:CE	2.33	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:57:GLY:HA3	1:C:79:HIS:ND1	2.18	0.58
1:B:201:ILE:O	1:B:205:GLU:HG2	2.03	0.58
1:D:29:LEU:HD11	1:D:211:LEU:HD22	1.85	0.58
1:B:81:SER:O	1:B:85:VAL:HG23	2.04	0.58
1:B:50:ILE:HD11	1:B:117:GLU:O	2.03	0.58
1:C:243:GLN:O	1:C:247:LYS:HG3	2.04	0.58
1:D:21:MET:CE	1:D:204:LEU:HD23	2.34	0.58
1:A:4:ARG:HG2	1:A:35:GLU:CD	2.24	0.58
1:D:248:ASN:HB3	4:D:731:HOH:O	2.03	0.58
1:B:147:THR:HA	1:B:189:THR:OG1	2.04	0.58
1:C:84:ILE:O	1:C:88:GLN:HG3	2.04	0.57
1:D:21:MET:HE3	1:D:204:LEU:HA	1.85	0.57
1:C:255:VAL:HG23	1:C:267:ASN:HD22	1.68	0.57
1:A:160:ILE:HG13	1:C:236:PHE:HB3	1.85	0.57
1:D:127:THR:HG23	1:D:130:ALA:HB3	1.87	0.57
1:A:204:LEU:O	1:A:208:LYS:HG3	2.04	0.57
1:D:6:LEU:HD12	1:D:37:VAL:O	2.03	0.57
1:A:7:ILE:HG21	1:A:22:LYS:HG2	1.85	0.57
1:A:200:ARG:NH1	3:A:601:FAD:H1B	2.20	0.57
1:A:238:MET:CE	1:A:243:GLN:HG2	2.34	0.57
1:D:143:VAL:CG1	1:D:184:LEU:HB2	2.26	0.56
1:C:17:PHE:HB2	3:C:603:FAD:H52A	1.87	0.56
1:B:236:PHE:CD2	1:D:160:ILE:HD12	2.39	0.56
1:B:50:ILE:HG22	1:B:50:ILE:O	2.03	0.56
1:B:158:GLN:HB3	1:D:238:MET:HE2	1.87	0.56
1:B:134:LYS:HA	1:B:138:ARG:HD3	1.86	0.56
1:B:148:THR:HG23	3:B:602:FAD:O2	2.06	0.56
1:B:147:THR:HA	1:B:189:THR:HG1	1.70	0.56
1:B:239:LYS:HB2	1:B:242:VAL:HG23	1.86	0.56
1:A:84:ILE:O	1:A:88:GLN:HG3	2.06	0.56
1:B:132:TYR:O	1:B:180:GLY:HA2	2.06	0.56
1:D:21:MET:CE	1:D:204:LEU:HA	2.36	0.56
1:A:197:ALA:O	1:A:201:ILE:HG12	2.06	0.56
1:D:72:VAL:O	1:D:76:LYS:HG3	2.06	0.56
1:C:176:LEU:O	1:C:181:PHE:HB2	2.06	0.56
1:D:4:ARG:HG3	1:D:35:GLU:HB2	1.88	0.56
1:A:238:MET:HE3	1:A:243:GLN:HA	1.88	0.55
1:C:24:ALA:O	1:C:208:LYS:HE3	2.06	0.55
1:D:240:LYS:CD	1:D:240:LYS:H	2.20	0.55
1:C:32:LYS:HE3	1:C:212:GLU:HB3	1.89	0.55
1:B:75:TYR:HB2	1:B:80:LEU:HD11	1.88	0.55
1:C:250:LYS:HE3	1:C:251:PHE:CZ	2.42	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:11:HIS:CE1	1:D:16:SER:HB3	2.42	0.55
1:C:146:ILE:HG22	1:C:147:THR:N	2.22	0.55
1:B:54:ASP:HA	1:B:81:SER:HB2	1.88	0.54
1:C:198:ASP:OD1	1:C:199:ALA:N	2.40	0.54
1:A:47:ASN:HB3	1:A:118:ARG:NH2	2.22	0.54
1:B:230:LEU:HD23	1:D:160:ILE:CD1	2.38	0.54
1:B:154:MET:CE	1:B:160:ILE:HD11	2.37	0.54
1:D:240:LYS:HD2	1:D:240:LYS:H	1.71	0.54
1:C:209:LYS:HD3	1:C:210:ARG:H	1.72	0.54
1:A:50:ILE:HG13	1:A:118:ARG:HG2	1.89	0.54
1:B:104:GLN:HA	3:B:602:FAD:C5X	2.38	0.54
1:C:169:TRP:CZ2	1:C:256:GLY:HA3	2.43	0.54
1:A:108:VAL:CG1	1:A:112:LEU:HB3	2.37	0.54
1:C:14:ARG:CB	1:C:14:ARG:HH11	2.21	0.54
1:C:151:SER:N	1:C:154:MET:HE3	2.18	0.54
1:A:160:ILE:CG1	1:C:236:PHE:HB3	2.37	0.54
1:C:14:ARG:HG2	1:C:19:TYR:CZ	2.43	0.54
1:A:91:LEU:HD11	1:A:120:PHE:HE1	1.73	0.53
1:D:250:LYS:HD3	1:D:251:PHE:CE2	2.43	0.53
1:A:202:GLN:CA	1:A:202:GLN:HE21	2.04	0.53
1:D:255:VAL:HG23	1:D:267:ASN:HD22	1.72	0.53
1:A:1:VAL:CG1	1:A:3:ARG:HH21	2.22	0.53
1:B:238:MET:HE2	1:B:243:GLN:HG2	1.89	0.53
1:A:231:ASN:HD21	1:A:233:GLN:HG2	1.74	0.53
1:A:14:ARG:NE	1:A:14:ARG:N	2.39	0.53
1:D:239:LYS:HB2	1:D:242:VAL:HG23	1.92	0.52
1:A:1:VAL:HG12	1:A:2:GLY:N	2.23	0.52
1:A:1:VAL:HG13	1:A:215:TRP:CD1	2.44	0.52
1:C:134:LYS:HB3	4:C:728:HOH:O	2.10	0.52
1:C:255:VAL:H	1:C:267:ASN:ND2	2.07	0.52
1:D:158:GLN:HE21	1:D:158:GLN:N	2.08	0.52
1:B:169:TRP:CZ2	1:B:256:GLY:HA3	2.44	0.52
1:D:227:LEU:HB3	1:D:242:VAL:HG11	1.92	0.52
1:B:144:LEU:HD12	1:B:172:GLN:HE21	1.74	0.52
1:C:89:LYS:HD2	4:C:731:HOH:O	2.10	0.52
1:B:132:TYR:HA	1:B:177:HIS:O	2.09	0.52
1:D:130:ALA:HB1	1:D:134:LYS:O	2.09	0.52
