



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 10:13 pm BST

PDB ID : 1VDV
Title : Bovine Milk Xanthine Dehydrogenase Y-700 Bound Form
Authors : Fukunari, A.; Okamoto, K.; Nishino, T.; Eger, B.T.; Pai, E.F.; Kamezawa, M.; Yamada, I.; Kato, N.
Deposited on : 2004-03-25
Resolution : 1.98 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

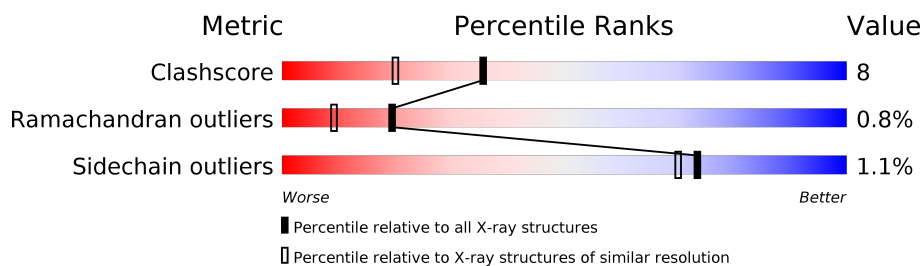
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)

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 respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1332	
1	B	1332	

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	MOS	B	4004	-	-	X	-
9	ACY	A	5201	-	-	X	-
9	ACY	B	5202	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 22610 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 Xanthine dehydrogenase/oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1299	Total	C	N	O	S	0	0	0
			10077	6404	1728	1884	61			
1	B	1296	Total	C	N	O	S	0	0	0
			10054	6391	1724	1878	61			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P80457
B	1	MET	-	INITIATING METHIONINE	UNP P80457

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

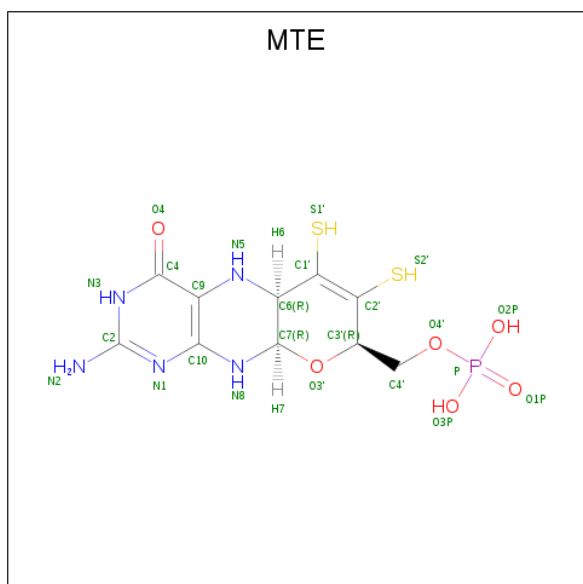
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	2	Total	Ca	0	0
			2	2		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



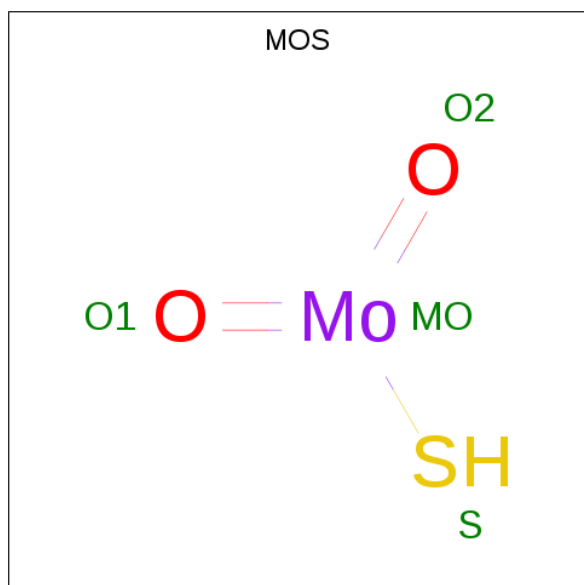
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: $C_{10}H_{14}N_5O_6P_2S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	
			24	10	5	6	1	2	0
4	B	1	Total	C	N	O	P	S	
			24	10	5	6	1	2	0

- Molecule 5 is DIOXOTHIO MOLYBDENUM(VI) ION (three-letter code: MOS) (formula: HMoO_2S).



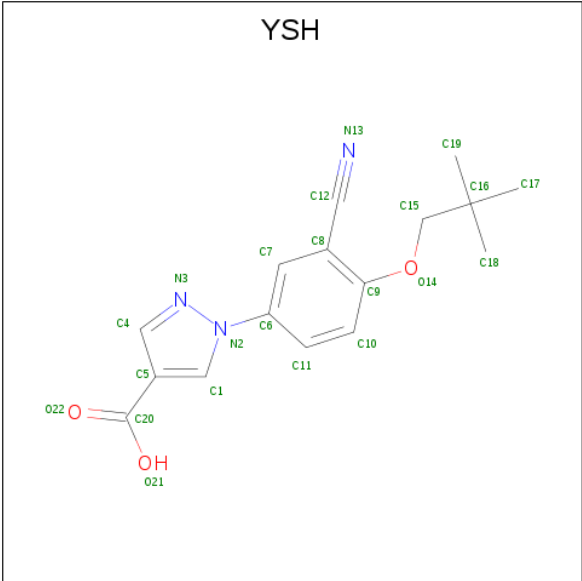
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	Mo	O	S		
			4	1	2	1	0	0
5	B	1	Total	Mo	O	S		
			4	1	2	1	0	0

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



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

- Molecule 7 is 1-[3-CYANO-4-(NEOPENTYLOXY)PHENYL]-1H-PYRAZOLE-4-CARBOXYLIC ACID (three-letter code: YSH) (formula: C₁₆H₁₇N₃O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			22	16	3	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			22	16	3	3		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



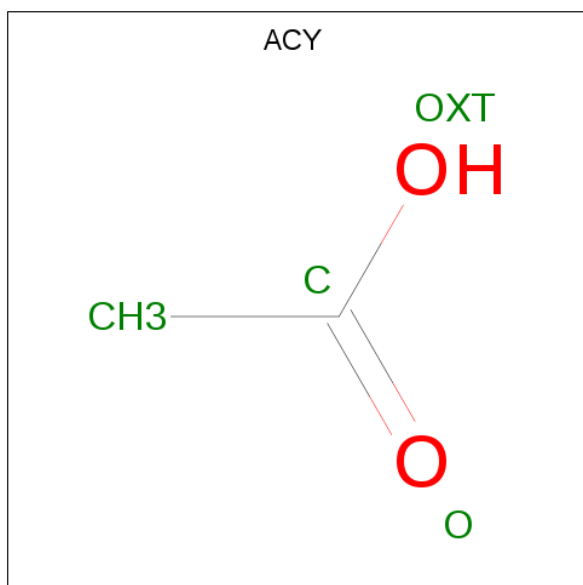
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 9 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total 4	C 2	O 2	0	0
9	B	1	Total 4	C 2	O 2	0	0

- Molecule 10 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1086	Total 1086	O 1086	0	0
10	B	1033	Total 1033	O 1033	0	0

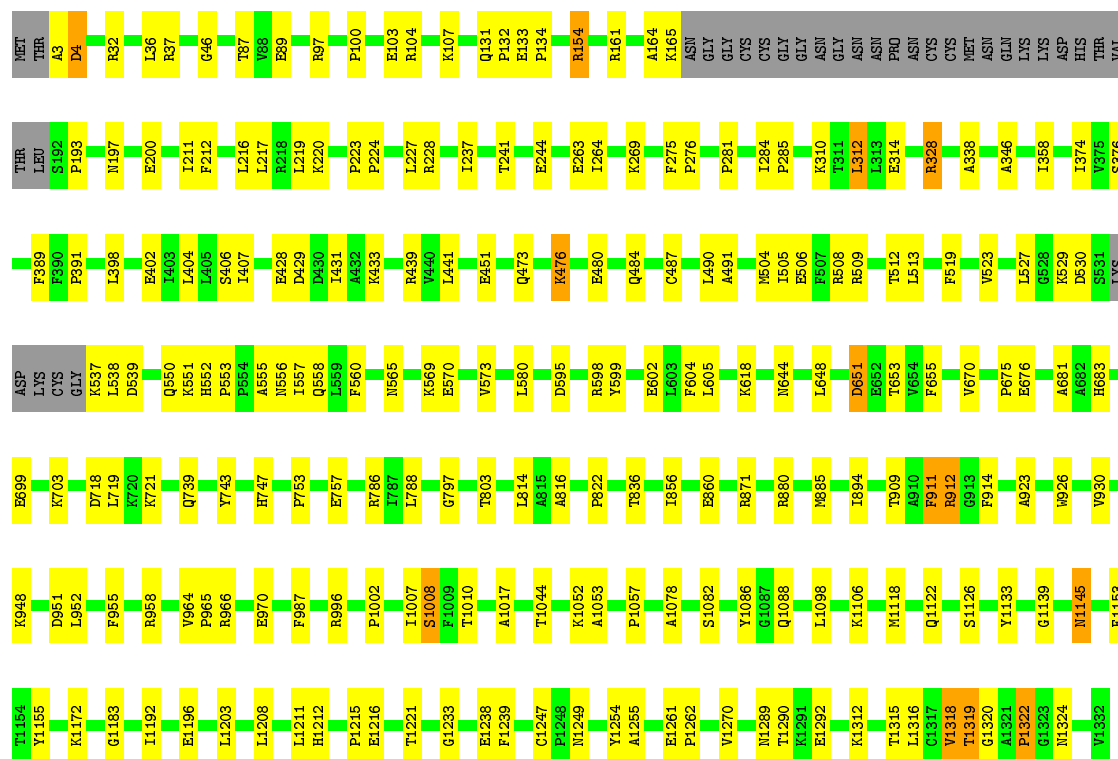
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

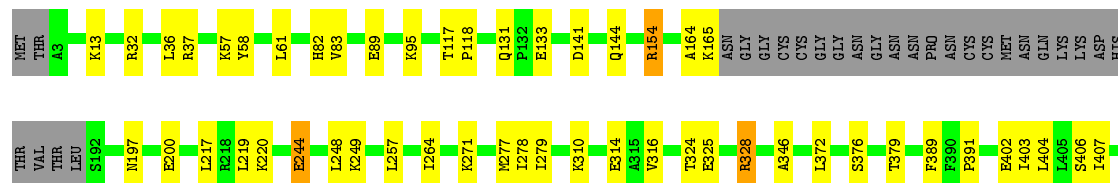
- Molecule 1: Xanthine dehydrogenase/oxidase

Chain A:  81% 15% ..



