Full wwPDB X-ray Structure Validation Report (i)

May 29, 2020 – 08:39 am BST

PDB ID	:	1IVH
Title	:	STRUCTURE OF HUMAN ISOVALERYL-COA DEHYDROGENASE AT 2.6 ANGSTROMS RESOLUTION: STRUCTURAL BASIS FOR SUBSTRATE SPECIFICITY
Authors	:	Tiffany, K.A.; Roberts, D.L.; Wang, M.; Paschke, R.; Mohsen, A.-W.A.; Vockley, J.; Kim, J.J.P.
Deposited on	:	1997-05-15
Resolution	:	2.60 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

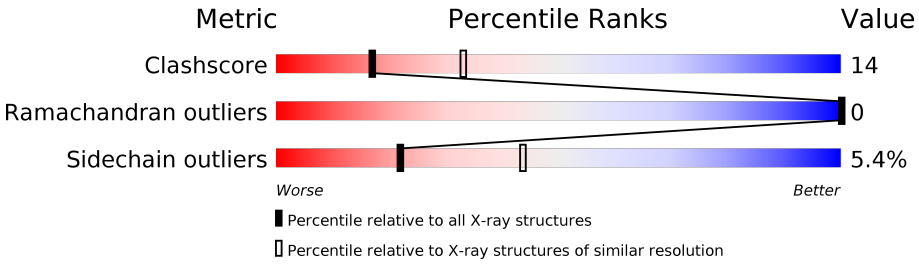
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA,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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	394	69% 26%
1	B	394	68% 28%
1	C	394	68% 30%
1	D	394	67% 30%

2 Entry composition

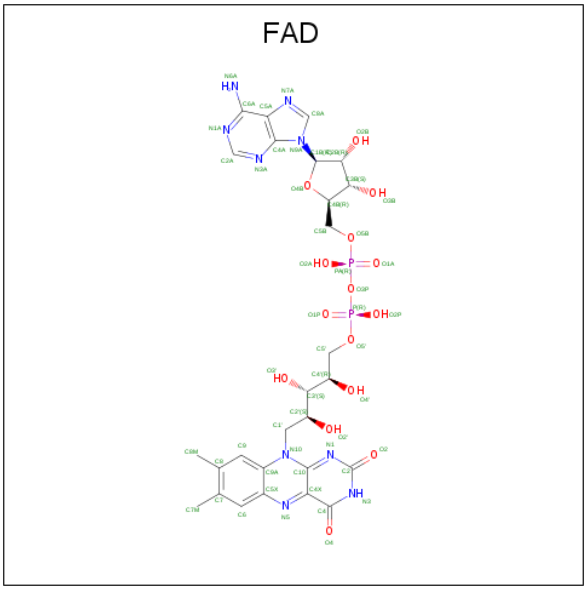
There are 4 unique types of molecules in this entry. The entry contains 12463 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ISOVALERYL-COA DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	0
			2960	1868	518	552	22			
1	B	387	Total	C	N	O	S	0	0	0
			2960	1868	518	552	22			
1	C	387	Total	C	N	O	S	0	0	0
			2960	1868	518	552	22			
1	D	387	Total	C	N	O	S	0	0	0
			2960	1868	518	552	22			

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



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

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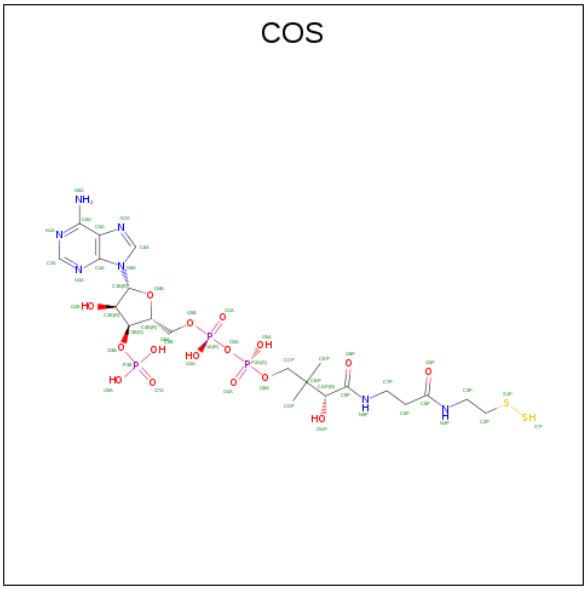
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is COENZYME A PERSULFIDE (three-letter code: COS) (formula: $C_{21}H_{36}N_7O_{16}P_3S_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		
3	B	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		
3	C	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		
3	D	1	Total	C	N	O	P	S	0	0
			49	21	7	16	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	50	Total	O	0	0
			50	50		
4	B	53	Total	O	0	0
			53	53		
4	C	51	Total	O	0	0
			51	51		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	61	Total O 61 61	0	0

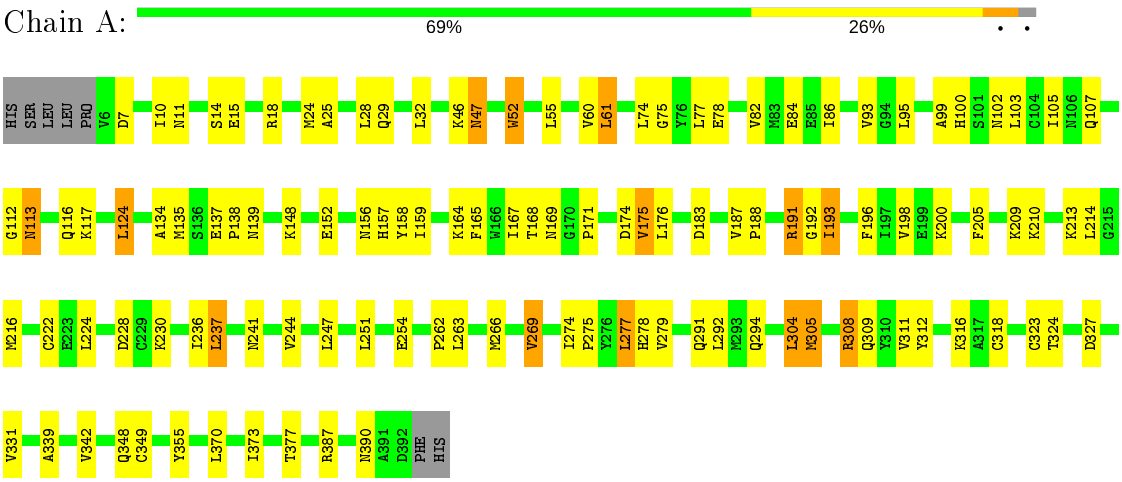
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

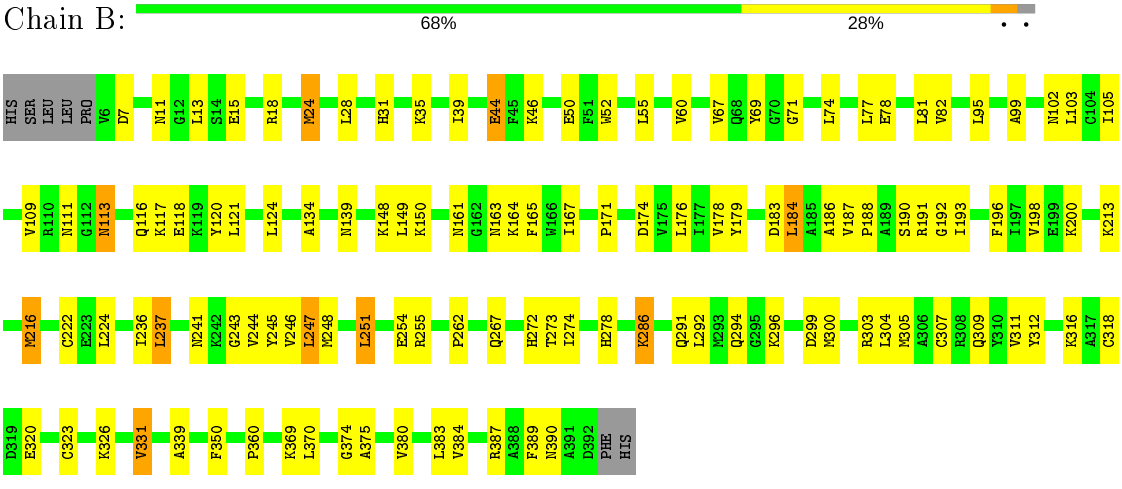
- Molecule 1: ISOVALERYL-COA DEHYDROGENASE

Chain A:



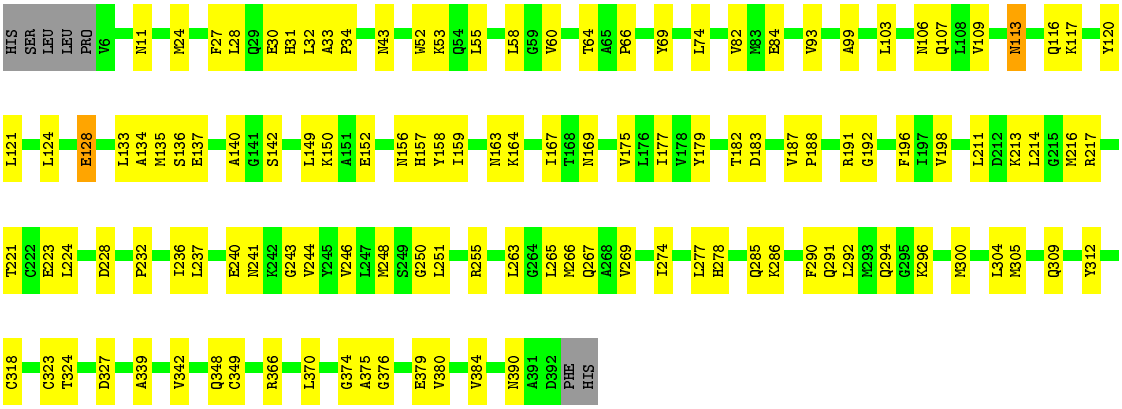
- Molecule 1: ISOVALERYL-COA DEHYDROGENASE

Chain B:



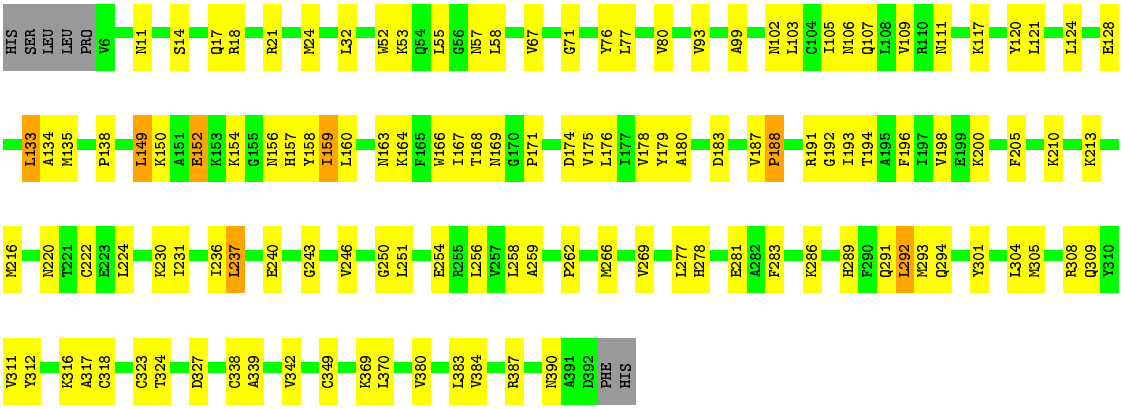
- Molecule 1: ISOVALERYL-COA DEHYDROGENASE

Chain C:



- Molecule 1: ISOVALERYL-COA DEHYDROGENASE

Chain D:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	94.00Å 97.70Å 181.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	82.5 (10.00-2.60)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.207 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12463	wwPDB-VP
Average B, all atoms (Å^2)	11.0	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: COS, 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	0.41	0/3011	0.62	0/4056
1	B	0.41	0/3011	0.62	1/4056 (0.0%)
1	C	0.40	0/3011	0.62	0/4056
1	D	0.41	0/3011	0.62	1/4056 (0.0%)
All	All	0.41	0/12044	0.62	2/16224 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	247	LEU	CA-CB-CG	6.51	130.27	115.30
1	D	188	PRO	N-CA-C	-5.01	99.06	112.10

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	2960	0	2964	86	0
1	B	2960	0	2964	85	0
1	C	2960	0	2964	92	0
1	D	2960	0	2964	92	0
2	A	53	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	53	0	31	0	0
2	C	53	0	31	0	0
2	D	53	0	31	1	0
3	A	49	0	32	1	0
3	B	49	0	32	0	0
3	C	49	0	32	3	0
3	D	49	0	32	2	0
4	A	50	0	0	0	0
4	B	53	0	0	1	0
4	C	51	0	0	3	0
4	D	61	0	0	2	0
All	All	12463	0	12108	336	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 14.