1:A:75:TYR:CZ	1:A:124:PHE:HB2	2.45	0.52
1:A:113:LYS:O	1:A:117:GLU:HG3	2.10	0.52
1:C:47:ASN:ND2	1:C:49:ILE:H	2.08	0.52
1:B:130:ALA:O	1:B:135:GLY:HA2	2.10	0.51
1:B:56:THR:HB	1:B:79:HIS:O	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:116:PHE:O	1:B:120:PHE:HB2	2.11	0.51
1:C:28:ALA:HA	1:C:31:LYS:HE2	1.92	0.51
1:D:21:MET:HE2	1:D:204:LEU:HD23	1.91	0.51
1:B:67:TYR:HB3	1:B:68:PRO:HD3	1.93	0.51
1:B:18:ASN:OD1	1:B:100:GLN:NE2	2.40	0.51
1:A:50:ILE:HD11	1:A:117:GLU:O	2.10	0.51
1:A:135:GLY:O	1:A:138:ARG:NH1	2.37	0.51
1:B:197:ALA:O	1:B:201:ILE:HG12	2.11	0.51
1:B:108:VAL:HG13	1:B:112:LEU:HD13	1.92	0.51
1:A:2:GLY:O	1:A:3:ARG:CZ	2.59	0.50
1:B:134:LYS:HB2	1:B:134:LYS:HZ3	1.75	0.50
1:A:17:PHE:HB2	3:A:601:FAD:C5B	2.36	0.50
1:B:271:ALA:O	1:B:272:ARG:HB2	2.10	0.50
1:D:122:GLY:C	1:D:124:PHE:H	2.14	0.50
1:C:68:PRO:O	1:C:72:VAL:HG23	2.12	0.50
1:B:50:ILE:HG13	1:B:118:ARG:HG2	1.92	0.50
1:D:172:GLN:HB2	1:D:268:GLN:HE22	1.76	0.50
1:C:150:GLY:HA2	1:C:154:MET:HE1	1.93	0.50
1:A:80:LEU:O	1:A:81:SER:C	2.50	0.50
1:A:50:ILE:CG1	1:A:118:ARG:HG2	2.42	0.50
1:C:207:TRP:O	1:C:211:LEU:HG	2.12	0.50
1:B:127:THR:HG22	1:B:129:ALA:N	2.27	0.50
1:D:104:GLN:HA	3:D:604:FAD:N5	2.27	0.50
1:B:230:LEU:CD2	1:D:160:ILE:HD13	2.42	0.50
1:B:236:PHE:HB3	1:D:160:ILE:HG13	1.94	0.50
1:B:108:VAL:HG13	1:B:112:LEU:HB3	1.92	0.50
1:C:273:LYS:HD2	1:C:273:LYS:H	1.77	0.50
1:A:238:MET:HE3	1:A:243:GLN:HG2	1.93	0.50
1:D:141:LYS:HA	1:D:182:GLN:O	2.12	0.50
1:B:57:GLY:H	1:B:79:HIS:CD2	2.30	0.49
1:A:52:ARG:HG2	4:A:704:HOH:O	2.11	0.49
1:A:13:GLU:OE1	1:A:14:ARG:NH2	2.45	0.49
1:D:64:ASN:HD21	1:D:66:GLN:NE2	2.08	0.49
1:A:202:GLN:CA	1:A:202:GLN:NE2	2.67	0.49
1:B:112:LEU:O	1:B:115:TRP:HB3	2.12	0.49
1:A:132:TYR:O	1:A:180:GLY:HA2	2.12	0.49
1:A:244:ASP:HA	1:A:247:LYS:HE3	1.95	0.49
1:C:104:GLN:HA	3:C:603:FAD:C5X	2.42	0.49
1:A:14:ARG:HA	1:A:19:TYR:CG	2.47	0.49
1:D:169:TRP:CZ2	1:D:256:GLY:HA3	2.47	0.49
1:B:238:MET:CE	1:D:158:GLN:HG3	2.42	0.49
1:B:155:TYR:HB3	1:B:164:MET:HB2	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:241:GLU:O	1:B:245:GLU:HG3	2.12	0.49
1:B:134:LYS:C	1:B:138:ARG:HD3	2.33	0.49
1:C:241:GLU:O	1:C:245:GLU:HB2	2.13	0.49
1:B:148:THR:HB	1:B:190:TYR:HA	1.94	0.49
1:B:195:THR:HG22	1:B:199:ALA:HB3	1.95	0.49
1:B:239:LYS:HB2	1:B:242:VAL:CG2	2.43	0.49
1:D:54:ASP:OD1	1:D:118:ARG:NH1	2.46	0.48
1:B:169:TRP:HA	1:B:268:GLN:HE21	1.77	0.48
1:B:236:PHE:O	1:D:160:ILE:HG13	2.13	0.48
1:C:65:PHE:CE1	1:C:70:GLU:HG3	2.48	0.48
1:B:238:MET:HE2	1:D:158:GLN:HG3	1.95	0.48
1:D:104:GLN:HA	3:D:604:FAD:C5X	2.44	0.48
1:B:29:LEU:CD1	1:B:211:LEU:HB3	2.43	0.48
1:B:158:GLN:HB3	1:D:238:MET:CE	2.43	0.48
1:B:257:HIS:HA	4:D:729:HOH:O	2.13	0.48
1:C:238:MET:HE2	1:C:259:LEU:HD21	1.95	0.47
1:D:264:PRO:HB2	1:D:273:LYS:HG2	1.96	0.47
1:B:91:LEU:O	1:B:140:LYS:HE3	2.14	0.47
1:C:271:ALA:O	1:C:272:ARG:CB	2.61	0.47
1:A:122:GLY:O	1:A:123:GLU:HB3	2.14	0.47
1:B:32:LYS:HE3	4:B:731:HOH:O	2.14	0.47
1:D:65:PHE:CD1	1:D:70:GLU:HG3	2.50	0.47
1:B:148:THR:CG2	1:B:149:GLY:N	2.78	0.47
1:B:106:PHE:N	1:B:106:PHE:CD1	2.83	0.47
1:A:50:ILE:HG23	1:A:67:TYR:CD1	2.49	0.47
1:C:57:GLY:HA3	1:C:79:HIS:CG	2.50	0.47
1:D:198:ASP:HA	1:D:201:ILE:HD12	1.97	0.47
1:D:59:LEU:HB2	1:D:62:PRO:HG3	1.97	0.47
1:C:172:GLN:HB2	1:C:268:GLN:NE2	2.30	0.47
1:A:45:ASN:HD22	1:A:45:ASN:HA	1.47	0.47
1:A:75:TYR:CE1	1:A:124:PHE:HB2	2.50	0.47
1:D:12:SER:HB3	1:D:42:TYR:CD1	2.50	0.47
1:A:243:GLN:O	1:A:247:LYS:HG3	2.15	0.47