- Molecule 1: Xanthine dehydrogenase/oxidase

Chain B: 83% 13% •



L1316	G1087	R895	N650	S412
C1317	Q1088	G896	N650	K433
V1318	L1098	T897	T853	L441
T1319	N1108	G898	V654	E451
G1320	P1109	B899	F655	
A1321	F1132	T909	K857	
P1322	Y1133	A910	D658	Q473
G1323	G1139	F911	E676	K476
N1324	N1445	R912	E699	I505
C1325	K1172	G913	L712	
K1326	N1173	F914	K713	R508
	I1192	R926	L719	R509
	E1196	V930	L719	T512
	F1199	K948	F723	K518
	L1203	D951	A726	L521
	T1221	L952	I736	G528
	T1226	F955	Y743	LYS
	P1236	R958	H747	ASP
	T1237	Y964	P753	SER
	E1238	P965	E757	LYS
	F1239	F987	K778	ASP
	N1249	C992	R786	LYS
	A1255	R993	G797	CYS
	E1261	K994	L814	GLY
	P1262	R995	A815	R537
	G1267	R996	A816	L538
	A1281	P1002	Y817	S544
	Q1284	I1007	K818	L548
	H1285	S1008	M826	K551
	T1286	F1009	T836	H552
	N1287	T1010	K847	Q558
	N1288	A1017	V857	N565
	N1289	L1030	E860	E570
	T1290	Q1048	R871	D571
	K1291	A1053	H875	T572
	E1292	P1057	R880	R575
	S1298	A1078		E589
	K1312	S1082		Y599
		Y1086		E600
				L635
				N644

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.82Å 123.94Å 148.89Å 90.00° 91.16° 90.00°	Depositor
Resolution (Å)	20.00 – 1.98	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.98)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.178 , 0.215	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	22610	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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: GOL, YSH, MOS, CA, FES, ACY, FAD, MTE

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	0.32	0/10298	0.60	0/13939
1	B	0.31	0/10275	0.60	0/13909
All	All	0.32	0/20573	0.60	0/27848

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10077	0	10076	172	0
1	B	10054	0	10053	155	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	8	0	0	1	0
3	B	8	0	0	0	0
4	A	24	0	10	1	0
4	B	24	0	10	1	0
5	A	4	0	0	1	0
5	B	4	0	0	2	0
6	A	53	0	31	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	53	0	31	3	0
7	A	22	0	16	3	0
7	B	22	0	16	3	0
8	A	66	0	88	8	0
8	B	60	0	80	8	0
9	A	4	0	3	4	0
9	B	4	0	3	4	0
10	A	1086	0	0	9	0
10	B	1033	0	0	7	0
All	All	22610	0	20417	331	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 8.