All (336) 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:B:187:VAL:HB	1:B:188:PRO:HD3	1.37	1.06
1:D:187:VAL:HB	1:D:188:PRO:HD3	1.39	1.04
1:A:187:VAL:HB	1:A:188:PRO:HD3	1.40	1.02
1:C:187:VAL:HB	1:C:188:PRO:HD3	1.41	1.00
1:C:124:LEU:HD21	1:C:175:VAL:HG11	1.48	0.95
1:B:188:PRO:HD2	1:B:191:ARG:HG3	1.52	0.90
1:A:74:LEU:HB3	1:A:78:GLU:HG3	1.53	0.89
1:D:124:LEU:HD21	1:D:175:VAL:HG11	1.53	0.88
1:D:216:MET:HG3	1:D:370:LEU:HD22	1.56	0.88
1:B:318:CYS:HG	1:B:323:CYS:HG	1.05	0.83
1:C:107:GLN:HE22	1:C:250:GLY:HA3	1.45	0.81
1:A:77:LEU:HD22	1:A:316:LYS:HG2	1.65	0.79
1:D:133:LEU:HD21	1:D:135:MET:HE2	1.64	0.78
1:B:291:GLN:HB2	1:D:291:GLN:HB2	1.66	0.78
1:D:171:PRO:HD3	1:D:222:CYS:SG	2.24	0.78
1:D:210:LYS:HE2	1:D:220:ASN:OD1	1.84	0.78
1:C:164:LYS:HB2	1:C:224:LEU:HB2	1.66	0.77
1:A:171:PRO:HD3	1:A:222:CYS:SG	2.25	0.76
1:A:124:LEU:HD21	1:A:175:VAL:HG11	1.68	0.76
1:D:277:LEU:HD11	1:D:349:CYS:HB3	1.68	0.75
1:A:157:HIS:ND1	1:A:230:LYS:HG2	2.02	0.74
1:D:53:LYS:HE3	1:D:128:GLU:HG2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LEU:HB2	1:A:198:VAL:HG22	1.70	0.73
1:B:311:VAL:HG22	1:B:331:VAL:HG13	1.69	0.73
1:D:187:VAL:HB	1:D:188:PRO:CD	2.17	0.73
1:C:99:ALA:HA	1:C:103:LEU:HG	1.71	0.73
1:D:191:ARG:HD3	4:D:684:HOH:O	1.90	0.72
1:B:187:VAL:HB	1:B:188:PRO:CD	2.18	0.71
1:B:318:CYS:CB	1:B:323:CYS:HG	2.02	0.71
1:D:196:PHE:CE1	1:D:236:ILE:HG22	2.26	0.71
1:D:188:PRO:HG2	1:D:191:ARG:HE	1.56	0.71
1:B:102:ASN:HD21	1:B:254:GLU:HA	1.54	0.71
1:D:149:LEU:HD12	1:D:164:LYS:HE2	1.72	0.71
1:C:318:CYS:CB	1:C:323:CYS:SG	2.79	0.70
1:B:164:LYS:HB2	1:B:224:LEU:HB2	1.73	0.70
1:D:198:VAL:HG12	1:D:231:ILE:HD11	1.72	0.70
1:D:269:VAL:HG21	1:D:342:VAL:HG12	1.74	0.70
1:B:318:CYS:CB	1:B:323:CYS:SG	2.79	0.70
1:B:318:CYS:HB3	1:B:323:CYS:SG	2.32	0.70
1:D:286:LYS:HB2	1:D:289:HIS:HD2	1.57	0.69
1:A:188:PRO:O	1:A:191:ARG:HG2	1.93	0.69
1:B:113:ASN:ND2	1:B:116:GLN:H	1.92	0.68
1:C:66:PRO:HG2	1:C:69:TYR:HD2	1.59	0.68
1:C:216:MET:HG3	1:C:370:LEU:HD22	1.75	0.68
1:B:278:HIS:HE1	1:C:390:ASN:HA	1.57	0.68
1:C:277:LEU:HD11	1:C:349:CYS:HB3	1.75	0.68
1:D:305:MET:O	1:D:309:GLN:HG2	1.94	0.67
1:A:216:MET:HG3	1:A:370:LEU:HD22	1.75	0.67
1:B:102:ASN:ND2	1:B:254:GLU:HA	2.09	0.67
1:D:188:PRO:HD2	1:D:191:ARG:HG3	1.76	0.67
1:B:99:ALA:HA	1:B:103:LEU:HG	1.75	0.67
1:B:67:VAL:HA	1:B:71:GLY:O	1.95	0.67
1:B:176:LEU:HB2	1:B:198:VAL:HG22	1.76	0.67
1:C:11:ASN:HB3	1:C:312:TYR:CD2	2.31	0.66
1:D:205:PHE:HE1	1:D:224:LEU:HG	1.60	0.66
1:C:183:ASP:HB3	1:C:192:GLY:HA2	1.77	0.66
1:D:164:LYS:HB2	1:D:224:LEU:HB2	1.79	0.65
1:C:274:ILE:O	1:C:278:HIS:HD2	1.79	0.65
1:B:95:LEU:HD22	1:B:216:MET:HG2	1.78	0.65
1:A:187:VAL:HB	1:A:188:PRO:CD	2.23	0.65
1:A:103:LEU:HD21	1:A:254:GLU:HG3	1.80	0.64
1:A:188:PRO:HD2	1:A:191:ARG:HG3	1.78	0.64
1:D:133:LEU:HD21	1:D:135:MET:CE	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:SER:O	1:A:18:ARG:HG3	1.98	0.64
1:C:318:CYS:HG	1:C:323:CYS:HG	0.65	0.63
1:B:116:GLN:O	1:B:120:TYR:HD1	1.81	0.63
1:C:84:GLU:HG3	1:C:263:LEU:HB3	1.79	0.63
1:C:318:CYS:CB	1:C:323:CYS:HG	2.12	0.62
1:D:196:PHE:CD1	1:D:236:ILE:HG22	2.34	0.62
1:C:196:PHE:CE1	1:C:236:ILE:HG22	2.33	0.62
1:D:150:LYS:HE2	1:D:152:GLU:HG2	1.81	0.62
1:D:138:PRO:HG2	1:D:163:ASN:HD21	1.63	0.61
1:C:53:LYS:NZ	1:C:128:GLU:HG3	2.15	0.61
1:A:113:ASN:ND2	1:A:116:GLN:H	1.97	0.61
1:C:66:PRO:HG2	1:C:69:TYR:CD2	2.35	0.61
1:D:198:VAL:HG12	1:D:231:ILE:CD1	2.31	0.61
1:B:171:PRO:HD3	1:B:222:CYS:SG	2.40	0.61
1:A:102:ASN:ND2	1:A:254:GLU:HA	2.16	0.61
1:C:188:PRO:HG2	1:C:191:ARG:HH11	1.64	0.60
1:B:139:ASN:HB2	1:B:148:LYS:HZ1	1.67	0.60
1:B:305:MET:O	1:B:309:GLN:HG2	2.02	0.60
1:C:188:PRO:HD2	1:C:191:ARG:HD2	1.81	0.60
1:A:55:LEU:HB3	1:A:61:LEU:HD13	1.82	0.60
1:C:318:CYS:HB3	1:C:323:CYS:SG	2.41	0.60
1:C:117:LYS:O	1:C:121:LEU:HB2	2.02	0.60
1:D:176:LEU:HB2	1:D:198:VAL:HG22	1.84	0.59
1:B:139:ASN:HB2	1:B:148:LYS:NZ	2.17	0.59
1:B:278:HIS:CE1	1:C:390:ASN:HA	2.36	0.59
1:A:205:PHE:HE1	1:A:224:LEU:HG	1.66	0.59
1:D:107:GLN:HE22	1:D:250:GLY:HA3	1.67	0.59
1:B:69:TYR:HE1	1:B:118:GLU:HG2	1.68	0.59
1:C:187:VAL:HB	1:C:188:PRO:CD	2.25	0.58
1:C:157:HIS:HD2	1:C:232:PRO:HA	1.67	0.58
1:C:192:GLY:HA2	1:C:241:ASN:HD22	1.68	0.58
1:B:179:TYR:HB3	1:B:193:ILE:HD11	1.83	0.58
1:D:318:CYS:CB	1:D:323:CYS:HG	2.16	0.58
1:C:159:ILE:HG23	1:C:228:ASP:HA	1.85	0.58
1:A:15:GLU:HA	1:A:18:ARG:HD2	1.85	0.58
1:C:106:ASN:O	1:C:109:VAL:HG22	2.03	0.58
1:A:305:MET:O	1:A:309:GLN:HG2	2.03	0.58
1:B:113:ASN:HD21	1:B:116:GLN:HG3	1.68	0.58
1:D:32:LEU:HD11	1:D:93:VAL:HG21	1.85	0.57
1:A:318:CYS:CB	1:A:323:CYS:SG	2.92	0.57
1:A:84:GLU:HG3	1:A:263:LEU:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:VAL:CB	1:D:188:PRO:HD3	2.27	0.57
1:D:77:LEU:HD22	1:D:316:LYS:HG2	1.86	0.57
1:D:338:CYS:O	1:D:342:VAL:HG23	2.05	0.57
1:B:274:ILE:O	1:B:278:HIS:HD2	1.88	0.57
1:C:296:LYS:O	1:C:300:MET:HG2	2.05	0.56
1:D:120:TYR:O	1:D:124:LEU:HD23	2.04	0.56
1:C:267:GLN:HG2	4:C:519:HOH:O	2.04	0.56
1:C:30:GLU:HG3	1:C:31:HIS:ND1	2.20	0.56
1:C:187:VAL:CB	1:C:188:PRO:HD3	2.27	0.56
1:D:243:GLY:O	1:D:246:VAL:HG22	2.05	0.56
1:D:380:VAL:O	1:D:384:VAL:HG23	2.06	0.56
1:D:24:MET:CE	1:D:58:LEU:HD13	2.35	0.56
1:A:387:ARG:HA	1:A:390:ASN:HD22	1.71	0.56
1:B:134:ALA:HA	1:B:167:ILE:HD12	1.87	0.56
1:C:24:MET:O	1:C:28:LEU:HD23	2.05	0.56
3:C:400:COS:H32	4:C:587:HOH:O	2.06	0.56
1:B:117:LYS:O	1:B:121:LEU:HB2	2.06	0.55
1:B:149:LEU:HD12	1:B:164:LYS:HE2	1.88	0.55
1:B:383:LEU:O	1:B:387:ARG:HG3	2.06	0.55
1:D:266:MET:O	1:D:269:VAL:HG22	2.07	0.55
1:B:111:ASN:HB2	1:B:237:LEU:HD22	1.89	0.55
1:C:134:ALA:HA	1:C:167:ILE:HD12	1.89	0.55
1:D:24:MET:HE3	1:D:58:LEU:HD13	1.88	0.55
1:B:196:PHE:CD2	1:B:236:ILE:HG22	2.42	0.55
1:D:67:VAL:HA	1:D:71:GLY:O	2.07	0.55
1:D:102:ASN:ND2	1:D:254:GLU:HA	2.22	0.55
1:D:324:THR:OG1	1:D:327:ASP:HB2	2.07	0.55
1:B:251:LEU:O	1:B:255:ARG:HG3	2.08	0.54
1:C:163:ASN:HB2	1:C:224:LEU:O	2.06	0.54
1:A:188:PRO:HD2	1:A:191:ARG:CG	2.38	0.54
1:C:24:MET:CE	1:C:58:LEU:HD13	2.36	0.54
1:A:278:HIS:HE1	1:D:390:ASN:OD1	1.90	0.54
1:A:135:MET:SD	1:A:247:LEU:HD11	2.47	0.54
1:C:113:ASN:ND2	1:C:116:GLN:H	2.06	0.54
1:B:120:TYR:O	1:B:124:LEU:HD23	2.08	0.54
1:C:380:VAL:O	1:C:384:VAL:HG23	2.08	0.54
1:D:99:ALA:O	1:D:103:LEU:HB2	2.07	0.54
1:A:95:LEU:HD22	1:A:216:MET:HE3	1.90	0.53
1:A:102:ASN:HD21	1:A:254:GLU:HA	1.73	0.53
1:C:137:GLU:HB2	1:C:140:ALA:HB3	1.90	0.53
1:B:291:GLN:HB3	1:D:292:LEU:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:274:ILE:O	1:C:278:HIS:CD2	2.60	0.53
1:D:179:TYR:HB3	1:D:193:ILE:HD11	1.90	0.53
1:D:111:ASN:HB2	1:D:237:LEU:HD22	1.90	0.53
1:D:183:ASP:HB3	1:D:192:GLY:HA2	1.90	0.53
1:A:75:GLY:O	1:A:78:GLU:HG2	2.09	0.53
1:A:275:PRO:O	1:A:279:VAL:HG23	2.09	0.52
1:A:311:VAL:HG22	1:A:331:VAL:HB	1.91	0.52
1:D:11:ASN:HB3	1:D:312:TYR:CD2	2.44	0.52
1:A:10:ILE:HG13	1:D:317:ALA:CB	2.39	0.52
1:A:113:ASN:HD21	1:A:116:GLN:HG3	1.74	0.52
1:D:134:ALA:HB3	1:D:178:VAL:HG22	1.90	0.52
1:D:254:GLU:O	1:D:258:LEU:HB2	2.10	0.52
1:D:387:ARG:HH12	3:D:400:COS:H122	1.74	0.52
1:A:32:LEU:HD11	1:A:93:VAL:HG21	1.90	0.52
1:C:53:LYS:HZ2	1:C:128:GLU:HG3	1.74	0.52
1:A:11:ASN:HB3	1:A:312:TYR:CD2	2.45	0.52
1:B:109:VAL:HG12	1:B:121:LEU:HD11	1.91	0.52
1:B:163:ASN:HB2	1:B:224:LEU:O	2.09	0.52
1:B:383:LEU:HD21	1:C:291:GLN:HG2	1.92	0.52
1:C:244:VAL:O	1:C:248:MET:HG2	2.09	0.52
1:A:304:LEU:HD11	1:A:308:ARG:NH2	2.25	0.51
1:A:112:GLY:O	1:A:117:LYS:HE3	2.11	0.51
1:D:318:CYS:CB	1:D:323:CYS:SG	2.97	0.51
1:B:150:LYS:HG3	1:B:184:LEU:HD11	1.92	0.51
1:C:188:PRO:HG2	1:C:191:ARG:NH1	2.24	0.51
1:B:11:ASN:HB3	1:B:312:TYR:CD2	2.45	0.51
1:D:17:GLN:HE22	1:D:77:LEU:HD23	1.74	0.51
1:C:192:GLY:HA2	1:C:241:ASN:ND2	2.24	0.51