1:D:42:TYR:HD2	4:D:703:HOH:O	1.97	0.47
1:B:240:LYS:HB3	1:B:240:LYS:HZ2	1.73	0.47
1:C:76:LYS:CE	1:C:123:GLU:HG3	2.44	0.47
1:D:189:THR:O	1:D:189:THR:OG1	2.33	0.47
1:D:60:LYS:HD2	1:D:73:LEU:CD2	2.45	0.46
1:B:27:ALA:O	1:B:31:LYS:HG3	2.15	0.46
1:D:30:LYS:C	1:D:32:LYS:H	2.18	0.46
1:C:59:LEU:HB2	1:C:62:PRO:HG3	1.98	0.46
1:D:83:ASP:OD2	1:D:118:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:55:ILE:HG23	1:B:74:ALA:HB2	1.97	0.46
1:B:236:PHE:HB3	1:D:160:ILE:CD1	2.44	0.46
1:D:239:LYS:HB2	1:D:242:VAL:CG2	2.46	0.46
1:C:113:LYS:O	1:C:117:GLU:HG3	2.15	0.46
1:C:207:TRP:CH2	1:C:211:LEU:HD21	2.50	0.46
1:C:72:VAL:HG13	1:C:123:GLU:HG2	1.96	0.46
1:C:17:PHE:HB2	3:C:603:FAD:C5B	2.46	0.46
1:A:271:ALA:C	1:A:272:ARG:HD3	2.36	0.46
1:C:205:GLU:HA	1:C:205:GLU:OE1	2.15	0.46
1:A:67:TYR:HB3	1:A:68:PRO:HD3	1.96	0.46
1:C:195:THR:CG2	1:C:200:ARG:HG3	2.46	0.46
1:D:176:LEU:O	1:D:181:PHE:HB2	2.15	0.46
1:C:4:ARG:HG2	1:C:35:GLU:HB3	1.97	0.46
1:C:52:ARG:C	1:C:54:ASP:H	2.19	0.46
1:C:40:ASP:HB3	1:C:43:ALA:HB3	1.96	0.46
1:A:127:THR:HG22	1:A:129:ALA:N	2.21	0.46
1:B:214:ILE:CG2	1:B:215:TRP:N	2.79	0.46
1:C:127:THR:OG1	1:C:130:ALA:N	2.49	0.46
1:D:185:GLU:HB3	1:D:269:ILE:O	2.16	0.46
1:A:116:PHE:O	1:A:120:PHE:HB2	2.15	0.46
1:B:4:ARG:HH21	1:B:93:ALA:HB1	1.81	0.46
1:D:271:ALA:O	1:D:272:ARG:HB2	2.17	0.45
1:D:78:GLY:HA2	4:D:723:HOH:O	2.16	0.45
1:C:209:LYS:HA	1:C:212:GLU:OE2	2.15	0.45
1:A:238:MET:HE2	1:A:243:GLN:HG2	1.97	0.45
1:A:91:LEU:HD11	1:A:120:PHE:CE1	2.52	0.45
1:D:229:ASP:OD1	1:D:239:LYS:HG2	2.15	0.45
1:C:14:ARG:HG2	1:C:19:TYR:CE1	2.51	0.45
1:C:9:LEU:CD2	1:C:22:LYS:HD3	2.46	0.45
1:A:66:GLN:HE21	1:A:66:GLN:CA	2.12	0.45
1:C:214:ILE:O	1:C:217:GLU:HB2	2.17	0.45
1:A:207:TRP:HA	1:A:207:TRP:CE3	2.52	0.45
1:C:31:LYS:C	1:C:33:GLY:H	2.20	0.45
1:D:172:GLN:HB2	1:D:268:GLN:NE2	2.31	0.45
1:A:94:ALA:O	1:A:140:LYS:NZ	2.38	0.45
1:A:11:HIS:NE2	3:A:601:FAD:O2P	2.48	0.45
1:C:99:PHE:HB2	1:C:144:LEU:HD23	1.98	0.45
1:B:271:ALA:O	1:B:272:ARG:CB	2.65	0.45
1:C:165:ASN:ND2	1:C:266:ASP:HA	2.32	0.45
1:B:122:GLY:O	1:B:123:GLU:CB	2.64	0.45
1:C:207:TRP:HZ3	1:C:210:ARG:HD3	1.82	0.45
1:A:132:TYR:HA	1:A:177:HIS:O	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:21:MET:HE3	1:D:204:LEU:HD23	1.98	0.45
1:C:36:VAL:HG12	1:C:37:VAL:N	2.31	0.45
1:D:19:TYR:O	1:D:22:LYS:HB3	2.16	0.45
1:B:221:TYR:HB2	1:B:273:LYS:HA	1.97	0.45
1:D:68:PRO:HG2	2:D:702:340:H453	1.98	0.45
1:C:145:SER:HA	1:C:187:GLN:HB3	1.97	0.45
1:C:1:VAL:CG1	1:C:2:GLY:H	2.25	0.44
1:D:97:VAL:HG21	1:D:181:PHE:HZ	1.82	0.44
1:C:246:GLU:HG3	4:C:716:HOH:O	2.17	0.44
1:B:61:ASP:OD1	1:B:64:ASN:HB2	2.18	0.44
1:C:125:ALA:O	1:C:136:PRO:HD2	2.16	0.44
1:A:117:GLU:OE2	1:C:109:PRO:HA	2.17	0.44
1:D:231:ASN:HD21	1:D:234:ALA:HB2	1.82	0.44
1:B:134:LYS:CA	1:B:138:ARG:HD3	2.47	0.44
1:A:237:LEU:HD22	1:C:158:GLN:HE21	1.82	0.44
1:B:4:ARG:NH2	1:B:93:ALA:HB1	2.33	0.44
1:A:207:TRP:HE3	1:A:207:TRP:HA	1.82	0.44
1:A:165:ASN:OD1	1:A:268:GLN:HB2	2.17	0.44
1:A:148:THR:HG22	1:A:150:GLY:N	2.32	0.44
1:D:258:HIS:HB3	1:D:263:ILE:HG12	1.99	0.44
1:C:224:PRO:HD2	1:C:227:LEU:HD11	2.00	0.44
1:D:21:MET:HA	1:D:21:MET:HE2	1.99	0.44
1:C:229:ASP:O	1:C:236:PHE:HA	2.17	0.44
1:B:134:LYS:HE3	1:B:225:SER:OG	2.18	0.44
1:B:202:GLN:NE2	1:B:202:GLN:HA	2.33	0.44
1:B:230:LEU:HD23	1:D:160:ILE:HD11	2.00	0.43
1:B:122:GLY:O	1:B:123:GLU:HB2	2.17	0.43
1:A:12:SER:HB3	1:A:42:TYR:CE1	2.52	0.43
1:B:104:GLN:HE21	1:D:117:GLU:CD	2.21	0.43