All (331) 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)
7:B:5102:YSH:C1	7:B:5102:YSH:N2	1.70	1.52
7:A:5101:YSH:C1	7:A:5101:YSH:N2	1.68	1.51
1:A:3:ALA:HB1	1:A:228:ARG:H	1.20	1.06
1:A:537:LYS:HG2	1:A:538:LEU:H	1.28	0.98
1:A:955:PHE:HA	1:A:1145:ASN:HD21	1.30	0.97
1:B:1286:THR:HG22	1:B:1287:ASN:H	1.32	0.94
1:A:439:ARG:HB3	1:A:439:ARG:HH11	1.32	0.93
1:A:131:GLN:HE21	1:A:133:GLU:H	1.14	0.90
1:B:955:PHE:HA	1:B:1145:ASN:HD21	1.36	0.89
1:B:1321:ALA:HB1	1:B:1322:PRO:HD2	1.56	0.87
1:A:1211:LEU:HA	1:A:1221:THR:HG21	1.57	0.86
1:B:404:LEU:HD21	1:B:407:ILE:HD11	1.57	0.86
1:A:36:LEU:HD22	1:A:89:GLU:HG3	1.57	0.84
1:A:3:ALA:HB1	1:A:228:ARG:N	1.93	0.83
1:B:131:GLN:HE21	1:B:133:GLU:H	1.26	0.83
1:B:1088:GLN:HG2	1:B:1133:TYR:CD1	2.15	0.82
1:B:328:ARG:HG2	1:B:328:ARG:HH11	1.45	0.80
1:B:551:LYS:NZ	1:B:551:LYS:HA	1.96	0.80
1:A:719:LEU:HD21	1:A:860:GLU:HG2	1.65	0.79
1:A:358:ILE:HD12	1:A:431:ILE:HG23	1.64	0.78
1:A:718:ASP:HB3	1:A:721:LYS:HE2	1.69	0.75
1:A:537:LYS:HG2	1:A:538:LEU:N	2.03	0.73
1:B:551:LYS:HZ2	1:B:552:HIS:H	1.32	0.73
1:B:36:LEU:HD22	1:B:89:GLU:HG3	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1088:GLN:HG2	1:A:1133:TYR:CD1	2.25	0.72
1:B:551:LYS:HZ2	1:B:551:LYS:HA	1.54	0.70
1:A:1118:MET:O	1:A:1122:GLN:HG2	1.92	0.70
1:B:1286:THR:HG22	1:B:1287:ASN:N	2.05	0.69
1:B:154:ARG:HD3	1:B:1196:GLU:OE2	1.92	0.69
1:B:552:HIS:CE1	1:B:1172:LYS:HZ3	2.09	0.69
1:A:406:SER:C	1:A:407:ILE:HD12	2.13	0.68
1:A:264:ILE:HD11	6:A:3005:FAD:H3B	1.75	0.68
1:B:1078:ALA:HB1	5:B:4004:MOS:O1	1.94	0.68
1:A:217:LEU:O	1:A:220:LYS:HG2	1.93	0.68
1:A:911:PHE:H	9:A:5201:ACY:H3	1.59	0.67
1:A:441:LEU:HB3	1:A:451:GLU:HB2	1.76	0.66
1:B:376:SER:HB3	1:B:379:THR:OG1	1.95	0.66
1:B:719:LEU:HD11	1:B:895:ARG:HB2	1.78	0.66
1:A:948:LYS:HG2	1:A:951:ASP:OD2	1.95	0.65
1:A:154:ARG:HD3	1:A:1196:GLU:OE2	1.96	0.65
1:B:948:LYS:HG2	1:B:951:ASP:OD2	1.97	0.65
1:A:538:LEU:HD12	8:A:5002:GOL:H31	1.77	0.65
1:A:428:GLU:OE2	1:A:1233:GLY:HA3	1.96	0.65
1:A:193:PRO:HG2	1:A:560:PHE:CE1	2.32	0.65
1:B:1312:LYS:O	1:B:1316:LEU:HD13	1.97	0.65
1:A:880:ARG:HD2	1:A:914:PHE:HB3	1.79	0.65
1:B:406:SER:O	1:B:407:ILE:HD12	1.97	0.65
1:A:131:GLN:HE21	1:A:133:GLU:N	1.92	0.64
1:A:439:ARG:HB3	1:A:439:ARG:NH1	2.09	0.64
1:B:551:LYS:HZ2	1:B:552:HIS:N	1.96	0.64
1:B:911:PHE:H	9:B:5202:ACY:H3	1.63	0.64
1:B:719:LEU:HD11	1:B:895:ARG:CB	2.28	0.63
1:A:580:LEU:HD13	1:A:1044:THR:HG23	1.80	0.63
1:A:358:ILE:CD1	1:A:431:ILE:HG23	2.28	0.63
1:A:328:ARG:HH11	1:A:328:ARG:HG2	1.63	0.63
1:A:217:LEU:HD12	1:A:220:LYS:HD3	1.82	0.62
1:A:164:ALA:O	1:A:165:LYS:HB2	2.00	0.61
1:B:1286:THR:CG2	1:B:1287:ASN:H	2.11	0.61
1:A:197:ASN:O	1:A:200:GLU:HG2	2.01	0.61
1:A:788:LEU:HB2	8:A:5011:GOL:H12	1.83	0.60
1:B:757:GLU:HB3	1:B:786:ARG:HE	1.66	0.60
5:B:4004:MOS:O2	5:B:4004:MOS:MO	1.73	0.60
1:B:310:LYS:O	1:B:314:GLU:HG3	2.02	0.59
1:B:911:PHE:N	9:B:5202:ACY:H3	2.16	0.59
1:A:3:ALA:HA	1:A:227:LEU:HD22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:ASP:HB3	10:A:5928:HOH:O	2.02	0.59
7:A:5101:YSH:C1	7:A:5101:YSH:C6	2.78	0.59
1:A:439:ARG:CB	1:A:439:ARG:HH11	2.13	0.59
1:A:911:PHE:N	9:A:5201:ACY:H3	2.18	0.59
1:A:328:ARG:HG2	10:A:5679:HOH:O	2.03	0.59
1:B:1318:VAL:HG22	1:B:1321:ALA:HB2	1.85	0.59
1:B:880:ARG:HD2	1:B:914:PHE:HB3	1.84	0.59
1:A:966:ARG:O	1:A:970:GLU:HG3	2.02	0.58
1:B:570:GLU:OE2	1:B:1057:PRO:HG3	2.03	0.58
1:A:3:ALA:HA	1:A:227:LEU:CD2	2.32	0.58
1:A:1010:THR:HG23	7:A:5101:YSH:O22	2.04	0.58
1:A:1203:LEU:HD13	1:A:1270:VAL:HG21	1.85	0.58
1:A:1172:LYS:HG3	8:A:5001:GOL:H31	1.87	0.57
1:B:1289:ASN:O	1:B:1290:THR:HB	2.05	0.57
1:B:372:LEU:HD23	1:B:407:ILE:HG13	1.86	0.57
1:A:241:THR:OG1	1:A:244:GLU:HG3	2.05	0.57
1:A:914:PHE:HA	9:A:5201:ACY:H2	1.87	0.56
1:B:473:GLN:O	1:B:476:LYS:HB2	2.05	0.56
1:B:713:LYS:HD3	1:B:897:THR:HG22	1.88	0.56
1:B:346:ALA:HB1	6:B:4005:FAD:H4'	1.86	0.56
1:A:552:HIS:CG	1:A:553:PRO:HD2	2.40	0.56
1:B:1326:LYS:HG3	10:B:5861:HOH:O	2.04	0.56
1:B:197:ASN:O	1:B:200:GLU:HG2	2.04	0.56
1:B:1287:ASN:O	1:B:1288:ASN:HB2	2.06	0.56
1:A:1312:LYS:O	1:A:1316:LEU:HD23	2.06	0.56
1:A:154:ARG:HD2	10:A:5453:HOH:O	2.06	0.56
1:A:651:ASP:CG	1:A:871:ARG:HH11	2.09	0.55
1:A:433:LYS:HE3	1:A:504:MET:SD	2.46	0.55
1:A:569:LYS:NZ	1:A:569:LYS:HB3	2.21	0.55
1:B:509:ARG:HH11	1:B:509:ARG:HG2	1.72	0.55
1:A:1318:VAL:HB	1:A:1322:PRO:HB3	1.88	0.55
1:B:404:LEU:HD21	1:B:407:ILE:CD1	2.33	0.55
1:B:1323:GLY:O	1:B:1325:CYS:N	2.41	0.54
1:A:1212:HIS:H	1:A:1221:THR:HG22	1.72	0.54
1:B:441:LEU:HB3	1:B:451:GLU:HB2	1.90	0.54
1:A:1249:ASN:O	1:A:1255:ALA:HA	2.08	0.54
1:A:909:THR:O	9:A:5201:ACY:H1	2.08	0.54
1:A:753:PRO:HD3	1:A:816:ALA:HB1	1.90	0.53
1:A:269:LYS:HE3	10:A:6386:HOH:O	2.09	0.53
1:A:97:ARG:HB2	1:A:97:ARG:NH1	2.23	0.53
1:B:1010:THR:HG23	7:B:5102:YSH:O22	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:THR:HG1	1:A:89:GLU:HG2	1.74	0.53
1:B:1312:LYS:HG2	10:B:6326:HOH:O	2.10	0.52
1:B:909:THR:O	9:B:5202:ACY:H1	2.08	0.52
1:A:1322:PRO:C	1:A:1324:ASN:H	2.12	0.52
1:A:473:GLN:O	1:A:476:LYS:HB2	2.09	0.52
1:A:599:TYR:HA	1:B:599:TYR:HA	1.91	0.52
1:A:131:GLN:NE2	1:A:133:GLU:H	1.96	0.52
1:B:521:LEU:HD22	1:B:538:LEU:HD11	1.91	0.52
1:B:264:ILE:HD11	6:B:4005:FAD:H3B	1.90	0.52
1:B:551:LYS:HZ3	1:B:551:LYS:HA	1.73	0.52
1:A:389:PHE:O	1:A:391:PRO:HD3	2.10	0.52
7:B:5102:YSH:C6	7:B:5102:YSH:C1	2.81	0.52
1:A:1082:SER:HB2	4:A:3003:MTE:O3P	2.10	0.52
1:B:154:ARG:HD2	10:B:5493:HOH:O	2.08	0.52
1:B:164:ALA:O	1:B:165:LYS:HB2	2.09	0.52
1:B:32:ARG:HH12	1:B:676:GLU:CD	2.13	0.52
1:A:885:MET:HE2	1:A:894:ILE:HD11	1.93	0.51
1:B:406:SER:C	1:B:407:ILE:HD12	2.30	0.51
1:A:338:ALA:HA	1:A:429:ASP:OD1	2.11	0.51
1:A:1078:ALA:HB1	5:A:3004:MOS:O1	2.09	0.51
1:A:537:LYS:CG	1:A:538:LEU:H	2.12	0.51
1:A:505:ILE:HD12	1:A:505:ILE:N	2.25	0.51
1:B:376:SER:HB2	1:B:402:GLU:HG2	1.92	0.51
1:A:1318:VAL:HG12	1:A:1319:THR:H	1.76	0.51
1:B:548:LEU:HA	8:B:5022:GOL:H12	1.93	0.50
1:A:1319:THR:HG23	1:A:1320:GLY:N	2.26	0.50
1:A:404:LEU:HD21	1:A:407:ILE:HD11	1.92	0.50
1:B:1249:ASN:O	1:B:1255:ALA:HA	2.11	0.50
1:B:1281:ALA:O	1:B:1284:GLN:HB3	2.12	0.50
1:B:723:PHE:CD2	1:B:847:LYS:HE2	2.47	0.50
1:A:480:GLU:O	1:A:484:GLN:HG3	2.11	0.50
1:A:747:HIS:CD2	1:A:836:THR:HG21	2.47	0.50
1:B:914:PHE:HA	9:B:5202:ACY:H2	1.92	0.50
1:A:1318:VAL:HG12	1:A:1319:THR:N	2.26	0.50
1:A:1289:ASN:HD22	1:A:1292:GLU:HB2	1.77	0.50
1:B:1289:ASN:HB3	1:B:1292:GLU:HB2	1.94	0.50
1:A:161:ARG:HD3	10:A:5307:HOH:O	2.11	0.49
1:A:598:ARG:HG3	1:B:600:GLU:HG2	1.94	0.49
1:A:604:PHE:CD2	1:A:675:PRO:HG3	2.46	0.49
1:B:747:HIS:CD2	1:B:836:THR:HG21	2.48	0.49
1:B:1172:LYS:HG3	8:B:5008:GOL:H31	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:551:LYS:HZ2	1:B:551:LYS:CA	2.23	0.49
1:B:58:TYR:CD2	1:B:220:LYS:HB2	2.47	0.49
1:A:1007:ILE:O	1:A:1008:SER:CB	2.61	0.49
1:B:1173:ASN:O	1:B:1236:PRO:HA	2.13	0.49
1:B:165:LYS:NZ	1:B:165:LYS:HB2	2.27	0.49
1:B:699:GLU:CD	1:B:699:GLU:H	2.14	0.49
1:A:1088:GLN:HG2	1:A:1133:TYR:CE1	2.48	0.49
1:A:237:ILE:N	1:A:237:ILE:HD12	2.28	0.49
1:A:644:ASN:O	1:A:653:THR:HA	2.13	0.49
1:A:856:ILE:N	1:A:856:ILE:HD12	2.27	0.49
1:B:650:ASN:HD21	1:B:778:LYS:HE3	1.78	0.49
1:A:739:GLN:HG2	1:A:911:PHE:CE1	2.48	0.49
1:B:964:VAL:HB	1:B:965:PRO:HD3	1.95	0.49
1:A:1017:ALA:HB1	1:A:1086:TYR:CD2	2.47	0.48
1:A:1106:LYS:NZ	1:A:1106:LYS:HB3	2.27	0.48
1:A:508:ARG:O	1:A:512:THR:HG23	2.13	0.48
1:A:527:LEU:C	1:A:529:LYS:H	2.17	0.48
1:B:1007:ILE:O	1:B:1008:SER:CB	2.61	0.48
1:B:1082:SER:HB2	4:B:4003:MTE:O3P	2.13	0.48
1:B:655:PHE:CE1	1:B:814:LEU:HD23	2.47	0.48