1:C:11:ASN:HB3	1:C:312:TYR:CE2	2.45	0.51
1:D:11:ASN:ND2	1:D:308:ARG:HG2	2.25	0.51
1:D:152:GLU:O	1:D:158:TYR:HA	2.11	0.51
1:A:192:GLY:HA2	1:A:241:ASN:ND2	2.25	0.51
1:A:24:MET:SD	1:A:60:VAL:HG11	2.50	0.51
1:A:99:ALA:HA	1:A:103:LEU:HG	1.93	0.51
1:B:74:LEU:HD13	1:B:78:GLU:HG2	1.92	0.50
1:C:11:ASN:HB3	1:C:312:TYR:HD2	1.75	0.50
1:D:160:LEU:HD11	1:D:231:ILE:HD12	1.92	0.50
1:D:339:ALA:HB3	4:D:707:HOH:O	2.11	0.50
1:C:149:LEU:HD12	1:C:164:LYS:HE2	1.93	0.50
1:C:348:GLN:HE21	1:D:369:LYS:NZ	2.10	0.50
1:D:134:ALA:HA	1:D:167:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:GLU:HB3	1:A:138:PRO:HD2	1.94	0.49
1:B:77:LEU:HD22	1:B:316:LYS:HG2	1.94	0.49
1:C:43:ASN:HB2	1:C:217:ARG:NH2	2.27	0.49
1:C:269:VAL:HG21	1:C:342:VAL:HG12	1.93	0.49
1:A:387:ARG:HH12	3:A:400:COS:H122	1.76	0.49
1:D:14:SER:O	1:D:18:ARG:HG3	2.12	0.49
1:A:28:LEU:HD13	1:A:86:ILE:HA	1.95	0.49
1:C:113:ASN:HD22	1:C:113:ASN:C	2.16	0.49
1:A:318:CYS:CB	1:A:323:CYS:HG	2.25	0.49
1:D:174:ASP:HA	1:D:200:LYS:HB2	1.95	0.49
1:B:183:ASP:HB3	1:B:192:GLY:HA2	1.95	0.49
1:C:216:MET:HG3	1:C:370:LEU:CD2	2.41	0.48
1:A:390:ASN:HD21	1:D:294:GLN:HE21	1.61	0.48
1:A:112:GLY:HA2	1:A:116:GLN:OE1	2.13	0.48
1:B:35:LYS:O	1:B:39:ILE:HG13	2.12	0.48
1:C:265:LEU:O	1:C:269:VAL:HG13	2.14	0.48
1:D:194:THR:HG23	1:D:240:GLU:HA	1.96	0.48
1:A:291:GLN:HB2	1:C:291:GLN:HB2	1.96	0.48
1:C:374:GLY:O	1:C:375:ALA:HB3	2.14	0.48
1:A:164:LYS:HB2	1:A:224:LEU:HB2	1.95	0.47
1:A:188:PRO:HG2	1:A:191:ARG:NH1	2.29	0.47
1:D:256:LEU:HD22	1:D:318:CYS:SG	2.53	0.47
1:A:152:GLU:O	1:A:158:TYR:HA	2.14	0.47
1:A:138:PRO:HD3	1:A:165:PHE:HB2	1.95	0.47
1:A:55:LEU:HD23	1:A:61:LEU:HD11	1.97	0.47
1:B:113:ASN:HD21	1:B:116:GLN:H	1.61	0.47
1:A:11:ASN:HB3	1:A:312:TYR:HD2	1.79	0.47
1:B:149:LEU:HD23	1:B:161:ASN:O	2.14	0.47
1:C:324:THR:OG1	1:C:327:ASP:HB2	2.14	0.47
1:D:105:ILE:O	1:D:109:VAL:HG13	2.15	0.47
1:B:294:GLN:HE21	1:C:390:ASN:ND2	2.12	0.47
1:B:174:ASP:HA	1:B:200:LYS:HB2	1.96	0.47
1:B:390:ASN:OD1	1:C:278:HIS:HE1	1.97	0.47
1:D:213:LYS:HB2	1:D:213:LYS:HE3	1.76	0.47
1:C:305:MET:O	1:C:309:GLN:HG2	2.15	0.47
1:D:281:GLU:HG2	1:D:286:LYS:HA	1.96	0.47
1:B:44:GLU:OE1	1:B:46:LYS:HE3	2.14	0.46
1:C:240:GLU:HG2	1:C:241:ASN:OD1	2.15	0.46
1:D:154:LYS:CG	1:D:159:ILE:HG13	2.45	0.46
1:A:52:TRP:NE1	1:A:100:HIS:ND1	2.59	0.46
1:B:113:ASN:HD22	1:B:113:ASN:C	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:LYS:HD3	1:C:152:GLU:CD	2.35	0.46
1:C:60:VAL:HB	1:C:82:VAL:HG11	1.98	0.46
1:B:267:GLN:HG2	4:B:637:HOH:O	2.16	0.46
1:A:274:ILE:O	1:A:278:HIS:HD2	1.98	0.46
1:C:266:MET:CG	1:C:339:ALA:HA	2.46	0.46
1:B:190:SER:HB2	1:B:244:VAL:HG21	1.97	0.46
1:B:24:MET:O	1:B:28:LEU:HD23	2.15	0.46
1:C:32:LEU:HD11	1:C:93:VAL:HG21	1.98	0.46
1:B:244:VAL:O	1:B:248:MET:HG2	2.15	0.46
1:A:134:ALA:HB2	1:A:167:ILE:HG12	1.97	0.45
1:A:95:LEU:HB2	1:A:216:MET:HE3	1.99	0.45
1:C:133:LEU:HD12	1:C:177:ILE:HB	1.98	0.45
1:C:213:LYS:HB2	1:C:213:LYS:HE3	1.77	0.45
1:A:294:GLN:NE2	1:D:383:LEU:HD23	2.30	0.45
1:B:15:GLU:HA	1:B:18:ARG:HD2	1.98	0.45
1:B:296:LYS:O	1:B:300:MET:HG3	2.16	0.45
1:B:262:PRO:HB3	1:B:339:ALA:HB2	1.98	0.45
1:D:259:ALA:HB3	1:D:311:VAL:HG21	1.98	0.45
1:B:186:ALA:HB1	1:B:191:ARG:HB2	1.99	0.45
1:B:192:GLY:HA2	1:B:241:ASN:HD22	1.81	0.45
3:C:400:COS:H133	1:D:283:PHE:CZ	2.53	0.44
3:C:400:COS:H133	1:D:283:PHE:HZ	1.81	0.44
1:C:379:GLU:HG2	1:D:293:MET:CE	2.47	0.44
1:A:278:HIS:CE1	1:D:390:ASN:HA	2.53	0.44
1:C:196:PHE:CD1	1:C:236:ILE:HG22	2.53	0.44
1:C:376:GLY:N	4:C:587:HOH:O	2.51	0.44
1:D:168:THR:O	1:D:169:ASN:HB2	2.18	0.44
1:A:318:CYS:HA	1:A:323:CYS:SG	2.58	0.44
1:B:243:GLY:O	1:B:246:VAL:HG22	2.18	0.44
1:C:243:GLY:O	1:C:246:VAL:HG22	2.17	0.44
1:D:103:LEU:HD21	1:D:254:GLU:HG3	2.00	0.44
1:B:11:ASN:HB3	1:B:312:TYR:HD2	1.82	0.44
1:B:31:HIS:O	1:B:35:LYS:HE2	2.18	0.44
1:C:348:GLN:HE21	1:D:369:LYS:HZ1	1.66	0.44
1:C:142:SER:HB3	1:C:380:VAL:HG21	2.00	0.44
1:D:301:TYR:O	1:D:305:MET:HG2	2.17	0.44
1:D:135:MET:SD	3:D:400:COS:H22	2.58	0.44
1:B:60:VAL:HB	1:B:82:VAL:HG11	2.00	0.44
1:A:196:PHE:CE1	1:A:236:ILE:HG12	2.52	0.43
1:A:244:VAL:O	1:A:247:LEU:HB3	2.18	0.43
1:B:188:PRO:CD	1:B:191:ARG:HG3	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:TYR:HE1	1:B:246:VAL:HG23	1.83	0.43
1:A:262:PRO:HB3	1:A:339:ALA:HB2	2.00	0.43
1:A:47:ASN:N	1:A:47:ASN:OD1	2.51	0.43
1:D:102:ASN:HD21	1:D:254:GLU:HA	1.82	0.43
1:A:159:ILE:CG2	1:A:228:ASP:HA	2.48	0.43
1:C:24:MET:HE3	1:C:58:LEU:HD13	1.99	0.43
1:D:179:TYR:HE2	1:D:246:VAL:CG2	2.31	0.43
1:A:266:MET:O	1:A:269:VAL:HG13	2.18	0.43
1:B:13:LEU:HD13	1:B:81:LEU:HD21	2.00	0.43
1:D:166:TRP:O	2:D:399:FAD:C4X	2.66	0.43
1:B:213:LYS:HE2	1:B:213:LYS:HB2	1.78	0.43
1:B:273:THR:HA	1:B:350:PHE:HE1	1.84	0.43
1:B:105:ILE:O	1:B:109:VAL:HG13	2.19	0.42
1:A:95:LEU:HB2	1:A:216:MET:CE	2.50	0.42
1:C:169:ASN:HD22	1:C:169:ASN:N	2.15	0.42
1:A:25:ALA:O	1:A:29:GLN:HB2	2.19	0.42
1:A:60:VAL:HB	1:A:82:VAL:HG11	2.01	0.42
1:A:174:ASP:HA	1:A:200:LYS:HB2	2.01	0.42
1:B:272:HIS:CE1	1:B:360:PRO:HG3	2.55	0.42
1:D:152:GLU:HG3	1:D:159:ILE:O	2.20	0.42
1:A:168:THR:O	1:A:169:ASN:HB2	2.20	0.42
1:A:176:LEU:HD22	1:A:224:LEU:HD21	2.02	0.42
1:A:373:ILE:HA	1:A:377:THR:HG22	2.01	0.42
1:C:152:GLU:O	1:C:158:TYR:HA	2.19	0.42
1:C:135:MET:HB3	1:C:179:TYR:CD2	2.55	0.42
1:B:374:GLY:O	1:B:375:ALA:HB3	2.20	0.42
1:D:154:LYS:HG2	1:D:159:ILE:HG13	2.02	0.42
1:A:277:LEU:HD11	1:A:349:CYS:HB3	2.02	0.42
1:B:307:CYS:O	1:B:311:VAL:HG23	2.20	0.42
1:A:355:TYR:CE2	1:B:370:LEU:HD23	2.55	0.42
1:C:27:PHE:HD2	1:C:28:LEU:HD22	1.85	0.41
1:A:183:ASP:HB3	1:A:192:GLY:HA2	2.02	0.41
1:B:299:ASP:O	1:B:303:ARG:HG3	2.20	0.41
1:C:211:LEU:HG	1:C:221:THR:O	2.20	0.41
1:C:33:ALA:N	1:C:34:PRO:HD2	2.36	0.41
1:C:64:THR:HA	1:C:74:LEU:O	2.21	0.41
1:D:117:LYS:O	1:D:121:LEU:HB2	2.19	0.41
1:D:180:ALA:HB3	1:D:196:PHE:HE2	1.85	0.41
1:D:259:ALA:O	1:D:262:PRO:HD2	2.20	0.41
1:A:193:ILE:O	1:A:241:ASN:HA	2.20	0.41
1:A:318:CYS:HB3	1:A:323:CYS:SG	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:106:ASN:O	1:D:109:VAL:HG22	2.20	0.41
1:D:157:HIS:ND1	1:D:230:LYS:HG2	2.34	0.41
1:C:163:ASN:HD22	1:C:223:GLU:HG3	1.85	0.41
1:B:390:ASN:HA	1:C:278:HIS:CE1	2.55	0.41
1:A:209:LYS:HG2	1:A:210:LYS:N	2.35	0.41
1:B:286:LYS:HD2	1:B:286:LYS:H	1.85	0.41
1:D:76:TYR:O	1:D:80:VAL:HG23	2.20	0.41
1:B:326:LYS:NZ	1:B:389:PHE:CE1	2.88	0.41
1:C:183:ASP:O	1:C:192:GLY:HA3	2.20	0.41
1:C:285:GLN:NE2	1:C:290:PHE:CE1	2.89	0.41
1:C:214:LEU:O	1:C:366:ARG:HD2	2.21	0.41
1:A:105:ILE:HD11	1:A:124:LEU:HB3	2.03	0.41
1:A:387:ARG:HA	1:A:390:ASN:HB2	2.01	0.41
1:A:348:GLN:HE21	1:B:369:LYS:NZ	2.19	0.41
1:B:380:VAL:O	1:B:384:VAL:HG23	2.20	0.41
1:C:120:TYR:O	1:C:124:LEU:HD23	2.21	0.41
1:A:103:LEU:O	1:A:107:GLN:HB2	2.20	0.40
1:C:251:LEU:O	1:C:255:ARG:HG3	2.21	0.40
1:A:148:LYS:HE2	1:A:148:LYS:HB2	1.93	0.40
1:B:134:ALA:HB3	1:B:178:VAL:HG22	2.03	0.40
1:C:183:ASP:HB3	1:C:192:GLY:CA	2.46	0.40
1:A:237:LEU:HD23	1:A:237:LEU:HA	1.86	0.40
1:A:269:VAL:HG11	1:A:342:VAL:HG12	2.02	0.40
1:C:103:LEU:N	1:C:103:LEU:HD23	2.37	0.40
1:B:390:ASN:ND2	1:C:294:GLN:HE21	2.18	0.40
1:A:324:THR:OG1	1:A:327:ASP:HB2	2.21	0.40
1:B:179:TYR:HE1	1:B:246:VAL:CG2	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	385/394 (98%)	367 (95%)	18 (5%)	0	100	100
1	B	385/394 (98%)	369 (96%)	16 (4%)	0	100	100
1	C	385/394 (98%)	369 (96%)	16 (4%)	0	100	100
1	D	385/394 (98%)	365 (95%)	20 (5%)	0	100	100
All	All	1540/1576 (98%)	1470 (96%)	70 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	308/315 (98%)	286 (93%)	22 (7%)	14	29
1	B	308/315 (98%)	289 (94%)	19 (6%)	18	37
1	C	308/315 (98%)	296 (96%)	12 (4%)	32	58
1	D	308/315 (98%)	294 (96%)	14 (4%)	27	52
All	All	1232/1260 (98%)	1165 (95%)	67 (5%)	22	44