1:B:64:ASN:ND2	4:B:716:HOH:O	2.50	0.43
1:D:196:PRO:O	1:D:200:ARG:HG3	2.18	0.43
1:C:25:ALA:HA	1:C:211:LEU:CD1	2.48	0.43
1:C:211:LEU:HA	1:C:214:ILE:HB	2.00	0.43
1:D:1:VAL:CG2	1:D:2:GLY:H	2.26	0.43
1:D:127:THR:HG23	1:D:130:ALA:N	2.33	0.43
1:B:50:ILE:CD1	1:B:117:GLU:HB3	2.46	0.43
1:B:74:ALA:HA	1:B:79:HIS:NE2	2.33	0.43
1:B:191:SER:HB2	1:B:194:HIS:HB2	2.01	0.43
1:B:25:ALA:O	1:B:29:LEU:HB2	2.19	0.43
1:C:143:VAL:HG12	1:C:144:LEU:N	2.33	0.43
1:B:141:LYS:HG2	1:B:182:GLN:HB2	2.01	0.43
1:B:169:TRP:CB	1:B:170:PRO:HD3	2.44	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:146:ILE:HG22	1:C:147:THR:H	1.83	0.43
1:C:169:TRP:CB	1:C:170:PRO:HD3	2.45	0.43
1:A:81:SER:O	1:A:85:VAL:HG23	2.19	0.43
1:D:56:THR:HG21	1:D:82:PRO:HD3	1.99	0.43
1:B:236:PHE:HD2	1:D:160:ILE:CD1	2.29	0.43
1:A:148:THR:HG22	1:A:149:GLY:N	2.33	0.43
1:B:238:MET:CE	1:B:243:GLN:HG2	2.49	0.43
1:C:6:LEU:O	1:C:97:VAL:HA	2.18	0.43
1:A:54:ASP:OD1	1:A:118:ARG:NH1	2.52	0.42
1:D:64:ASN:ND2	1:D:66:GLN:HE21	2.13	0.42
1:D:48:PRO:O	1:D:114:GLY:HA3	2.19	0.42
1:C:272:ARG:HA	4:C:702:HOH:O	2.19	0.42
1:C:238:MET:HE3	1:C:238:MET:HB2	1.82	0.42
1:D:68:PRO:O	1:D:72:VAL:HG23	2.19	0.42
1:A:229:ASP:O	1:A:231:ASN:N	2.52	0.42
1:B:128:TYR:O	1:B:131:MET:HG3	2.20	0.42
1:C:150:GLY:HA2	1:C:154:MET:CE	2.49	0.42
1:B:154:MET:O	1:B:161:HIS:HB2	2.18	0.42
1:A:42:TYR:HB2	4:A:706:HOH:O	2.19	0.42
1:B:105:TRP:CZ2	1:D:120:PHE:HB3	2.54	0.42
1:B:46:PHE:O	1:B:48:PRO:HD3	2.19	0.42
1:A:4:ARG:CG	1:A:35:GLU:OE2	2.67	0.42
1:D:48:PRO:HB2	1:D:114:GLY:HA3	2.00	0.42
1:B:148:THR:CG2	1:B:150:GLY:O	2.68	0.42
1:C:132:TYR:O	1:C:180:GLY:HA2	2.18	0.42
1:B:54:ASP:O	1:B:81:SER:N	2.49	0.42
1:B:138:ARG:HH11	1:B:138:ARG:HG3	1.83	0.42
1:A:67:TYR:N	1:A:68:PRO:CD	2.83	0.42
1:C:130:ALA:O	1:C:135:GLY:HA2	2.20	0.42
1:B:47:ASN:ND2	1:B:47:ASN:C	2.71	0.42
1:A:148:THR:CG2	1:A:149:GLY:N	2.82	0.42
1:C:67:TYR:HB3	1:C:68:PRO:HD3	2.02	0.42
1:C:239:LYS:HB3	1:C:241:GLU:OE2	2.20	0.42
1:D:12:SER:HB3	1:D:42:TYR:CE1	2.55	0.42
1:C:197:ALA:HA	1:C:200:ARG:CZ	2.49	0.41
1:C:122:GLY:HA2	1:C:126:TYR:CE1	2.55	0.41
1:B:211:LEU:HA	1:B:214:ILE:HB	2.02	0.41
1:B:204:LEU:O	1:B:208:LYS:HG3	2.19	0.41
1:B:104:GLN:HA	3:B:602:FAD:N5	2.34	0.41
1:A:254:SER:HB2	1:A:267:ASN:HD21	1.85	0.41
1:A:232:PHE:CD1	1:A:232:PHE:N	2.88	0.41
1:C:242:VAL:O	1:C:246:GLU:HB2	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:11:HIS:CE1	1:B:16:SER:HB3	2.55	0.41
1:C:257:HIS:HA	4:C:709:HOH:O	2.20	0.41
1:A:235:GLY:O	1:A:236:PHE:HB2	2.20	0.41
1:B:50:ILE:HD11	1:B:117:GLU:C	2.40	0.41
1:B:158:GLN:HB3	1:B:158:GLN:HE21	1.68	0.41
1:A:166:VAL:HG13	1:C:166:VAL:HG13	2.03	0.41
1:A:47:ASN:ND2	4:A:738:HOH:O	2.54	0.41
1:A:4:ARG:HD3	1:A:93:ALA:O	2.20	0.41
1:B:31:LYS:NZ	1:B:208:LYS:NZ	2.69	0.41
1:C:195:THR:HG22	1:C:200:ARG:HG3	2.01	0.41
1:C:254:SER:HB2	1:C:267:ASN:ND2	2.36	0.41
1:B:77:GLU:HB2	1:B:79:HIS:CE1	2.56	0.41
1:C:155:TYR:HB3	1:C:164:MET:HB2	2.03	0.41
1:C:273:LYS:N	1:C:273:LYS:NZ	2.68	0.41
1:D:187:GLN:HG2	1:D:207:TRP:CE3	2.56	0.41
1:C:238:MET:HE3	1:C:243:GLN:HG2	2.02	0.41
1:C:224:PRO:O	1:C:227:LEU:HG	2.21	0.41
1:A:57:GLY:H	1:A:79:HIS:CD2	2.39	0.41
1:A:214:ILE:HG23	1:A:215:TRP:N	2.36	0.41
1:C:192:ILE:CG2	3:C:603:FAD:H5'1	2.51	0.41
1:C:89:LYS:HG3	4:C:730:HOH:O	2.21	0.41
1:B:195:THR:HA	1:B:196:PRO:HD3	1.85	0.41
1:B:132:TYR:O	1:B:134:LYS:N	2.53	0.41
1:D:215:TRP:CD1	1:D:215:TRP:O	2.74	0.41
1:D:195:THR:HG21	1:D:203:ILE:HD11	2.02	0.41