1:B:826:MET:HB3	8:B:5014:GOL:H31	1.94	0.48
1:B:1323:GLY:O	1:B:1324:ASN:C	2.51	0.48
1:B:719:LEU:HD13	1:B:860:GLU:OE2	2.14	0.48
8:A:5011:GOL:O3	1:B:1030:LEU:HD22	2.14	0.48
1:A:1318:VAL:HG21	1:A:1322:PRO:CB	2.44	0.48
1:A:211:ILE:HG12	1:A:212:PHE:N	2.29	0.48
1:A:346:ALA:HB1	6:A:3005:FAD:H4'	1.96	0.48
1:B:726:ALA:HB2	1:B:857:VAL:CG2	2.44	0.48
1:B:1321:ALA:HB1	1:B:1322:PRO:CD	2.38	0.48
1:B:655:PHE:HE1	1:B:814:LEU:HD23	1.78	0.48
1:B:952:LEU:HD23	1:B:958:ARG:HA	1.94	0.48
1:A:310:LYS:O	1:A:314:GLU:HG3	2.14	0.47
1:B:558:GLN:HB3	1:B:1192:ILE:HD13	1.96	0.47
1:A:604:PHE:HE2	8:A:5006:GOL:H31	1.79	0.47
1:B:433:LYS:HG3	10:B:5852:HOH:O	2.14	0.47
1:A:1215:PRO:HD2	1:A:1216:GLU:OE2	2.15	0.47
1:A:555:ALA:HB3	1:A:1238:GLU:HG3	1.95	0.47
1:B:544:SER:HB2	1:B:994:LYS:HD2	1.97	0.47
1:A:374:ILE:HD13	1:A:398:LEU:CD2	2.45	0.47
1:A:529:LYS:O	1:A:530:ASP:HB2	2.14	0.47
1:A:1318:VAL:CB	1:A:1322:PRO:HB3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:ILE:H	1:A:505:ILE:HD12	1.80	0.47
1:B:911:PHE:O	1:B:912:ARG:C	2.53	0.47
1:B:325:GLU:HB2	1:B:412:SER:HB3	1.96	0.47
1:A:885:MET:CE	1:A:894:ILE:HD11	2.45	0.47
1:A:987:PHE:CD2	1:A:996:ARG:HG3	2.50	0.47
1:B:1318:VAL:O	1:B:1320:GLY:N	2.47	0.47
1:A:558:GLN:HB3	1:A:1192:ILE:HD13	1.96	0.46
1:A:926:TRP:O	1:A:930:VAL:HG23	2.14	0.46
1:A:655:PHE:HE1	1:A:814:LEU:HD23	1.80	0.46
1:B:328:ARG:HH11	1:B:328:ARG:CG	2.20	0.46
1:B:736:ILE:O	1:B:736:ILE:HG23	2.16	0.46
1:A:1052:LYS:HD3	1:A:1254:TYR:CZ	2.51	0.46
1:B:994:LYS:HE3	8:B:5008:GOL:O2	2.15	0.46
1:B:217:LEU:O	1:B:220:LYS:HG2	2.15	0.46
1:A:1322:PRO:C	1:A:1324:ASN:N	2.68	0.46
1:A:223:PRO:HA	1:A:224:PRO:HD3	1.86	0.46
1:B:117:THR:HB	1:B:118:PRO:HD3	1.97	0.46
1:B:1203:LEU:HD11	10:B:5736:HOH:O	2.14	0.46
1:B:1053:ALA:O	1:B:1098:LEU:HD11	2.16	0.46
1:A:37:ARG:HD3	1:A:595:ASP:O	2.16	0.46
1:A:648:LEU:HD11	1:A:803:THR:HG21	1.97	0.46
1:B:726:ALA:HB2	1:B:857:VAL:HG21	1.98	0.46
1:A:911:PHE:O	1:A:912:ARG:C	2.53	0.46
1:B:635:LEU:HD21	1:B:818:LYS:HG2	1.97	0.45
1:A:757:GLU:HB3	1:A:786:ARG:HE	1.80	0.45
1:B:1261:GLU:N	1:B:1262:PRO:CD	2.79	0.45
1:B:37:ARG:HD3	8:B:5013:GOL:O3	2.15	0.45
1:A:407:ILE:N	1:A:407:ILE:HD12	2.31	0.45
1:A:602:GLU:HA	1:A:822:PRO:HG2	1.99	0.45
1:B:1221:THR:HG22	1:B:1226:THR:HB	1.98	0.45
1:B:57:LYS:HE2	1:B:83:VAL:HG22	1.98	0.45
1:A:193:PRO:HG2	1:A:560:PHE:CZ	2.52	0.45
1:B:389:PHE:O	1:B:391:PRO:HD3	2.16	0.45
1:A:964:VAL:HB	1:A:965:PRO:HD3	1.98	0.45
1:A:1126:SER:HB2	1:B:1132:PHE:CD1	2.52	0.45
1:A:164:ALA:O	1:A:165:LYS:CB	2.64	0.45
1:B:736:ILE:HG13	1:B:1298:SER:HB3	1.99	0.45
1:B:987:PHE:CD2	1:B:996:ARG:HG3	2.52	0.45
1:A:605:LEU:C	1:A:605:LEU:HD23	2.37	0.45
1:B:508:ARG:O	1:B:512:THR:HG23	2.17	0.45
1:A:1261:GLU:N	1:A:1262:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1153:PHE:HB2	1:A:1155:TYR:CZ	2.52	0.45
1:A:952:LEU:HD23	1:A:958:ARG:HA	2.00	0.44
1:A:699:GLU:H	1:A:699:GLU:CD	2.21	0.44
1:A:604:PHE:CE2	8:A:5006:GOL:H31	2.52	0.44
1:B:1324:ASN:O	1:B:1325:CYS:C	2.56	0.44
1:A:683:HIS:HA	8:A:5019:GOL:H12	1.99	0.44
1:A:573:VAL:HG21	1:A:1052:LYS:HD2	2.00	0.44
1:B:644:ASN:O	1:B:653:THR:HA	2.18	0.44
1:A:161:ARG:HH12	1:A:556:ASN:ND2	2.16	0.43
1:B:1088:GLN:HG2	1:B:1133:TYR:CE1	2.52	0.43
1:B:1088:GLN:HG3	10:B:5797:HOH:O	2.18	0.43
1:B:328:ARG:HG2	1:B:328:ARG:NH1	2.19	0.43
1:B:403:ILE:C	1:B:403:ILE:HD12	2.38	0.43
1:B:95:LYS:HG3	1:B:589:GLU:OE1	2.18	0.43
1:B:1017:ALA:HB1	1:B:1086:TYR:CD2	2.53	0.43
6:B:4005:FAD:HM73	10:B:5428:HOH:O	2.18	0.43
1:A:911:PHE:HD2	1:A:912:ARG:N	2.17	0.43
1:B:723:PHE:CE2	1:B:847:LYS:HE2	2.52	0.43
1:B:871:ARG:HH11	1:B:871:ARG:HG3	1.83	0.43
6:A:3005:FAD:HM73	10:A:5425:HOH:O	2.18	0.43
1:A:374:ILE:HG21	1:A:398:LEU:HD22	2.00	0.43
1:B:154:ARG:CD	1:B:1196:GLU:OE2	2.65	0.43
1:B:141:ASP:O	1:B:144:GLN:HG3	2.18	0.43
1:B:61:LEU:HD23	1:B:61:LEU:C	2.38	0.43
1:A:1053:ALA:O	1:A:1098:LEU:HD11	2.19	0.43
1:A:328:ARG:HG3	10:A:5888:HOH:O	2.17	0.43
1:A:487:CYS:HB3	1:A:513:LEU:HD13	2.00	0.43
1:A:651:ASP:OD1	1:A:871:ARG:NH1	2.52	0.43
1:A:1315:THR:O	1:A:1318:VAL:HG22	2.19	0.43
1:B:955:PHE:CA	1:B:1145:ASN:HD21	2.20	0.43
1:B:926:TRP:O	1:B:930:VAL:HG23	2.19	0.43
1:A:404:LEU:CD2	1:A:407:ILE:HD11	2.49	0.43
1:B:826:MET:H	8:B:5014:GOL:C3	2.30	0.43
1:A:1290:THR:HG22	1:A:1290:THR:O	2.19	0.43
1:B:1199:PHE:CE1	1:B:1267:GLY:HA2	2.53	0.43
1:B:82:HIS:NE2	1:B:219:LEU:HD13	2.33	0.43
1:A:570:GLU:CD	1:A:1057:PRO:HG3	2.40	0.43
1:B:992:CYS:SG	1:B:1285:HIS:NE2	2.92	0.43
1:B:948:LYS:HG2	1:B:951:ASP:CG	2.39	0.43
1:A:131:GLN:O	1:A:134:PRO:HD3	2.19	0.42
1:A:100:PRO:O	1:A:104:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:LEU:HD23	1:A:219:LEU:HD12	2.00	0.42
1:B:909:THR:OG1	1:B:910:ALA:N	2.51	0.42
1:A:491:ALA:O	1:A:509:ARG:NH2	2.52	0.42
1:A:87:THR:OG1	1:A:89:GLU:HG2	2.19	0.42
1:B:1108:ASN:N	1:B:1109:PRO:HD3	2.34	0.42
1:B:753:PRO:HD3	1:B:816:ALA:HB1	2.01	0.42
1:A:275:PHE:HA	1:A:276:PRO:HD2	1.91	0.42
1:B:257:LEU:HA	1:B:279:ILE:O	2.18	0.42
1:A:1183:GLY:HA2	1:A:1247:CYS:O	2.19	0.42
1:A:519:PHE:O	1:A:523:VAL:HG23	2.20	0.42
1:B:249:LYS:HG3	1:B:403:ILE:CG2	2.50	0.42
1:B:572:THR:HA	1:B:575:ARG:HD2	2.01	0.42
1:B:719:LEU:HD11	1:B:895:ARG:HB3	2.00	0.42
1:A:103:GLU:HG3	1:A:107:LYS:HE2	2.02	0.42
1:A:651:ASP:OD2	1:A:871:ARG:HG3	2.19	0.42
1:B:572:THR:OG1	1:B:1048:GLN:HG2	2.19	0.42
1:A:703:LYS:HB3	1:A:703:LYS:NZ	2.35	0.42
1:A:46:GLY:HA2	3:A:3002:FES:S1	2.60	0.42
1:A:376:SER:HB3	1:A:402:GLU:HG2	2.02	0.42
1:B:316:VAL:HA	1:B:324:THR:HG21	2.01	0.42
1:B:325:GLU:HB2	1:B:412:SER:CB	2.50	0.42
1:B:473:GLN:HA	1:B:473:GLN:NE2	2.35	0.42
1:B:271:LYS:NZ	8:B:5020:GOL:H32	2.35	0.41
1:A:312:LEU:HA	1:A:312:LEU:HD12	1.89	0.41
1:B:217:LEU:HA	1:B:217:LEU:HD12	1.93	0.41
1:B:551:LYS:NZ	1:B:552:HIS:H	2.09	0.41
1:A:1319:THR:HG23	1:A:1320:GLY:H	1.85	0.41
1:B:505:ILE:N	1:B:505:ILE:HD12	2.36	0.41
1:B:518:LYS:HZ3	8:B:5022:GOL:C3	2.32	0.41
1:A:1318:VAL:HG11	1:A:1322:PRO:HA	2.02	0.41
1:A:670:VAL:HG11	1:A:681:ALA:HB3	2.01	0.41
1:B:1325:CYS:O	1:B:1326:LYS:CB	2.67	0.41
1:B:244:GLU:O	1:B:248:LEU:HG	2.19	0.41
1:B:13:LYS:C	1:B:13:LYS:HD3	2.41	0.41
1:B:552:HIS:HB2	1:B:1237:THR:HG21	2.03	0.41
1:B:1287:ASN:O	1:B:1288:ASN:CB	2.67	0.41
1:A:1216:GLU:CD	1:A:1216:GLU:H	2.23	0.41
1:B:657:LYS:O	1:B:658:ASP:HB2	2.21	0.41
1:B:899:ARG:HD2	1:B:899:ARG:HA	1.87	0.41
1:A:1088:GLN:HG3	10:A:5686:HOH:O	2.19	0.41
1:A:923:ALA:HA	1:A:926:TRP:NE1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1289:ASN:O	1:B:1290:THR:CB	2.69	0.41
1:B:992:CYS:HA	1:B:1284:GLN:HE21	1.86	0.41
1:A:433:LYS:HA	1:A:433:LYS:HD3	1.81	0.40
1:A:32:ARG:HH12	1:A:676:GLU:CD	2.24	0.40
1:B:1325:CYS:O	1:B:1326:LYS:HB3	2.20	0.40
1:B:58:TYR:CZ	1:B:220:LYS:HD2	2.56	0.40
1:B:328:ARG:CG	1:B:328:ARG:NH1	2.79	0.40
1:A:284:ILE:HA	1:A:285:PRO:HD2	1.91	0.40
1:B:712:LEU:HD21	1:B:875:HIS:CE1	2.56	0.40
1:A:1212:HIS:H	1:A:1221:THR:CG2	2.34	0.40
1:A:3:ALA:HA	1:A:227:LEU:HD23	2.04	0.40
1:A:490:LEU:HB2	1:A:513:LEU:CD2	2.52	0.40
1:A:539:ASP:H	8:A:5002:GOL:C3	2.35	0.40
1:A:551:LYS:HE3	10:A:6123:HOH:O	2.21	0.40
1:A:556:ASN:O	1:A:557:ILE:HD13	2.21	0.40
1:A:655:PHE:CE1	1:A:814:LEU:HD23	2.57	0.40
1:A:131:GLN:HA	1:A:132:PRO:HD2	1.95	0.40
1:A:263:GLU:HB2	6:A:3005:FAD:H52A	2.02	0.40
1:A:506:GLU:CD	1:A:506:GLU:H	2.24	0.40
1:B:277:MET:HE3	1:B:278:ILE:N	2.35	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	1293/1332 (97%)	1244 (96%)	41 (3%)	8 (1%)	25	14
1	B	1290/1332 (97%)	1234 (96%)	44 (3%)	12 (1%)	17	8
All	All	2583/2664 (97%)	2478 (96%)	85 (3%)	20 (1%)	19	9