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASP
1	A	46	LYS
1	A	47	ASN
1	A	52	TRP
1	A	61	LEU
1	A	113	ASN
1	A	124	LEU
1	A	139	ASN
1	A	156	ASN
1	A	175	VAL
1	A	191	ARG
1	A	193	ILE
1	A	213	LYS

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Mol	Chain	Res	Type
1	A	214	LEU
1	A	237	LEU
1	A	251	LEU
1	A	269	VAL
1	A	277	LEU
1	A	292	LEU
1	A	304	LEU
1	A	305	MET
1	A	308	ARG
1	B	7	ASP
1	B	24	MET
1	B	44	GLU
1	B	50	GLU
1	B	52	TRP
1	B	55	LEU
1	B	113	ASN
1	B	165	PHE
1	B	184	LEU
1	B	216	MET
1	B	237	LEU
1	B	245	TYR
1	B	247	LEU
1	B	251	LEU
1	B	286	LYS
1	B	292	LEU
1	B	304	LEU
1	B	320	GLU
1	B	331	VAL
1	C	52	TRP
1	C	55	LEU
1	C	113	ASN
1	C	128	GLU
1	C	136	SER
1	C	156	ASN
1	C	182	THR
1	C	198	VAL
1	C	237	LEU
1	C	286	LYS
1	C	292	LEU
1	C	304	LEU
1	D	21	ARG
1	D	52	TRP

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Mol	Chain	Res	Type
1	D	55	LEU
1	D	57	ASN
1	D	133	LEU
1	D	149	LEU
1	D	152	GLU
1	D	156	ASN
1	D	159	ILE
1	D	237	LEU
1	D	251	LEU
1	D	278	HIS
1	D	292	LEU
1	D	304	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	43	ASN
1	A	68	GLN
1	A	79	HIS
1	A	102	ASN
1	A	113	ASN
1	A	241	ASN
1	A	278	HIS
1	A	289	HIS
1	A	294	GLN
1	A	348	GLN
1	A	390	ASN
1	B	11	ASN
1	B	29	GLN
1	B	37	GLN
1	B	54	GLN
1	B	68	GLN
1	B	102	ASN
1	B	113	ASN
1	B	139	ASN
1	B	169	ASN
1	B	241	ASN
1	B	278	HIS
1	B	390	ASN
1	C	68	GLN
1	C	107	GLN

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Mol	Chain	Res	Type
1	C	113	ASN
1	C	157	HIS
1	C	163	ASN
1	C	169	ASN
1	C	241	ASN
1	C	278	HIS
1	C	289	HIS
1	C	341	GLN
1	C	348	GLN
1	C	390	ASN
1	D	31	HIS
1	D	54	GLN
1	D	57	ASN
1	D	102	ASN
1	D	139	ASN
1	D	169	ASN
1	D	241	ASN
1	D	341	GLN
1	D	390	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	COS	C	400	-	42,51,51	1.58	5 (11%)	54,76,76	1.20	7 (12%)
2	FAD	A	399	-	51,58,58	1.27	5 (9%)	60,89,89	2.86	14 (23%)
2	FAD	C	399	-	51,58,58	1.21	6 (11%)	60,89,89	3.06	14 (23%)
3	COS	D	400	-	42,51,51	1.47	6 (14%)	54,76,76	1.19	5 (9%)
2	FAD	B	399	-	51,58,58	1.34	8 (15%)	60,89,89	3.06	13 (21%)
2	FAD	D	399	-	51,58,58	1.11	6 (11%)	60,89,89	2.84	13 (21%)
3	COS	B	400	-	42,51,51	1.15	5 (11%)	54,76,76	1.22	7 (12%)
3	COS	A	400	-	42,51,51	1.40	5 (11%)	54,76,76	1.25	6 (11%)

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	COS	C	400	-	-	9/44/65/65	0/3/3/3
2	FAD	A	399	-	-	2/30/50/50	0/6/6/6
2	FAD	C	399	-	-	2/30/50/50	0/6/6/6
3	COS	D	400	-	-	9/44/65/65	0/3/3/3
2	FAD	B	399	-	-	2/30/50/50	0/6/6/6
2	FAD	D	399	-	-	2/30/50/50	0/6/6/6
3	COS	B	400	-	-	10/44/65/65	0/3/3/3
3	COS	A	400	-	-	9/44/65/65	0/3/3/3

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	400	COS	P3B-O3B	5.62	1.69	1.59
3	D	400	COS	P3B-O3B	4.90	1.68	1.59
3	A	400	COS	O4B-C1B	4.86	1.47	1.41
3	A	400	COS	P3B-O3B	4.65	1.68	1.59
3	D	400	COS	O4B-C1B	4.34	1.47	1.41
3	C	400	COS	O4B-C1B	4.10	1.46	1.41
2	A	399	FAD	C1'-N10	-4.09	1.44	1.48
3	D	400	COS	C9P-N8P	3.88	1.42	1.33
3	B	400	COS	P3B-O3B	3.71	1.66	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	399	FAD	C1'-N10	-3.62	1.44	1.48
3	C	400	COS	C9P-N8P	3.61	1.41	1.33
2	A	399	FAD	C4-N3	3.26	1.38	1.33
2	D	399	FAD	C1'-N10	-3.20	1.44	1.48
3	C	400	COS	OAP-CAP	3.18	1.48	1.42
2	B	399	FAD	C4-N3	3.08	1.38	1.33
2	B	399	FAD	C9A-N10	3.07	1.42	1.38
3	A	400	COS	C5P-N4P	3.04	1.40	1.33
2	B	399	FAD	C4X-N5	3.00	1.37	1.33
2	C	399	FAD	C10-N1	2.92	1.37	1.33
3	C	400	COS	C5P-N4P	2.89	1.40	1.33
2	D	399	FAD	C10-N1	2.88	1.37	1.33
3	B	400	COS	O4B-C1B	2.76	1.44	1.41
2	C	399	FAD	C4X-N5	2.69	1.37	1.33
2	A	399	FAD	C10-N1	2.53	1.36	1.33
2	B	399	FAD	C8M-C8	2.51	1.56	1.51
2	A	399	FAD	C4X-N5	2.50	1.36	1.33
2	B	399	FAD	C8A-N7A	-2.50	1.30	1.34
2	B	399	FAD	C10-N1	2.47	1.36	1.33
2	C	399	FAD	C8A-N7A	-2.45	1.30	1.34
3	B	400	COS	C8A-N7A	-2.44	1.30	1.34
2	C	399	FAD	C1'-N10	-2.41	1.45	1.48
3	B	400	COS	C9P-N8P	2.39	1.38	1.33
3	A	400	COS	C9P-N8P	2.39	1.38	1.33
2	A	399	FAD	C8A-N7A	-2.34	1.30	1.34
2	C	399	FAD	C8M-C8	2.31	1.55	1.51
2	C	399	FAD	C4-N3	2.31	1.37	1.33
3	D	400	COS	C5P-N4P	2.31	1.38	1.33
2	D	399	FAD	C4-N3	2.27	1.37	1.33
3	A	400	COS	C8A-N7A	-2.25	1.30	1.34
3	B	400	COS	C5P-N4P	2.21	1.38	1.33
3	D	400	COS	P1A-O5B	2.18	1.68	1.59
3	D	400	COS	OAP-CAP	2.15	1.46	1.42
2	D	399	FAD	C8A-N7A	-2.15	1.30	1.34
2	B	399	FAD	C4X-C10	2.11	1.40	1.38
2	D	399	FAD	C4X-N5	2.09	1.36	1.33
2	D	399	FAD	C9A-N10	2.02	1.41	1.38