1:A:3:ARG:HA	1:A:3:ARG:NH1	2.35	0.41
1:B:14:ARG:HE	1:B:14:ARG:HA	1.85	0.41
1:D:240:LYS:HD2	1:D:240:LYS:N	2.36	0.40
1:A:58:LYS:CD	1:A:58:LYS:N	2.83	0.40
1:B:227:LEU:HB3	1:B:242:VAL:HG11	2.03	0.40
1:A:13:GLU:HA	1:A:14:ARG:HH21	1.85	0.40
1:B:50:ILE:O	1:B:50:ILE:CG2	2.69	0.40
1:C:272:ARG:O	1:C:273:LYS:O	2.39	0.40
1:B:59:LEU:HB3	1:B:70:GLU:OE2	2.22	0.40
1:B:17:PHE:HB2	3:B:602:FAD:C5B	2.43	0.40
1:B:117:GLU:HG2	1:D:105:TRP:HD1	1.86	0.40
1:B:147:THR:HG22	1:B:189:THR:OG1	2.21	0.40
1:A:244:ASP:HA	1:A:247:LYS:CE	2.52	0.40
1:C:17:PHE:O	1:C:21:MET:HG2	2.22	0.40
1:C:31:LYS:HB2	1:C:31:LYS:HE2	1.87	0.40
1:A:74:ALA:HB1	1:A:79:HIS:O	2.21	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	271/273 (99%)	244 (90%)	23 (8%)	4 (2%)	15	13
1	B	271/273 (99%)	248 (92%)	19 (7%)	4 (2%)	15	13
1	C	271/273 (99%)	247 (91%)	19 (7%)	5 (2%)	13	10
1	D	271/273 (99%)	247 (91%)	18 (7%)	6 (2%)	10	7
All	All	1084/1092 (99%)	986 (91%)	79 (7%)	19 (2%)	13	10

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	272	ARG
1	C	272	ARG
1	B	123	GLU
1	A	245	GLU
1	B	272	ARG
1	D	41	LEU
1	D	191	SER
1	D	230	LEU
1	B	133	ASP
1	B	191	SER
1	C	132	TYR
1	A	230	LEU
1	C	32	LYS
1	D	31	LYS
1	C	57	GLY
1	C	129	ALA
1	D	132	TYR
1	D	272	ARG
1	A	57	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of

similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	227/227 (100%)	210 (92%)	17 (8%)	19	23
1	B	227/227 (100%)	219 (96%)	8 (4%)	48	63
1	C	227/227 (100%)	213 (94%)	14 (6%)	26	33
1	D	227/227 (100%)	216 (95%)	11 (5%)	35	46
All	All	908/908 (100%)	858 (94%)	50 (6%)	30	39

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	14	ARG
1	A	29	LEU
1	A	45	ASN
1	A	60	LYS
1	A	66	GLN
1	A	112	LEU
1	A	121	ILE
1	A	158	GLN
1	A	160	ILE
1	A	182	GLN
1	A	202	GLN
1	A	207	TRP
1	A	231	ASN
1	A	248	ASN
1	A	261	LYS
1	A	272	ARG
1	B	14	ARG
1	B	47	ASN
1	B	50	ILE
1	B	112	LEU
1	B	158	GLN
1	B	218	THR
1	B	240	LYS
1	B	248	ASN
1	C	29	LEU
1	C	38	GLU
1	C	60	LYS
1	C	66	GLN
1	C	81	SER

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Mol	Chain	Res	Type
1	C	133	ASP
1	C	158	GLN
1	C	209	LYS
1	C	233	GLN
1	C	240	LYS
1	C	241	GLU
1	C	245	GLU
1	C	265	THR
1	C	273	LYS
1	D	14	ARG
1	D	23	GLU
1	D	48	PRO
1	D	52	ARG
1	D	60	LYS
1	D	82	PRO
1	D	143	VAL
1	D	158	GLN
1	D	189	THR
1	D	240	LYS
1	D	241	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	47	ASN
1	A	66	GLN
1	A	79	HIS
1	A	202	GLN
1	A	267	ASN
1	A	268	GLN
1	B	47	ASN
1	B	66	GLN
1	B	79	HIS
1	B	104	GLN
1	B	158	GLN
1	B	172	GLN
1	B	202	GLN
1	B	231	ASN
1	B	267	ASN
1	B	268	GLN
1	C	47	ASN

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Mol	Chain	Res	Type
1	C	158	GLN
1	C	172	GLN
1	C	233	GLN
1	C	267	ASN
1	C	268	GLN
1	D	45	ASN
1	D	47	ASN
1	D	66	GLN
1	D	158	GLN
1	D	172	GLN
1	D	243	GLN
1	D	267	ASN
1	D	268	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

8 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	$\# Z > 2$
3	FAD	A	601	-	58,58,58	2.37	18 (31%)	85,89,89	1.59	16 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	340	A	703	-	25,25,25	3.16	15 (60%)	34,36,36	3.85	16 (47%)
3	FAD	B	602	-	58,58,58	2.40	19 (32%)	85,89,89	1.45	13 (15%)
2	340	B	704	-	25,25,25	2.99	16 (64%)	34,36,36	3.46	15 (44%)
3	FAD	C	603	-	58,58,58	2.49	21 (36%)	85,89,89	1.50	13 (15%)
2	340	C	701	-	25,25,25	3.20	13 (52%)	34,36,36	4.25	12 (35%)
3	FAD	D	604	-	58,58,58	2.39	14 (24%)	85,89,89	1.56	13 (15%)
2	340	D	702	-	25,25,25	3.15	14 (56%)	34,36,36	3.25	14 (41%)