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	1008	SER
1	B	1008	SER
1	B	1287	ASN
1	B	1324	ASN
1	B	1326	LYS
1	A	1319	THR
1	B	244	GLU
1	B	1325	CYS
1	A	912	ARG
1	A	1322	PRO
1	B	912	ARG
1	B	1139	GLY
1	B	1319	THR
1	A	797	GLY
1	A	1318	VAL
1	B	797	GLY
1	B	1322	PRO
1	B	1323	GLY
1	A	1139	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	1101/1128 (98%)	1086 (99%)	15 (1%)	67	62
1	B	1098/1128 (97%)	1088 (99%)	10 (1%)	78	77
All	All	2199/2256 (98%)	2174 (99%)	25 (1%)	73	70

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	ARG
1	A	281	PRO
1	A	312	LEU
1	A	328	ARG

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Mol	Chain	Res	Type
1	A	476	LYS
1	A	550	GLN
1	A	565	ASN
1	A	618	LYS
1	A	651	ASP
1	A	743	TYR
1	A	911	PHE
1	A	1002	PRO
1	A	1145	ASN
1	A	1208	LEU
1	A	1239	PHE
1	B	154	ARG
1	B	328	ARG
1	B	551	LYS
1	B	565	ASN
1	B	600	GLU
1	B	743	TYR
1	B	911	PHE
1	B	1002	PRO
1	B	1145	ASN
1	B	1239	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN
1	A	252	HIS
1	A	272	ASN
1	A	351	ASN
1	A	471	GLN
1	A	473	GLN
1	A	550	GLN
1	A	556	ASN
1	A	565	ASN
1	A	626	GLN
1	A	650	ASN
1	A	1145	ASN
1	A	1212	HIS
1	A	1284	GLN
1	A	1289	ASN
1	A	1324	ASN
1	B	131	GLN

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Mol	Chain	Res	Type
1	B	146	ASN
1	B	351	ASN
1	B	471	GLN
1	B	473	GLN
1	B	484	GLN
1	B	565	ASN
1	B	626	GLN
1	B	650	ASN
1	B	875	HIS
1	B	976	GLN
1	B	1145	ASN
1	B	1284	GLN
1	B	1287	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](#)

Of 39 ligands modelled in this entry, 4 are monoatomic - leaving 35 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	GOL	A	5017	-	5,5,5	0.28	0	5,5,5	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GOL	B	5014	-	5,5,5	0.21	0	5,5,5	0.38	0
8	GOL	B	5020	-	5,5,5	0.25	0	5,5,5	0.34	0
8	GOL	A	5011	-	5,5,5	0.21	0	5,5,5	0.36	0
8	GOL	A	5003	-	5,5,5	0.31	0	5,5,5	0.32	0
6	FAD	A	3005	-	51,58,58	2.87	21 (41%)	60,89,89	2.84	24 (40%)
9	ACY	A	5201	-	1,3,3	1.09	0	0,3,3	0.00	-
8	GOL	B	5008	-	5,5,5	0.26	0	5,5,5	0.39	0
5	MOS	B	4004	4	0,3,3	0.00	-	-	-	-
8	GOL	A	5018	-	5,5,5	0.34	0	5,5,5	0.27	0
5	MOS	A	3004	4	0,3,3	0.00	-	-	-	-
8	GOL	B	5022	-	5,5,5	0.23	0	5,5,5	0.36	0
6	FAD	B	4005	-	51,58,58	2.95	24 (47%)	60,89,89	2.82	24 (40%)
3	FES	B	4001	1	0,4,4	0.00	-	-	-	-
7	YSH	B	5102	-	19,23,23	5.82	11 (57%)	25,33,33	3.83	5 (20%)
8	GOL	B	5021	-	5,5,5	0.27	0	5,5,5	0.39	0
8	GOL	A	5016	-	5,5,5	0.27	0	5,5,5	0.48	0
8	GOL	A	5004	-	5,5,5	0.28	0	5,5,5	0.32	0
3	FES	A	3002	1	0,4,4	0.00	-	-	-	-
8	GOL	B	5007	-	5,5,5	0.28	0	5,5,5	0.32	0
3	FES	A	3001	1	0,4,4	0.00	-	-	-	-
4	MTE	B	4003	5	21,26,26	6.02	13 (61%)	21,40,40	4.41	9 (42%)
8	GOL	A	5019	-	5,5,5	0.32	0	5,5,5	0.29	0
8	GOL	A	5006	-	5,5,5	0.24	0	5,5,5	0.41	0
8	GOL	A	5002	-	5,5,5	0.22	0	5,5,5	0.36	0
8	GOL	B	5015	-	5,5,5	0.26	0	5,5,5	0.30	0
8	GOL	B	5012	-	5,5,5	0.22	0	5,5,5	0.42	0
3	FES	B	4002	1	0,4,4	0.00	-	-	-	-
4	MTE	A	3003	5	21,26,26	6.25	13 (61%)	21,40,40	4.02	8 (38%)
8	GOL	B	5009	-	5,5,5	0.31	0	5,5,5	0.29	0
9	ACY	B	5202	-	1,3,3	1.54	0	0,3,3	0.00	-
8	GOL	B	5013	-	5,5,5	0.23	0	5,5,5	0.29	0
8	GOL	A	5005	-	5,5,5	0.31	0	5,5,5	0.34	0
8	GOL	A	5001	-	5,5,5	0.31	0	5,5,5	0.39	0
7	YSH	A	5101	-	19,23,23	5.73	10 (52%)	25,33,33	3.82	5 (20%)

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
8	GOL	A	5017	-	-	0/4/4/4	-
8	GOL	B	5014	-	-	0/4/4/4	-
8	GOL	B	5020	-	-	0/4/4/4	-
8	GOL	A	5011	-	-	0/4/4/4	-
8	GOL	A	5003	-	-	0/4/4/4	-
6	FAD	A	3005	-	-	4/30/50/50	0/6/6/6
8	GOL	B	5008	-	-	0/4/4/4	-
8	GOL	A	5018	-	-	0/4/4/4	-
8	GOL	B	5022	-	-	0/4/4/4	-
6	FAD	B	4005	-	-	2/30/50/50	0/6/6/6
3	FES	B	4001	1	-	-	0/1/1/1
7	YSH	B	5102	-	-	3/12/16/16	0/2/2/2
8	GOL	B	5021	-	-	0/4/4/4	-
8	GOL	A	5016	-	-	0/4/4/4	-
8	GOL	A	5004	-	-	0/4/4/4	-
3	FES	A	3002	1	-	-	0/1/1/1
8	GOL	B	5007	-	-	0/4/4/4	-
3	FES	A	3001	1	-	-	0/1/1/1
4	MTE	B	4003	5	-	6/6/34/34	0/3/3/3
8	GOL	A	5019	-	-	0/4/4/4	-
8	GOL	A	5006	-	-	0/4/4/4	-
8	GOL	A	5002	-	-	0/4/4/4	-
8	GOL	B	5015	-	-	0/4/4/4	-
8	GOL	B	5012	-	-	0/4/4/4	-
3	FES	B	4002	1	-	-	0/1/1/1
4	MTE	A	3003	5	-	4/6/34/34	0/3/3/3
8	GOL	B	5009	-	-	0/4/4/4	-
8	GOL	B	5013	-	-	0/4/4/4	-
8	GOL	A	5005	-	-	0/4/4/4	-
8	GOL	A	5001	-	-	0/4/4/4	-
7	YSH	A	5101	-	-	3/12/16/16	0/2/2/2