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	399	FAD	C4-N3-C2	15.72	128.41	115.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	399	FAD	C4-N3-C2	14.79	127.63	115.14
2	D	399	FAD	C4-N3-C2	13.99	126.95	115.14
2	A	399	FAD	C4-N3-C2	13.40	126.45	115.14
2	B	399	FAD	C10-C4X-N5	10.65	128.62	121.26
2	D	399	FAD	C10-C4X-N5	9.99	128.17	121.26
2	C	399	FAD	C10-C4X-N5	9.77	128.02	121.26
2	A	399	FAD	C10-C4X-N5	9.55	127.86	121.26
2	C	399	FAD	C4X-C4-N3	-6.88	114.02	123.43
2	A	399	FAD	C4X-C4-N3	-6.38	114.71	123.43
2	B	399	FAD	C4X-C4-N3	-6.17	115.00	123.43
2	D	399	FAD	C4X-C4-N3	-5.76	115.55	123.43
2	B	399	FAD	C4-C4X-C10	-5.41	116.37	119.95
2	B	399	FAD	C4X-N5-C5X	-5.20	111.58	116.77
2	A	399	FAD	C1'-N10-C10	5.11	122.98	118.41
2	A	399	FAD	C4X-N5-C5X	-5.02	111.75	116.77
2	C	399	FAD	C4X-N5-C5X	-4.81	111.96	116.77
2	D	399	FAD	C4X-N5-C5X	-4.41	112.36	116.77
2	B	399	FAD	C4X-C10-N10	-4.33	115.86	120.30
2	A	399	FAD	C4X-C10-N10	-4.23	115.95	120.30
2	B	399	FAD	O4B-C1B-C2B	-4.23	100.75	106.93
2	D	399	FAD	C4-C4X-C10	-4.20	117.17	119.95
2	A	399	FAD	C4-C4X-C10	-4.12	117.22	119.95
2	D	399	FAD	C4X-C10-N10	-4.05	116.14	120.30
2	C	399	FAD	C4X-C10-N10	-4.04	116.15	120.30
2	C	399	FAD	C4-C4X-C10	-3.97	117.33	119.95
2	A	399	FAD	C6-C5X-N5	-3.69	114.99	119.05
2	B	399	FAD	C1'-N10-C10	3.58	121.62	118.41
2	D	399	FAD	C4-C4X-N5	-3.58	114.50	118.60
2	C	399	FAD	C4-C4X-N5	-3.51	114.58	118.60
2	D	399	FAD	O4B-C1B-C2B	-3.49	101.83	106.93
2	A	399	FAD	C9A-C5X-N5	3.41	127.69	122.36
3	B	400	COS	CEP-CBP-CCP	-3.36	102.74	108.23
2	A	399	FAD	O4B-C1B-C2B	-3.36	102.02	106.93
2	B	399	FAD	C6-C5X-N5	-3.35	115.35	119.05
3	C	400	COS	CEP-CBP-CAP	3.32	114.58	108.82
2	A	399	FAD	C4-C4X-N5	-3.26	114.87	118.60
3	A	400	COS	CEP-CBP-CCP	-3.25	102.94	108.23
2	C	399	FAD	C6-C5X-N5	-3.23	115.49	119.05
2	B	399	FAD	C4-C4X-N5	-3.23	114.90	118.60
2	B	399	FAD	C9A-C5X-N5	3.21	127.38	122.36
3	C	400	COS	CDP-CBP-CAP	3.18	114.34	108.82
2	C	399	FAD	C1'-N10-C10	3.16	121.24	118.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	399	FAD	C9A-C5X-N5	3.12	127.24	122.36
2	D	399	FAD	C6-C5X-N5	-3.10	115.63	119.05
3	D	400	COS	CDP-CBP-CAP	3.08	114.15	108.82
3	A	400	COS	CDP-CBP-CAP	3.08	114.15	108.82
3	B	400	COS	CEP-CBP-CAP	3.02	114.06	108.82
2	D	399	FAD	C1'-N10-C10	2.95	121.05	118.41
2	C	399	FAD	O4B-C1B-C2B	-2.94	102.62	106.93
3	A	400	COS	CEP-CBP-CAP	2.93	113.90	108.82
2	B	399	FAD	C2B-C3B-C4B	-2.80	97.21	102.64
2	D	399	FAD	C9A-C5X-N5	2.79	126.72	122.36
3	C	400	COS	C2B-C3B-C4B	-2.74	98.36	103.22
3	D	400	COS	CEP-CBP-CCP	-2.58	104.03	108.23
3	B	400	COS	O4B-C1B-C2B	-2.57	103.17	106.93
3	A	400	COS	C6P-C5P-N4P	2.53	120.68	116.42
2	C	399	FAD	C9A-N10-C10	-2.51	118.61	121.91
2	A	399	FAD	C2B-C3B-C4B	-2.51	97.76	102.64
3	B	400	COS	O3B-P3B-O7A	-2.51	99.72	109.39
3	A	400	COS	O4B-C1B-C2B	-2.41	103.40	106.93
3	C	400	COS	O4B-C1B-C2B	-2.40	103.41	106.93
3	B	400	COS	CDP-CBP-CAP	2.39	112.97	108.82
2	B	399	FAD	C9A-N10-C10	-2.37	118.81	121.91
2	C	399	FAD	C1'-N10-C9A	2.36	120.15	118.29
3	D	400	COS	CEP-CBP-CAP	2.35	112.90	108.82
3	C	400	COS	CEP-CBP-CCP	-2.32	104.45	108.23
2	D	399	FAD	C9A-N10-C10	-2.27	118.93	121.91
3	B	400	COS	O5B-C5B-C4B	2.20	116.55	108.99
2	D	399	FAD	C1'-N10-C9A	2.19	120.02	118.29
3	A	400	COS	O5P-C5P-N4P	-2.18	118.90	123.01
3	C	400	COS	O3B-P3B-O7A	-2.14	101.12	109.39
2	A	399	FAD	P-O3P-PA	-2.14	125.48	132.83
3	D	400	COS	C2B-C3B-C4B	-2.13	99.45	103.22
3	B	400	COS	C2B-C3B-C4B	-2.09	99.52	103.22
3	D	400	COS	O3B-P3B-O7A	-2.09	101.32	109.39
2	C	399	FAD	C2B-C3B-C4B	-2.05	98.65	102.64
3	C	400	COS	O9A-P3B-O8A	2.01	115.32	107.64
2	A	399	FAD	C5A-C6A-N6A	2.00	123.39	120.35

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	400	COS	C5B-O5B-P1A-O1A

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Mol	Chain	Res	Type	Atoms
3	C	400	COS	CCP-O6A-P2A-O5A
3	C	400	COS	CAP-CBP-CCP-O6A
3	D	400	COS	C5B-O5B-P1A-O1A
3	D	400	COS	C5B-O5B-P1A-O3A
3	D	400	COS	CCP-O6A-P2A-O5A
3	B	400	COS	C5B-O5B-P1A-O1A
3	B	400	COS	C5B-O5B-P1A-O3A
3	B	400	COS	CCP-O6A-P2A-O4A
3	B	400	COS	CCP-O6A-P2A-O5A
3	B	400	COS	CAP-CBP-CCP-O6A
3	A	400	COS	C5B-O5B-P1A-O1A
3	A	400	COS	CCP-O6A-P2A-O5A
3	A	400	COS	CAP-CBP-CCP-O6A
3	C	400	COS	CDP-CBP-CCP-O6A
3	A	400	COS	CDP-CBP-CCP-O6A
3	D	400	COS	CDP-CBP-CCP-O6A
3	B	400	COS	CDP-CBP-CCP-O6A
3	A	400	COS	CEP-CBP-CCP-O6A
2	C	399	FAD	PA-O3P-P-O1P
3	C	400	COS	CEP-CBP-CCP-O6A
3	C	400	COS	C5B-O5B-P1A-O3A
3	D	400	COS	CCP-O6A-P2A-O3A
3	B	400	COS	C3B-O3B-P3B-O8A
3	B	400	COS	CCP-O6A-P2A-O3A
3	A	400	COS	C5B-O5B-P1A-O3A
3	A	400	COS	CCP-O6A-P2A-O3A
3	C	400	COS	CCP-O6A-P2A-O4A
3	D	400	COS	CCP-O6A-P2A-O4A
3	A	400	COS	CCP-O6A-P2A-O4A
3	D	400	COS	CAP-CBP-CCP-O6A
3	D	400	COS	CEP-CBP-CCP-O6A
3	B	400	COS	CEP-CBP-CCP-O6A
2	C	399	FAD	PA-O3P-P-O2P
2	D	399	FAD	PA-O3P-P-O1P
3	C	400	COS	C5P-C6P-C7P-N8P
3	B	400	COS	C5P-C6P-C7P-N8P
2	A	399	FAD	PA-O3P-P-O1P
2	A	399	FAD	PA-O3P-P-O2P
2	B	399	FAD	PA-O3P-P-O1P
3	D	400	COS	P1A-O3A-P2A-O6A
3	C	400	COS	CCP-O6A-P2A-O3A
2	B	399	FAD	PA-O3P-P-O2P

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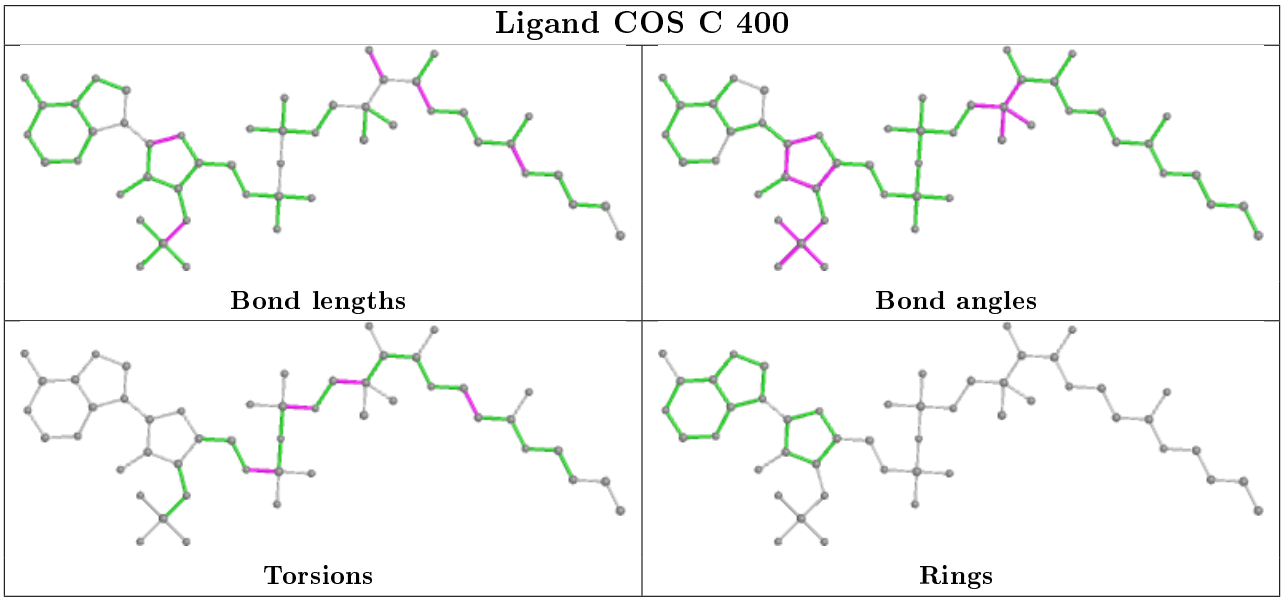
Mol	Chain	Res	Type	Atoms
2	D	399	FAD	PA-O3P-P-O2P
3	A	400	COS	C9P-CAP-CBP-CCP

There are no ring outliers.