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
3	FAD	A	601	-	-	0/34/50/50	0/1/6/6
2	340	A	703	-	-	0/5/23/23	0/1/3/3
3	FAD	B	602	-	-	0/34/50/50	0/1/6/6
2	340	B	704	-	-	0/5/23/23	0/1/3/3
3	FAD	C	603	-	-	0/34/50/50	0/1/6/6
2	340	C	701	-	-	0/5/23/23	0/1/3/3
3	FAD	D	604	-	-	0/34/50/50	0/1/6/6
2	340	D	702	-	-	0/5/23/23	0/1/3/3

All (130) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	701	340	C3-C2	-12.59	1.38	1.50
2	D	702	340	C3-C2	-12.00	1.39	1.50
2	A	703	340	C3-C2	-11.20	1.39	1.50
2	B	704	340	C3-C2	-10.29	1.40	1.50
3	C	603	FAD	P-O3P	-7.91	1.45	1.59
3	B	602	FAD	P-O3P	-7.52	1.46	1.59
3	D	604	FAD	P-O3P	-7.32	1.46	1.59
3	A	601	FAD	C9A-N10	7.28	1.49	1.38
3	A	601	FAD	P-O3P	-7.04	1.47	1.59
3	B	602	FAD	C9A-N10	6.66	1.48	1.38
3	D	604	FAD	C1'-C2'	6.58	1.57	1.51
3	C	603	FAD	C9A-N10	6.53	1.48	1.38
3	D	604	FAD	C9A-N10	6.29	1.48	1.38
3	B	602	FAD	C1'-C2'	5.71	1.57	1.51
3	C	603	FAD	C1'-C2'	5.34	1.56	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	FAD	O4B-C1B	5.18	1.49	1.41
3	C	603	FAD	C4X-C10	5.18	1.49	1.40
3	A	601	FAD	C4X-C10	5.16	1.49	1.40
3	D	604	FAD	O4B-C1B	4.90	1.48	1.41
3	D	604	FAD	C4X-C10	4.76	1.49	1.40
3	B	602	FAD	C4X-C10	4.62	1.48	1.40
3	C	603	FAD	C4-C4X	4.53	1.48	1.41
3	A	601	FAD	C1'-C2'	4.40	1.55	1.51
3	C	603	FAD	PA-O2A	-4.39	1.35	1.55
3	B	602	FAD	PA-O2A	-4.29	1.35	1.55
3	C	603	FAD	O4B-C1B	4.27	1.47	1.41
3	B	602	FAD	O4B-C1B	4.11	1.47	1.41
3	A	601	FAD	PA-O2A	-4.04	1.37	1.55
3	D	604	FAD	PA-O2A	-4.01	1.37	1.55
3	B	602	FAD	P-O2P	-3.99	1.37	1.55
2	B	704	340	C25-C24	3.90	1.46	1.38
3	A	601	FAD	P-O2P	-3.88	1.37	1.55
2	D	702	340	C8-C9	-3.79	1.32	1.39
2	A	703	340	C29-C24	3.73	1.46	1.38
2	A	703	340	C25-C24	3.73	1.46	1.38
2	C	701	340	C8-C9	-3.66	1.32	1.39
3	D	604	FAD	P-O2P	-3.61	1.38	1.55
3	C	603	FAD	P-O2P	-3.57	1.39	1.55
2	B	704	340	C8-C9	-3.52	1.32	1.39
3	A	601	FAD	PA-O3P	3.50	1.66	1.59
3	B	602	FAD	C2-N3	3.49	1.44	1.37
2	A	703	340	O44-C6	3.49	1.42	1.36
3	D	604	FAD	C2-N3	3.46	1.44	1.37
2	D	702	340	C25-C24	3.42	1.45	1.38
2	A	703	340	O20-C24	3.40	1.45	1.37
3	B	602	FAD	O5'-C5'	3.40	1.58	1.44
3	D	604	FAD	O5'-C5'	3.37	1.58	1.44
3	C	603	FAD	C2-N3	3.37	1.43	1.37
2	D	702	340	C29-C24	3.27	1.45	1.38
3	C	603	FAD	O5'-C5'	3.26	1.58	1.44
3	D	604	FAD	C4-C4X	3.25	1.46	1.41
3	B	602	FAD	PA-O3P	3.13	1.65	1.59
2	C	701	340	C25-C24	3.12	1.45	1.38
3	A	601	FAD	C2-N3	3.03	1.43	1.37
2	C	701	340	C1-C2	2.97	1.52	1.44
3	A	601	FAD	O5'-C5'	2.96	1.57	1.44
2	C	701	340	C29-C24	2.95	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	703	340	C8-C9	-2.93	1.33	1.39
2	B	704	340	C1-C2	2.92	1.51	1.44
3	A	601	FAD	C4-C4X	2.91	1.46	1.41
2	B	704	340	C29-C24	2.91	1.44	1.38
3	C	603	FAD	C5X-N5	2.91	1.39	1.35
2	C	701	340	O44-C6	2.84	1.41	1.36
3	B	602	FAD	C8-C7	2.83	1.49	1.40
2	B	704	340	O20-C24	2.78	1.44	1.37
2	A	703	340	C1-C2	2.78	1.51	1.44
2	A	703	340	C4-C3	2.76	1.45	1.40
3	C	603	FAD	C4A-N3A	2.76	1.39	1.35
3	D	604	FAD	C8-C7	2.72	1.48	1.40
3	D	604	FAD	C4A-N3A	2.71	1.39	1.35
2	B	704	340	C4-C3	2.70	1.44	1.40
3	C	603	FAD	C8-C7	2.68	1.48	1.40
2	D	702	340	C27-C26	2.68	1.45	1.37
2	B	704	340	O44-C6	2.65	1.41	1.36
2	A	703	340	C6-C5	2.65	1.54	1.49
2	C	701	340	C4-C3	2.63	1.44	1.40
2	B	704	340	C28-C27	2.62	1.45	1.37
2	D	702	340	O44-C6	2.61	1.41	1.36
2	A	703	340	C27-C26	2.60	1.45	1.37
3	B	602	FAD	C6-C5X	2.59	1.44	1.41
3	B	602	FAD	C2A-N1A	2.58	1.39	1.33
2	A	703	340	C26-C25	2.54	1.44	1.39
2	D	702	340	C1-C2	2.52	1.50	1.44