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3003	MTE	C7-C6	19.00	1.68	1.53
4	B	4003	MTE	C7-C6	18.55	1.68	1.53
7	B	5102	YSH	C1-C5	17.56	1.71	1.38
7	A	5101	YSH	C1-C5	17.30	1.71	1.38
7	B	5102	YSH	C11-C6	12.18	1.62	1.38
7	A	5101	YSH	C11-C6	12.11	1.62	1.38
4	A	3003	MTE	C9-N5	11.68	1.62	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	4003	MTE	C9-N5	11.49	1.61	1.38
4	A	3003	MTE	C9-C10	10.82	1.61	1.41
4	B	4003	MTE	C9-C10	10.80	1.61	1.41
6	A	3005	FAD	C10-N1	9.36	1.45	1.33
6	B	4005	FAD	C10-N1	8.93	1.44	1.33
7	B	5102	YSH	C10-C9	8.75	1.57	1.39
7	A	5101	YSH	C10-C9	8.52	1.57	1.39
6	B	4005	FAD	C4X-C10	7.34	1.46	1.38
6	A	3005	FAD	C9A-N10	7.21	1.48	1.38
6	B	4005	FAD	C9A-N10	7.19	1.48	1.38
6	A	3005	FAD	C4X-C10	7.06	1.45	1.38
4	B	4003	MTE	P-O4'	-6.93	1.37	1.60
4	A	3003	MTE	P-O4'	-6.77	1.38	1.60
6	B	4005	FAD	C4-N3	6.74	1.44	1.33
6	A	3005	FAD	C4-N3	6.62	1.44	1.33
4	A	3003	MTE	C6-N5	-6.52	1.36	1.45
7	A	5101	YSH	C8-C12	5.91	1.53	1.44
7	B	5102	YSH	C8-C12	5.73	1.53	1.44
4	B	4003	MTE	P-O3P	-5.05	1.35	1.54
4	A	3003	MTE	P-O3P	-4.99	1.35	1.54
6	B	4005	FAD	C4X-N5	4.88	1.40	1.33
6	B	4005	FAD	C1'-N10	4.77	1.53	1.48
6	A	3005	FAD	C4X-N5	4.63	1.39	1.33
4	B	4003	MTE	C4'-C3'	-4.51	1.45	1.52
7	B	5102	YSH	O14-C9	4.50	1.46	1.37
4	B	4003	MTE	C4-C9	4.45	1.47	1.41
4	A	3003	MTE	C4-C9	4.40	1.47	1.41
4	A	3003	MTE	C4'-C3'	-4.34	1.46	1.52
6	A	3005	FAD	C1'-N10	4.09	1.52	1.48
7	B	5102	YSH	C6-N2	4.09	1.55	1.44
7	A	5101	YSH	O14-C9	4.07	1.45	1.37
6	B	4005	FAD	C4A-N3A	4.01	1.41	1.35
7	A	5101	YSH	C6-N2	3.78	1.54	1.44
4	B	4003	MTE	C4-N3	3.78	1.39	1.33
6	A	3005	FAD	C4A-N3A	3.76	1.40	1.35
6	B	4005	FAD	O4B-C1B	3.58	1.46	1.41
4	A	3003	MTE	C4-N3	3.57	1.39	1.33
6	A	3005	FAD	O4B-C1B	3.53	1.46	1.41
7	B	5102	YSH	C7-C6	3.42	1.42	1.38
6	B	4005	FAD	C2A-N3A	3.36	1.37	1.32
4	A	3003	MTE	O4'-C4'	-3.30	1.32	1.44
6	A	3005	FAD	C2A-N3A	3.26	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	5101	YSH	C7-C6	3.25	1.42	1.38
6	B	4005	FAD	C9A-C5X	3.25	1.49	1.42
6	B	4005	FAD	C6-C7	3.07	1.45	1.37
4	B	4003	MTE	C6-N5	-3.06	1.40	1.45
6	B	4005	FAD	C9-C9A	3.04	1.46	1.40
6	B	4005	FAD	C8-C7	3.01	1.48	1.40
6	B	4005	FAD	C5X-N5	2.99	1.40	1.35
6	A	3005	FAD	C8-C7	2.98	1.48	1.40
6	A	3005	FAD	C9-C9A	2.94	1.46	1.40
6	A	3005	FAD	C6-C7	2.92	1.45	1.37
7	A	5101	YSH	C11-C10	-2.91	1.33	1.38
4	A	3003	MTE	C2-N1	2.86	1.40	1.35
6	A	3005	FAD	C2A-N1A	2.82	1.39	1.33
6	A	3005	FAD	C9A-C5X	2.80	1.48	1.42
7	B	5102	YSH	O14-C15	2.73	1.53	1.42
6	A	3005	FAD	C5X-N5	2.72	1.39	1.35
4	A	3003	MTE	O4-C4	2.72	1.31	1.24
6	B	4005	FAD	C5'-C4'	2.68	1.55	1.51
7	A	5101	YSH	O14-C15	2.66	1.53	1.42
6	B	4005	FAD	C2A-N1A	2.65	1.38	1.33
6	B	4005	FAD	C4'-C3'	2.62	1.58	1.53
6	B	4005	FAD	C2-N3	2.55	1.43	1.38
4	B	4003	MTE	O3'-C3'	2.55	1.47	1.43
6	A	3005	FAD	C2-N3	2.49	1.43	1.38
4	B	4003	MTE	C2-N1	2.43	1.39	1.35
6	B	4005	FAD	C2'-C3'	2.42	1.58	1.53
4	B	4003	MTE	O4-C4	2.42	1.30	1.24
7	B	5102	YSH	C4-N3	2.39	1.40	1.33
6	B	4005	FAD	C6-C5X	2.35	1.45	1.41
6	A	3005	FAD	C6-C5X	2.34	1.45	1.41
7	A	5101	YSH	C4-N3	2.33	1.39	1.33
6	B	4005	FAD	P-O1P	2.30	1.59	1.50
6	A	3005	FAD	PA-O1A	2.28	1.59	1.50
6	A	3005	FAD	C4'-C3'	2.28	1.57	1.53
6	A	3005	FAD	P-O1P	2.23	1.58	1.50
6	B	4005	FAD	PA-O1A	2.21	1.58	1.50
7	B	5102	YSH	C11-C10	-2.20	1.34	1.38
4	A	3003	MTE	P-O2P	-2.13	1.46	1.54
6	A	3005	FAD	C5'-C4'	2.13	1.54	1.51
4	B	4003	MTE	P-O2P	-2.12	1.46	1.54
7	B	5102	YSH	N3-N2	-2.09	1.33	1.38
6	B	4005	FAD	C8M-C8	2.04	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	4005	FAD	C9-C8	2.02	1.42	1.37

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	5102	YSH	C4-N3-N2	14.75	114.44	103.70
7	A	5101	YSH	C4-N3-N2	14.27	114.09	103.70
4	A	3003	MTE	C4-C9-N5	13.22	130.22	119.12
4	B	4003	MTE	C4-C9-N5	12.89	129.94	119.12
7	A	5101	YSH	C6-N2-N3	11.19	128.73	118.80
4	B	4003	MTE	P-O4'-C4'	11.08	148.82	118.30
6	B	4005	FAD	C1'-N10-C9A	10.83	126.81	118.29
6	A	3005	FAD	C1'-N10-C9A	10.72	126.73	118.29
7	B	5102	YSH	C6-N2-N3	10.53	128.15	118.80
6	A	3005	FAD	C4X-N5-C5X	7.94	124.71	116.77
6	B	4005	FAD	C4X-N5-C5X	7.86	124.62	116.77
6	A	3005	FAD	C4-N3-C2	7.22	121.24	115.14
6	B	4005	FAD	C4-N3-C2	7.10	121.14	115.14
6	A	3005	FAD	N3A-C2A-N1A	-7.04	117.67	128.68
6	B	4005	FAD	N3A-C2A-N1A	-6.95	117.81	128.68
4	A	3003	MTE	P-O4'-C4'	6.69	136.73	118.30
4	B	4003	MTE	C2-N1-C10	5.82	127.58	114.54
4	A	3003	MTE	C2-N1-C10	5.65	127.21	114.54
6	A	3005	FAD	C1'-N10-C10	-5.52	113.47	118.41
6	B	4005	FAD	C1'-N10-C10	-5.28	113.68	118.41
4	A	3003	MTE	C4-N3-C2	4.52	123.12	115.93
4	B	4003	MTE	N2-C2-N3	4.46	124.19	117.25
4	B	4003	MTE	C4-N3-C2	4.41	122.94	115.93
4	A	3003	MTE	N2-C2-N3	4.31	123.96	117.25
6	B	4005	FAD	O4'-C4'-C3'	4.08	119.01	109.10
6	A	3005	FAD	O4'-C4'-C3'	3.99	118.79	109.10
4	B	4003	MTE	N3-C2-N1	-3.79	119.48	125.42
4	A	3003	MTE	N3-C2-N1	-3.78	119.50	125.42
6	A	3005	FAD	C3B-C2B-C1B	3.65	106.47	100.98
6	B	4005	FAD	C3B-C2B-C1B	3.50	106.25	100.98
4	B	4003	MTE	O3'-C7-C6	-3.48	106.64	108.96
4	A	3003	MTE	O3'-C7-C6	-3.36	106.73	108.96
6	A	3005	FAD	C5'-C4'-C3'	-3.31	105.80	112.20
6	B	4005	FAD	C4-C4X-N5	3.31	122.38	118.60
4	A	3003	MTE	O3'-C7-N8	-3.29	105.19	108.57
6	A	3005	FAD	C4-C4X-N5	3.19	122.24	118.60
6	B	4005	FAD	C5'-C4'-C3'	-3.13	106.15	112.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	3005	FAD	O3'-C3'-C4'	2.82	115.62	108.81
6	B	4005	FAD	C10-C4X-N5	-2.80	119.32	121.26
6	A	3005	FAD	C10-C4X-N5	-2.62	119.45	121.26
6	A	3005	FAD	O2'-C2'-C1'	2.52	115.66	109.59
6	A	3005	FAD	O3B-C3B-C4B	-2.51	103.80	111.05
6	B	4005	FAD	O3B-C3B-C4B	-2.50	103.81	111.05
6	B	4005	FAD	C4-C4X-C10	-2.50	118.29	119.95
6	B	4005	FAD	O2'-C2'-C1'	2.50	115.61	109.59
6	B	4005	FAD	O3'-C3'-C4'	2.49	114.83	108.81
6	A	3005	FAD	C4-C4X-C10	-2.47	118.31	119.95
6	A	3005	FAD	C8M-C8-C7	2.46	125.77	120.74
7	B	5102	YSH	C7-C6-N2	-2.45	115.94	119.07
6	B	4005	FAD	O2B-C2B-C3B	2.45	119.74	111.82
6	B	4005	FAD	C2A-N1A-C6A	2.42	122.90	118.75
6	A	3005	FAD	C2A-N1A-C6A	2.42	122.90	118.75
6	A	3005	FAD	O5B-PA-O1A	2.41	118.47	109.07
4	B	4003	MTE	O3'-C7-N8	-2.40	106.10	108.57
6	A	3005	FAD	C8M-C8-C9	-2.36	114.71	120.34
7	A	5101	YSH	C1-C5-C4	2.34	112.35	105.21
6	A	3005	FAD	C9A-C5X-N5	-2.34	118.70	122.36
6	B	4005	FAD	C8M-C8-C7	2.34	125.52	120.74
6	B	4005	FAD	C8M-C8-C9	-2.31	114.81	120.34
6	A	3005	FAD	O2B-C2B-C3B	2.30	119.27	111.82
6	B	4005	FAD	C9A-C5X-N5	-2.27	118.80	122.36
6	B	4005	FAD	C4X-C4-N3	-2.26	120.35	123.43
6	B	4005	FAD	O5B-PA-O1A	2.24	117.83	109.07
4	B	4003	MTE	O2P-P-O4'	2.23	112.66	106.73
7	B	5102	YSH	C1-C5-C4	2.20	111.94	105.21
6	A	3005	FAD	C4X-C4-N3	-2.19	120.44	123.43
7	A	5101	YSH	C10-C11-C6	-2.18	115.90	119.07
6	A	3005	FAD	O5'-P-O1P	2.15	117.45	109.07
7	A	5101	YSH	C7-C6-N2	-2.14	116.35	119.07
6	A	3005	FAD	O2'-C2'-C3'	2.10	114.21	109.10
6	A	3005	FAD	C7M-C7-C6	-2.09	115.34	120.34
7	B	5102	YSH	C10-C11-C6	-2.09	116.03	119.07
6	B	4005	FAD	O5'-P-O1P	2.06	117.13	109.07
6	B	4005	FAD	C1B-N9A-C4A	-2.02	123.10	126.64
6	B	4005	FAD	O2'-C2'-C3'	2.02	114.00	109.10