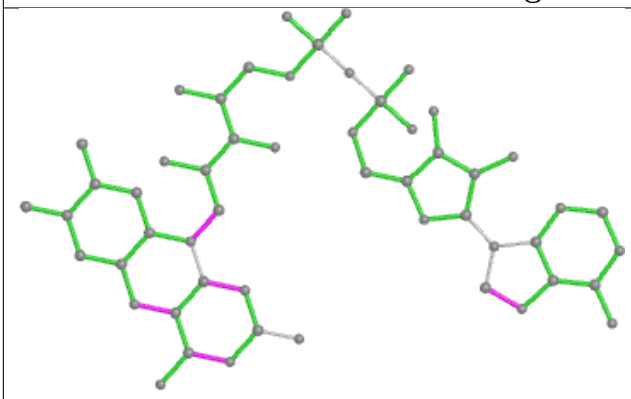
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	400	COS	3	0
3	D	400	COS	2	0
2	D	399	FAD	1	0
3	A	400	COS	1	0

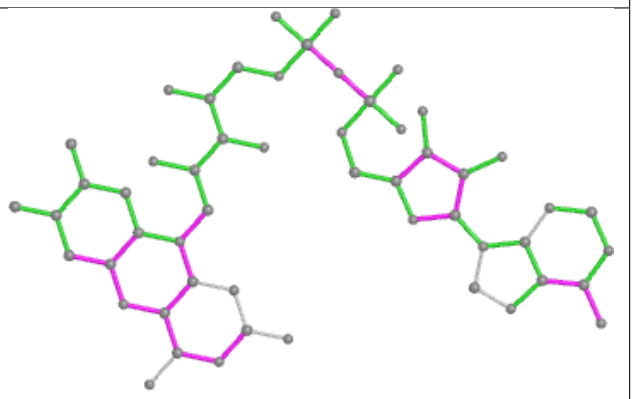
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