2	B	704	340	C8-N7	2.51	1.42	1.39
3	C	603	FAD	C2B-C1B	-2.50	1.49	1.53
2	C	701	340	C6-C5	2.49	1.54	1.49
3	B	602	FAD	C4-C4X	2.49	1.45	1.41
2	D	702	340	C4-C3	2.45	1.44	1.40
3	D	604	FAD	C1'-N10	2.43	1.50	1.48
2	D	702	340	C26-C25	2.41	1.44	1.39
2	B	704	340	C26-C25	2.39	1.44	1.39
2	B	704	340	C28-C29	2.39	1.44	1.39
2	B	704	340	C27-C26	2.38	1.44	1.37
2	A	703	340	C4-C5	-2.38	1.40	1.46
3	C	603	FAD	PA-O3P	2.36	1.64	1.59
2	D	702	340	C4-C5	-2.34	1.40	1.46
2	B	704	340	C4-C5	-2.33	1.40	1.46
2	A	703	340	C28-C27	2.33	1.44	1.37
2	D	702	340	C6-C5	2.32	1.53	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	703	340	C28-C29	2.28	1.44	1.39
3	C	603	FAD	C5B-C4B	2.28	1.59	1.51
3	D	604	FAD	PA-O3P	2.27	1.64	1.59
2	B	704	340	C6-C5	2.25	1.53	1.49
3	C	603	FAD	C9A-C5X	2.24	1.47	1.42
3	A	601	FAD	C6-C5X	2.22	1.44	1.41
3	C	603	FAD	O4B-C4B	2.21	1.50	1.45
2	C	701	340	O20-C24	2.21	1.42	1.37
2	D	702	340	C28-C27	2.20	1.44	1.37
2	C	701	340	C27-C26	2.20	1.44	1.37
3	A	601	FAD	C5B-C4B	2.19	1.58	1.51
3	C	603	FAD	C6-C5X	2.19	1.44	1.41
2	C	701	340	C26-C25	2.16	1.44	1.39
2	A	703	340	C8-N7	2.15	1.41	1.39
3	C	603	FAD	C4-N3	2.14	1.40	1.37
2	D	702	340	O20-C24	2.14	1.42	1.37
2	C	701	340	C28-C27	2.13	1.44	1.37
3	C	603	FAD	C2A-N1A	2.13	1.38	1.33
2	C	701	340	C37-C8	2.12	1.54	1.49
3	B	602	FAD	PA-O5B	-2.12	1.49	1.59
2	D	702	340	C28-C29	2.10	1.43	1.39
3	A	601	FAD	C2A-N1A	2.10	1.38	1.33
3	B	602	FAD	C5X-N5	2.09	1.38	1.35
3	B	602	FAD	C5B-C4B	2.08	1.58	1.51
3	B	602	FAD	C4A-N3A	2.08	1.38	1.35
3	A	601	FAD	C4A-N3A	2.05	1.38	1.35
2	B	704	340	C37-C8	2.04	1.54	1.49
3	A	601	FAD	PA-O5B	-2.02	1.50	1.59
3	B	602	FAD	C2A-N3A	2.01	1.36	1.32
3	A	601	FAD	C5X-N5	2.01	1.38	1.35
3	A	601	FAD	C8-C7	2.00	1.46	1.40

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	701	340	C19-O20-C24	18.59	167.34	117.66
2	A	703	340	C19-O20-C24	15.64	159.45	117.66
2	B	704	340	O20-C19-C9	9.61	129.61	107.73
2	D	702	340	C4-C9-C8	7.43	116.80	105.61
2	C	701	340	C4-C9-C8	7.38	116.72	105.61
2	B	704	340	C4-C9-C8	7.30	116.60	105.61
2	D	702	340	O20-C24-C25	7.14	155.28	119.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	701	340	O20-C19-C9	7.07	123.82	107.73
2	A	703	340	O20-C19-C9	7.07	123.82	107.73
2	D	702	340	O20-C24-C29	-6.95	85.58	119.96
2	A	703	340	C4-C9-C8	6.94	116.06	105.61
2	B	704	340	O20-C24-C25	6.70	153.09	119.96
2	D	702	340	O44-C6-C5	6.69	117.07	111.13
2	C	701	340	O44-C6-C5	6.68	117.06	111.13
2	B	704	340	O20-C24-C29	-6.45	88.07	119.96
2	A	703	340	O44-C6-C5	6.30	116.72	111.13
2	D	702	340	O20-C19-C9	6.26	121.98	107.73
3	C	603	FAD	C2-N1-C10	6.24	121.26	114.98
2	B	704	340	O44-C6-C5	5.97	116.43	111.13
3	D	604	FAD	C2-N1-C10	5.91	120.94	114.98
3	A	601	FAD	C2-N1-C10	5.61	120.63	114.98
3	B	602	FAD	C2-N1-C10	5.52	120.54	114.98
2	C	701	340	C3-C4-C9	-5.02	100.87	107.05
2	D	702	340	C19-C9-C8	-4.98	118.50	127.25
3	C	603	FAD	O4B-C1B-N9A	-4.89	103.89	108.44
2	B	704	340	C12-N7-C3	4.86	129.82	124.45
2	C	701	340	C19-C9-C8	-4.82	118.77	127.25
2	D	702	340	C3-C4-C9	-4.81	101.13	107.05
2	A	703	340	C12-N7-C3	4.75	129.70	124.45
3	D	604	FAD	O4B-C1B-N9A	-4.75	104.02	108.44
2	B	704	340	C19-O20-C24	4.59	129.93	117.66
2	D	702	340	C12-N7-C3	4.56	129.49	124.45
2	B	704	340	C3-C4-C9	-4.46	101.57	107.05
2	B	704	340	C19-C9-C8	-4.41	119.50	127.25
3	A	601	FAD	C4X-C10-N10	-4.37	118.33	120.51
2	C	701	340	C12-N7-C3	4.32	129.22	124.45
3	A	601	FAD	O4B-C1B-N9A	-4.31	104.43	108.44