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	3005	FAD	N10-C1'-C2'-O2'
6	A	3005	FAD	N10-C1'-C2'-C3'
6	B	4005	FAD	N10-C1'-C2'-O2'
6	B	4005	FAD	N10-C1'-C2'-C3'
7	B	5102	YSH	N13-C12-C8-C9
4	B	4003	MTE	C2'-C3'-C4'-O4'
4	B	4003	MTE	O3'-C3'-C4'-O4'
4	B	4003	MTE	C3'-C4'-O4'-P
4	B	4003	MTE	C4'-O4'-P-O2P
4	B	4003	MTE	C4'-O4'-P-O3P
4	A	3003	MTE	C4'-O4'-P-O2P
4	A	3003	MTE	C4'-O4'-P-O3P
7	A	5101	YSH	N13-C12-C8-C9
7	A	5101	YSH	C7-C6-N2-C1
7	A	5101	YSH	C11-C6-N2-C1
4	B	4003	MTE	C4'-O4'-P-O1P
4	A	3003	MTE	C4'-O4'-P-O1P
7	B	5102	YSH	C7-C6-N2-C1
6	A	3005	FAD	C2'-C3'-C4'-O4'
4	A	3003	MTE	C3'-C4'-O4'-P
7	B	5102	YSH	C11-C6-N2-C1
6	A	3005	FAD	O3'-C3'-C4'-O4'

There are no ring outliers.

21 monomers are involved in 43 short contacts:

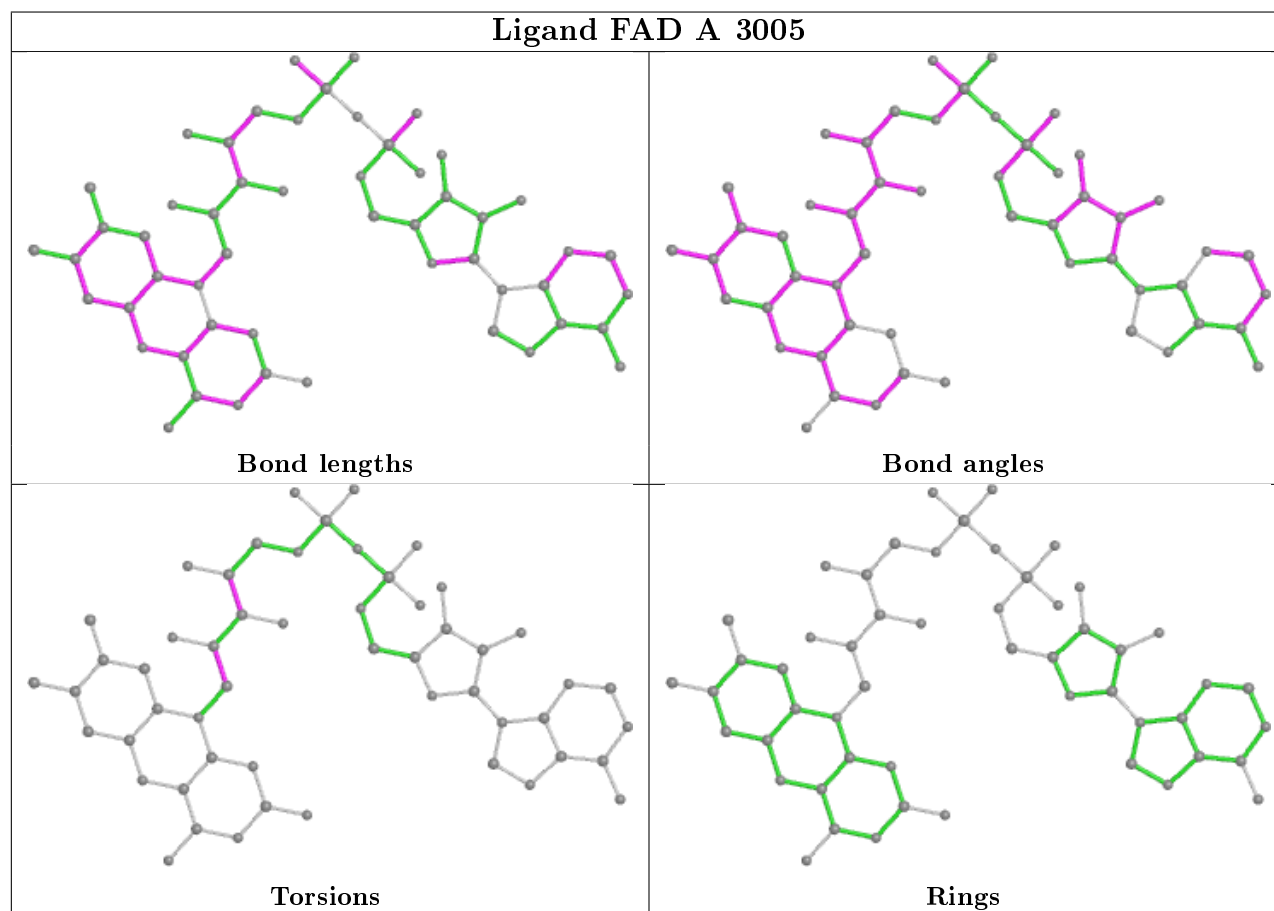
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	5014	GOL	2	0
8	B	5020	GOL	1	0
8	A	5011	GOL	2	0
6	A	3005	FAD	4	0
9	A	5201	ACY	4	0
8	B	5008	GOL	2	0
5	B	4004	MOS	2	0
5	A	3004	MOS	1	0
8	B	5022	GOL	2	0
6	B	4005	FAD	3	0
7	B	5102	YSH	3	0
3	A	3002	FES	1	0
4	B	4003	MTE	1	0
8	A	5019	GOL	1	0
8	A	5006	GOL	2	0
8	A	5002	GOL	2	0