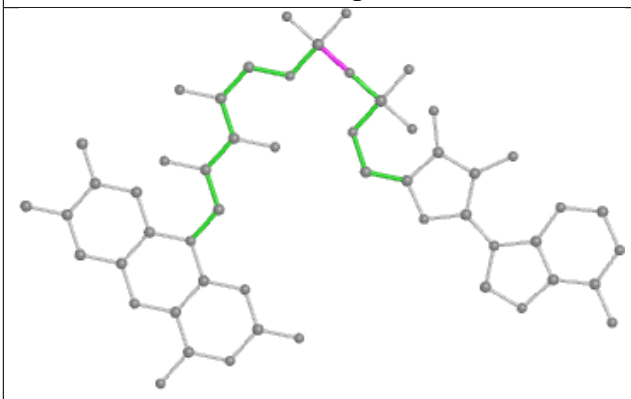
Ligand FAD A 399



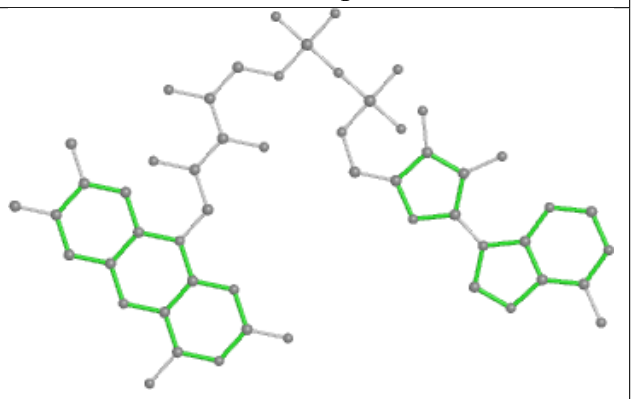
Bond lengths



Bond angles

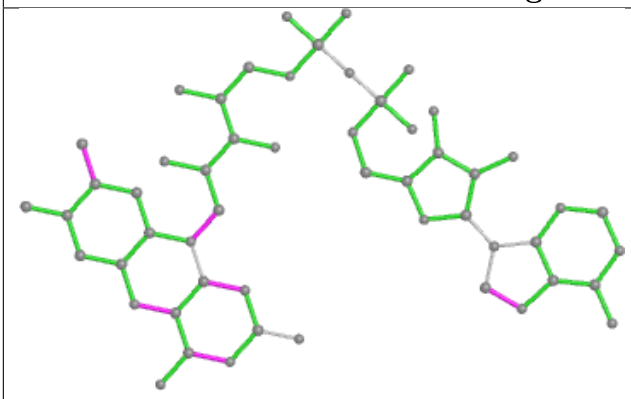


Torsions

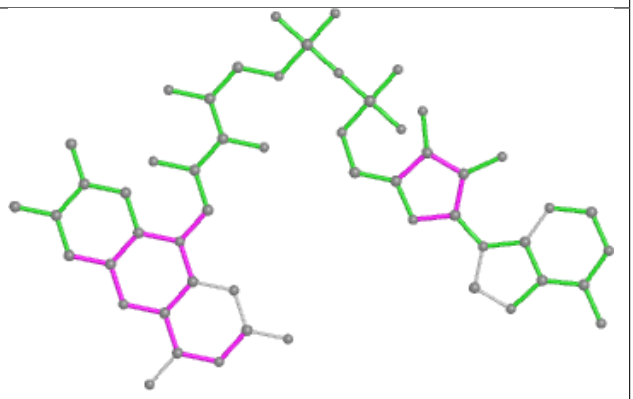


Rings

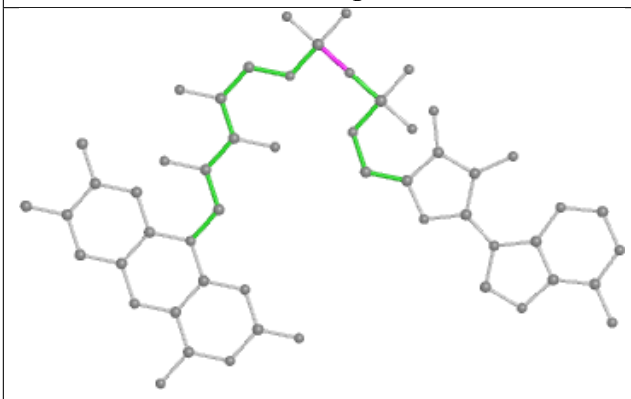
Ligand FAD C 399



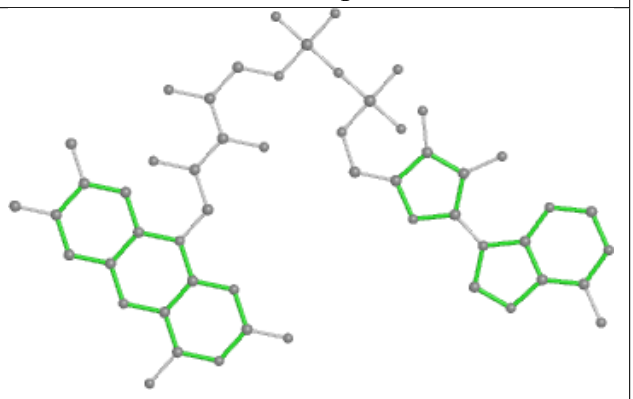
Bond lengths



Bond angles

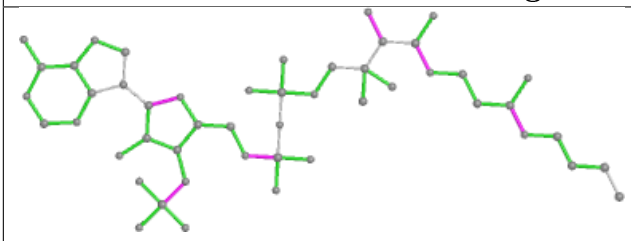


Torsions

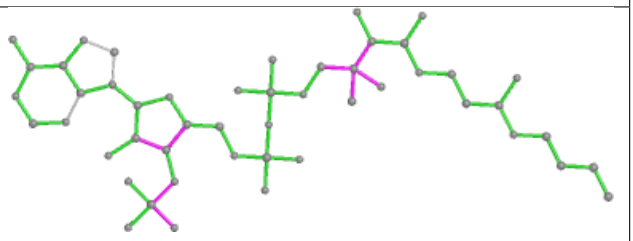


Rings

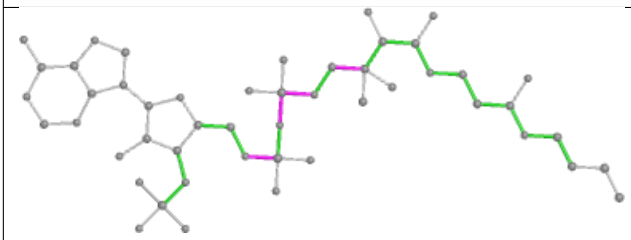
Ligand COS D 400



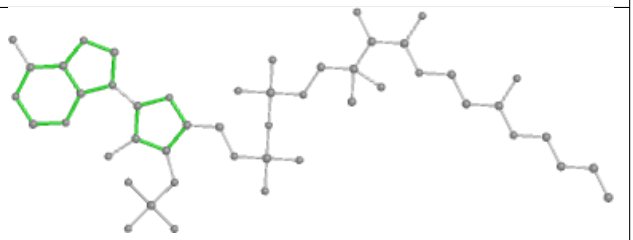
Bond lengths



Bond angles

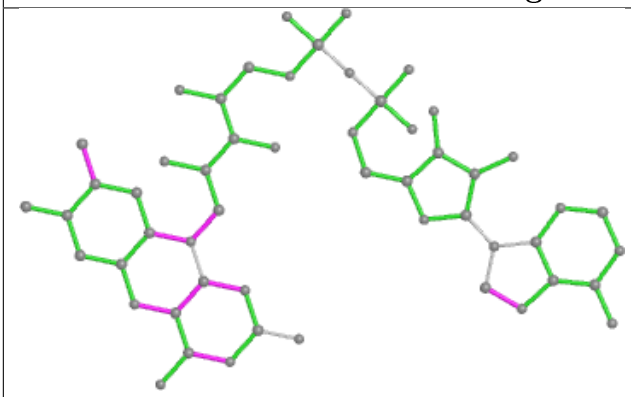


Torsions

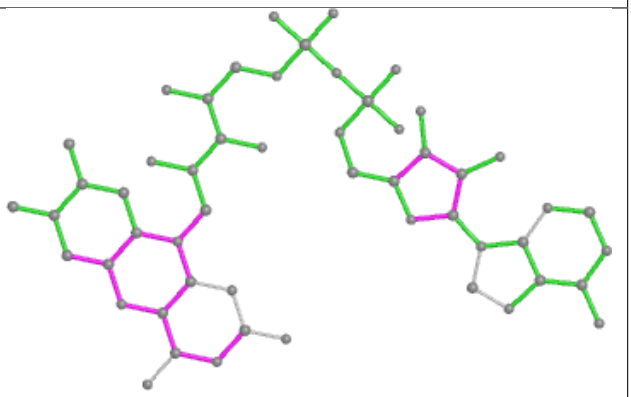


Rings

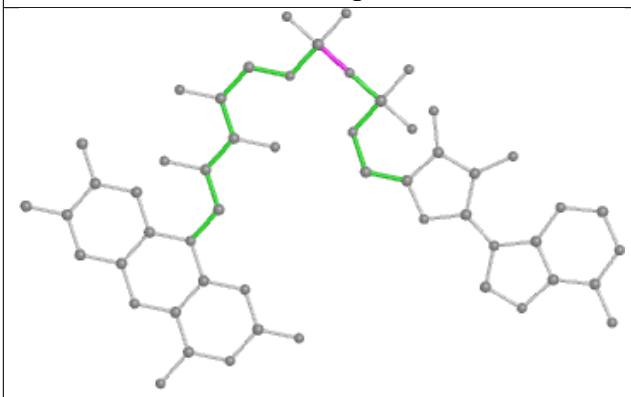
Ligand FAD B 399



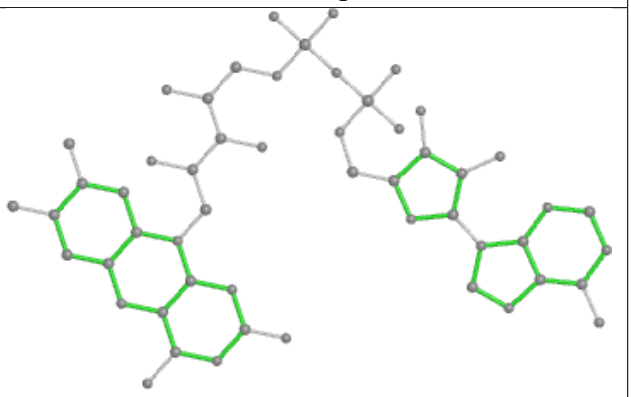
Bond lengths



Bond angles

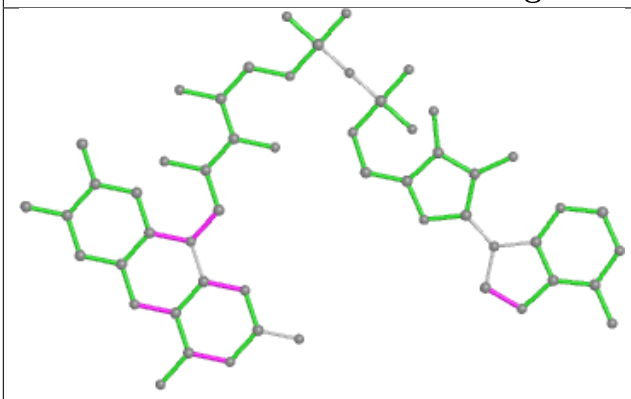


Torsions

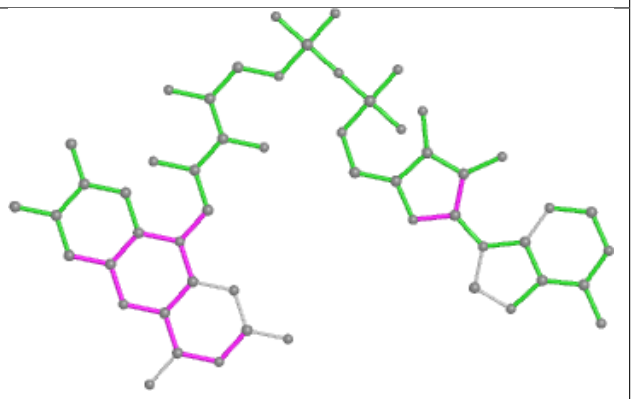


Rings

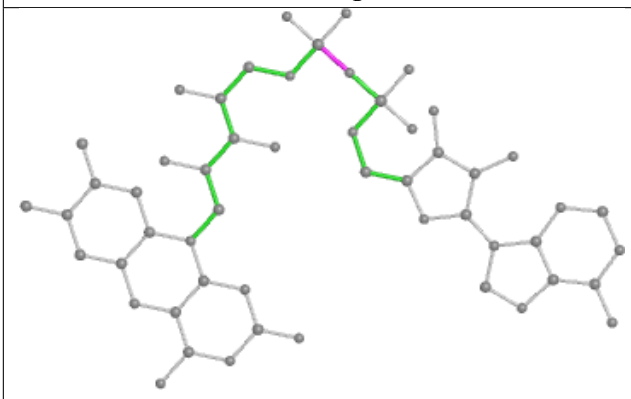
Ligand FAD D 399



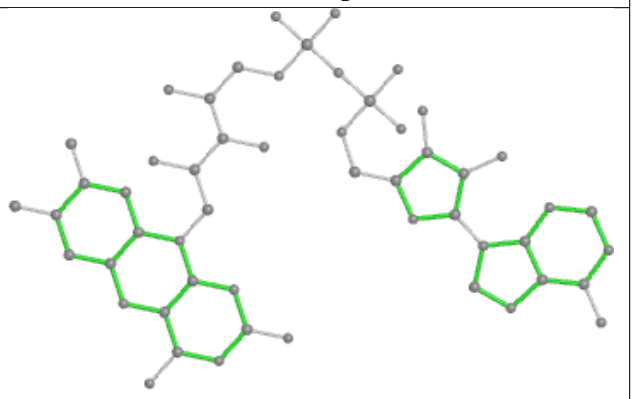
Bond lengths



Bond angles

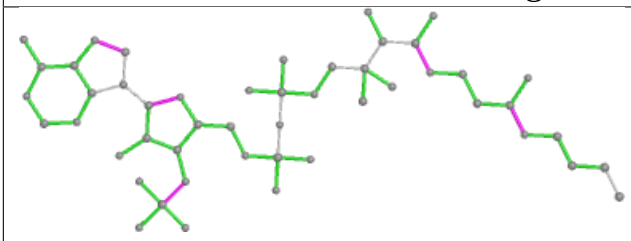


Torsions

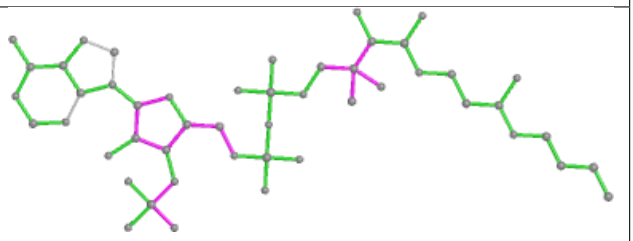


Rings

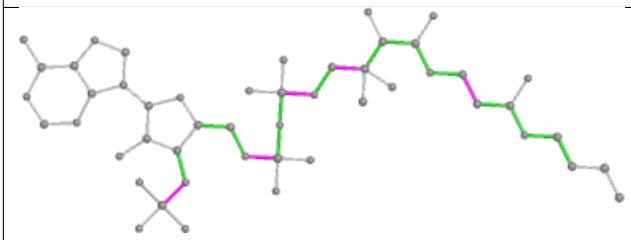
Ligand COS B 400



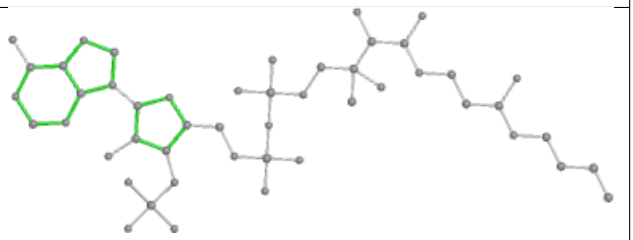
Bond lengths



Bond angles

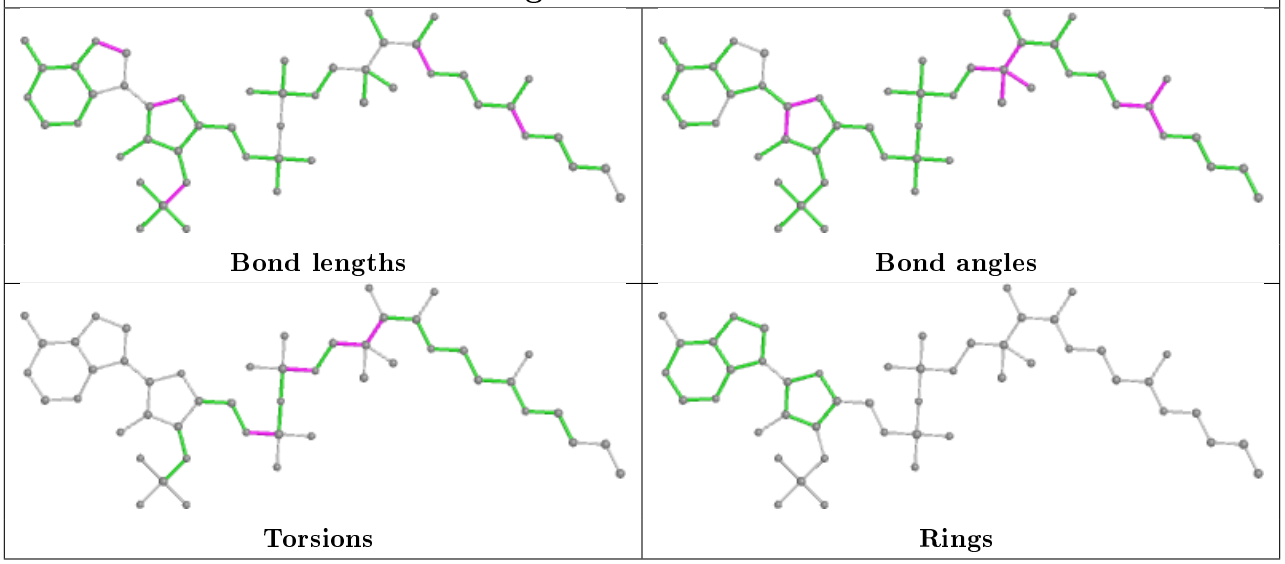


Torsions



Rings

Ligand COS A 400



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.