2	A	703	340	C3-C4-C9	-4.23	101.85	107.05
3	B	602	FAD	C4X-C10-N10	-4.10	118.46	120.51
3	B	602	FAD	O4B-C1B-N9A	-4.02	104.70	108.44
3	D	604	FAD	C4X-C10-N10	-3.93	118.55	120.51
3	A	601	FAD	P-O3P-PA	3.82	142.90	131.68
3	D	604	FAD	P-O3P-PA	3.77	142.73	131.68
3	D	604	FAD	N3A-C2A-N1A	-3.59	125.71	128.71
3	C	603	FAD	N3A-C2A-N1A	-3.51	125.78	128.71
2	A	703	340	C19-C9-C8	-3.45	121.18	127.25
3	C	603	FAD	P-O3P-PA	3.15	140.93	131.68
3	D	604	FAD	O5B-PA-O1A	-3.14	97.09	109.37
3	B	602	FAD	P-O3P-PA	3.12	140.83	131.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	603	FAD	C4X-C10-N10	-3.12	118.95	120.51
3	A	601	FAD	O5B-PA-O1A	-3.08	97.29	109.37
3	B	602	FAD	N3A-C2A-N1A	-3.03	126.18	128.71
3	A	601	FAD	N3A-C2A-N1A	-3.02	126.18	128.71
3	C	603	FAD	O5B-PA-O1A	-3.00	97.64	109.37
3	B	602	FAD	O5B-PA-O1A	-2.94	97.84	109.37
2	C	701	340	C9-C4-C5	2.83	137.97	131.29
2	D	702	340	C9-C4-C5	2.78	137.85	131.29
3	A	601	FAD	C4X-C10-N1	-2.71	120.03	122.73
3	A	601	FAD	O3P-PA-O5B	2.65	115.27	103.41
2	A	703	340	O20-C24-C29	2.62	132.91	119.96
2	B	704	340	C9-C4-C5	2.57	137.35	131.29
3	C	603	FAD	C5A-C4A-N9A	-2.50	103.55	107.16
3	A	601	FAD	O3P-P-O5'	2.45	114.38	103.41
3	D	604	FAD	O3P-PA-O5B	2.44	114.32	103.41
3	C	603	FAD	C2A-N1A-C6A	2.43	123.16	118.77
2	A	703	340	C1-C6-C5	-2.42	117.95	122.50
3	A	601	FAD	C5'-C4'-C3'	-2.40	107.53	112.06
2	B	704	340	O11-C2-C1	-2.39	117.34	121.72
2	D	702	340	C12-N7-C8	-2.38	121.77	124.09
3	D	604	FAD	C2A-N1A-C6A	2.37	123.06	118.77
2	A	703	340	C9-C4-C5	2.37	136.89	131.29
3	B	602	FAD	C5A-C4A-N9A	-2.36	103.76	107.16
2	A	703	340	O11-C2-C1	-2.34	117.44	121.72
2	C	701	340	C1-C6-C5	-2.33	118.11	122.50
2	B	704	340	C12-N7-C8	-2.31	121.83	124.09
2	A	703	340	C3-C2-C1	2.30	120.69	116.39
3	D	604	FAD	C5A-C4A-N9A	-2.30	103.84	107.16
3	C	603	FAD	C4X-C10-N1	-2.28	120.45	122.73
2	A	703	340	C12-N7-C8	-2.27	121.87	124.09
3	D	604	FAD	C4X-C10-N1	-2.27	120.46	122.73
2	A	703	340	C19-C9-C4	-2.27	122.76	128.84
3	C	603	FAD	O3P-PA-O5B	2.26	113.53	103.41
3	A	601	FAD	C2A-N1A-C6A	2.26	122.86	118.77
3	D	604	FAD	N3A-C4A-N9A	2.26	129.52	125.43
2	D	702	340	O11-C2-C1	-2.26	117.58	121.72
3	D	604	FAD	O3P-P-O5'	2.26	113.50	103.41
2	D	702	340	C9-C8-N7	-2.26	104.82	106.86
2	C	701	340	C9-C8-N7	-2.26	104.82	106.86
2	A	703	340	O20-C24-C25	-2.25	108.81	119.96
3	A	601	FAD	C5A-C4A-N9A	-2.25	103.92	107.16
3	C	603	FAD	N3A-C4A-N9A	2.24	129.48	125.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	702	340	C1-C6-C5	-2.24	118.27	122.50
3	C	603	FAD	C5'-C4'-C3'	-2.24	107.83	112.06
3	D	604	FAD	C4A-C5A-N7A	2.24	111.44	109.52
3	B	602	FAD	C5'-C4'-C3'	-2.23	107.86	112.06
3	B	602	FAD	C4A-C5A-N7A	2.22	111.43	109.52
2	B	704	340	C3-C2-C1	2.21	120.52	116.39
2	B	704	340	C1-C6-C5	-2.21	118.33	122.50
2	D	702	340	C3-C2-C1	2.19	120.49	116.39
3	A	601	FAD	N3A-C4A-N9A	2.19	129.38	125.43
3	B	602	FAD	N3A-C4A-N9A	2.18	129.37	125.43
2	C	701	340	C3-C2-C1	2.17	120.45	116.39
3	A	601	FAD	N1-C10-N10	2.16	121.65	115.97
3	B	602	FAD	C4X-C10-N1	-2.16	120.58	122.73
3	A	601	FAD	C1'-N10-C10	2.15	122.21	119.17
2	C	701	340	C12-N7-C8	-2.14	122.00	124.09
3	C	603	FAD	C4A-C5A-N7A	2.11	111.33	109.52
2	B	704	340	C4-C5-C6	2.10	120.19	117.38
3	B	602	FAD	O3P-PA-O5B	2.09	112.77	103.41
3	A	601	FAD	O5B-C5B-C4B	-2.08	101.28	108.94
3	B	602	FAD	C2A-N1A-C6A	2.08	122.52	118.77
2	A	703	340	C45-O44-C6	2.02	120.94	116.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.