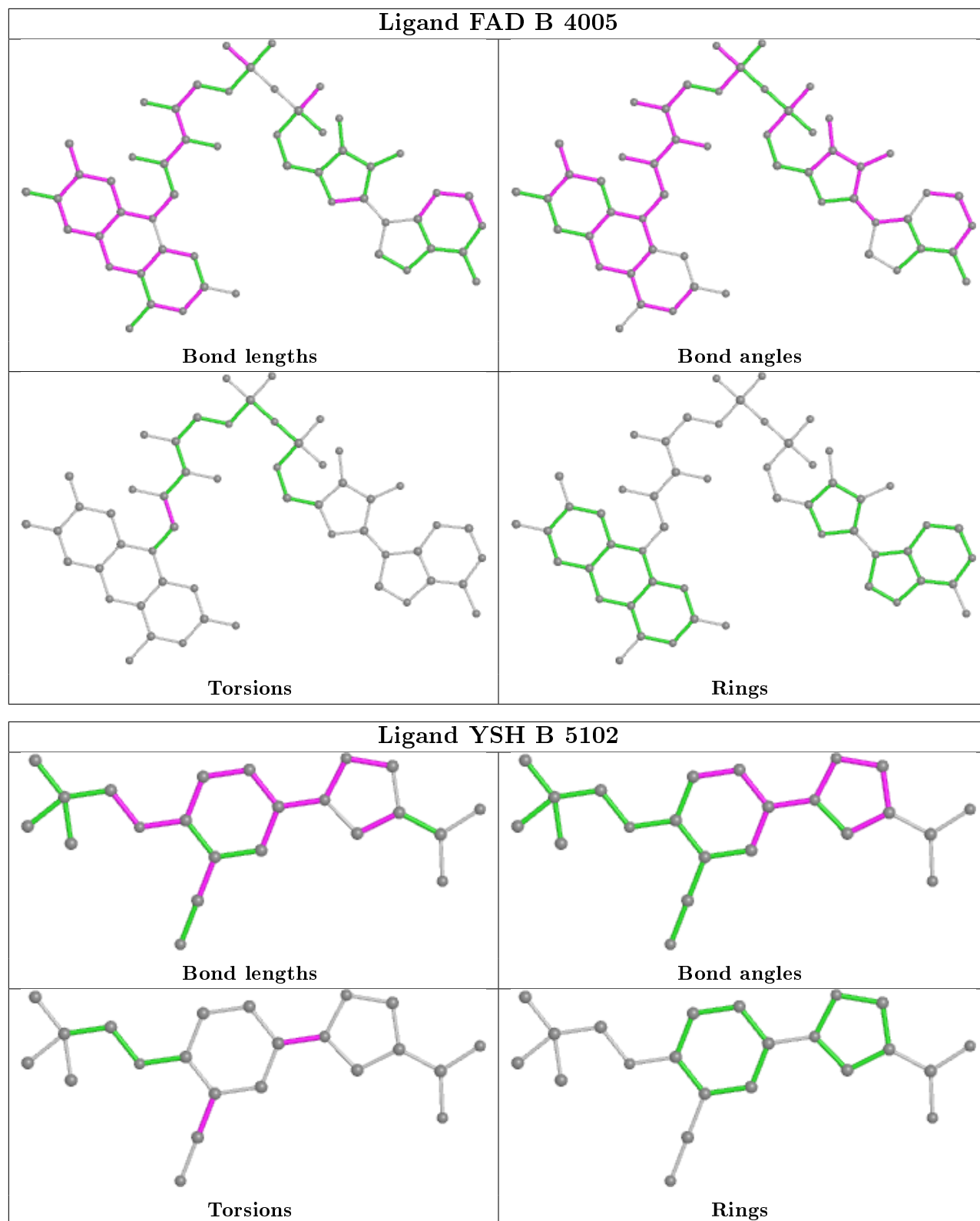
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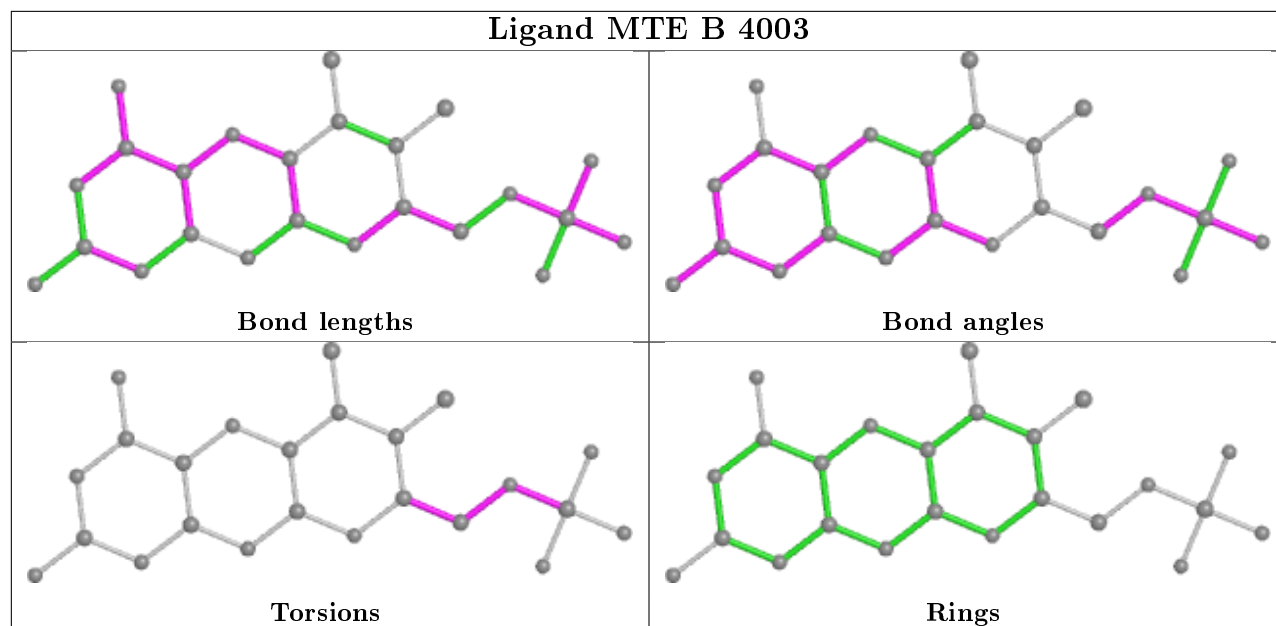
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3003	MTE	1	0
9	B	5202	ACY	4	0
8	B	5013	GOL	1	0
8	A	5001	GOL	1	0
7	A	5101	YSH	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

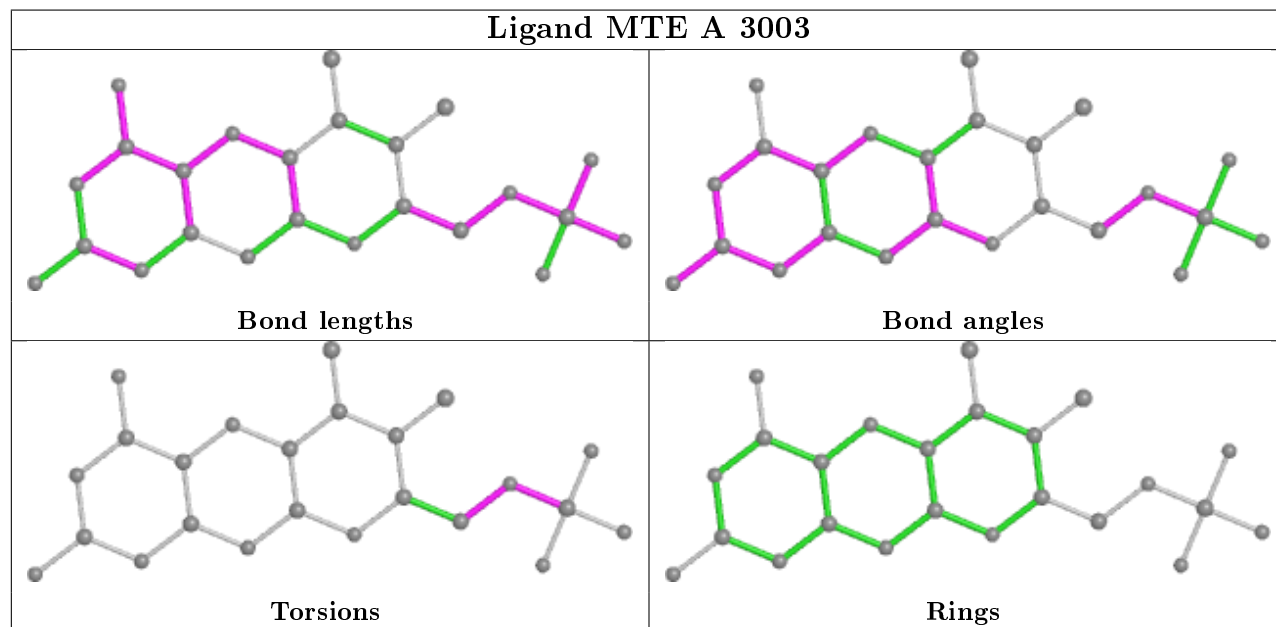


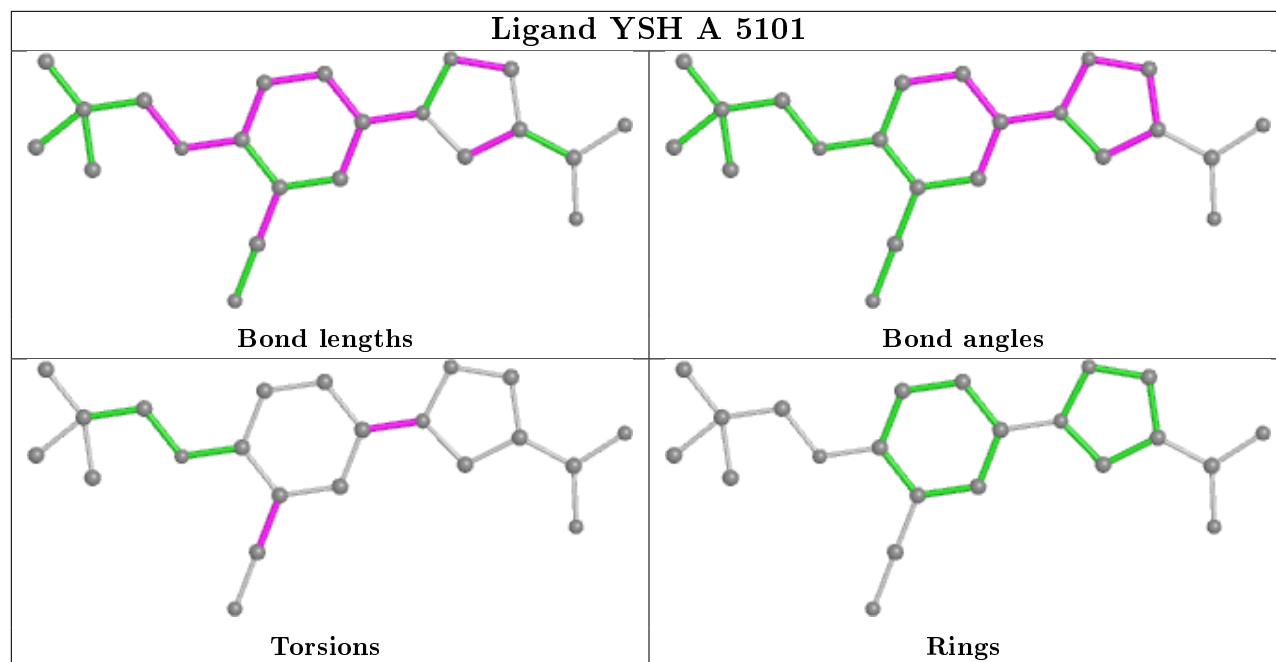


Ligand MTE B 4003



Ligand MTE A 3003





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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.