



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:11 AM UTC

PDB ID : 2CFY / pdb_00002cfy
Title : Crystal structure of human thioredoxin reductase 1
Authors : Debreczeni, J.E.; Johansson, C.; Kavanagh, K.; Savitsky, P.; Sundstrom, M.;
Arrowsmith, C.; Weigelt, J.; Edwards, A.; von Delft, F.; Oppermann, U.
Deposited on : 2006-02-26
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

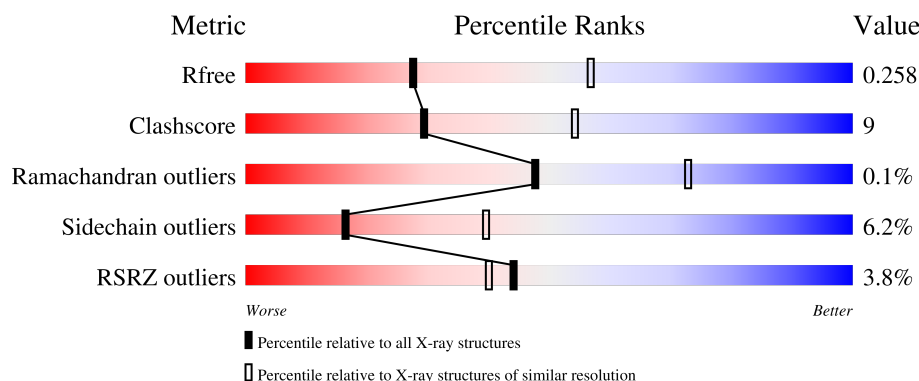
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 of 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	521	9% 76% 15% 7%
1	B	521	79% 13% 7%
1	C	521	78% 13% 7%
1	D	521	77% 14% 7%
1	E	521	9% 75% 17% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	521	9% 74% 17% • 7%

2 Entry composition [i](#)

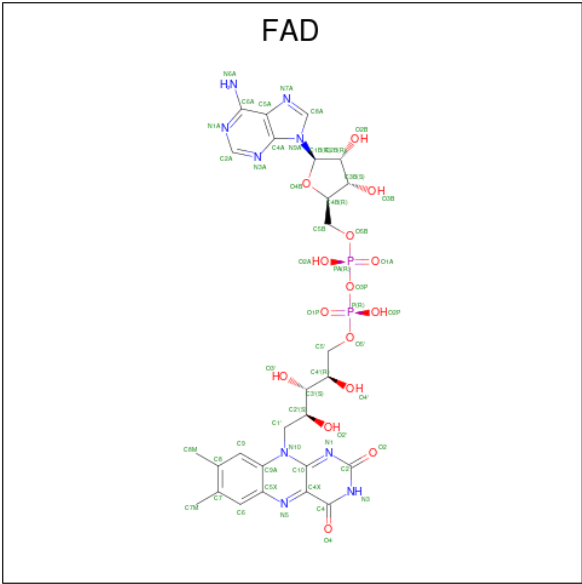
There are 3 unique types of molecules in this entry. The entry contains 22479 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 THIOREDOXIN REDUCTASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3687	2354	619	695	19			
1	B	484	Total	C	N	O	S	0	1	0
			3698	2363	619	697	19			
1	C	484	Total	C	N	O	S	0	0	0
			3702	2360	624	699	19			
1	D	484	Total	C	N	O	S	0	0	0
			3692	2356	618	699	19			
1	E	484	Total	C	N	O	S	0	0	0
			3576	2282	593	682	19			
1	F	484	Total	C	N	O	S	0	0	0
			3624	2314	602	689	19			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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		
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		
2	E	1	Total	C	N	O	P	0	0
			33	14	5	12	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

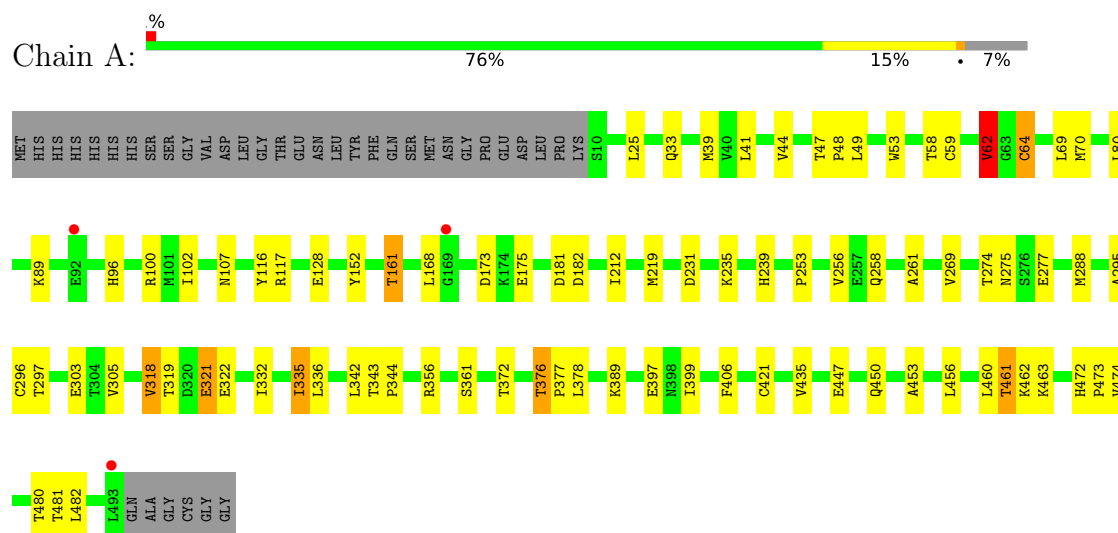
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total	O	0	0
			52	52		
3	B	53	Total	O	0	0
			53	53		
3	C	57	Total	O	0	0
			57	57		
3	D	59	Total	O	0	0
			59	59		
3	E	1	Total	O	0	0
			1	1		
3	F	6	Total	O	0	0
			6	6		

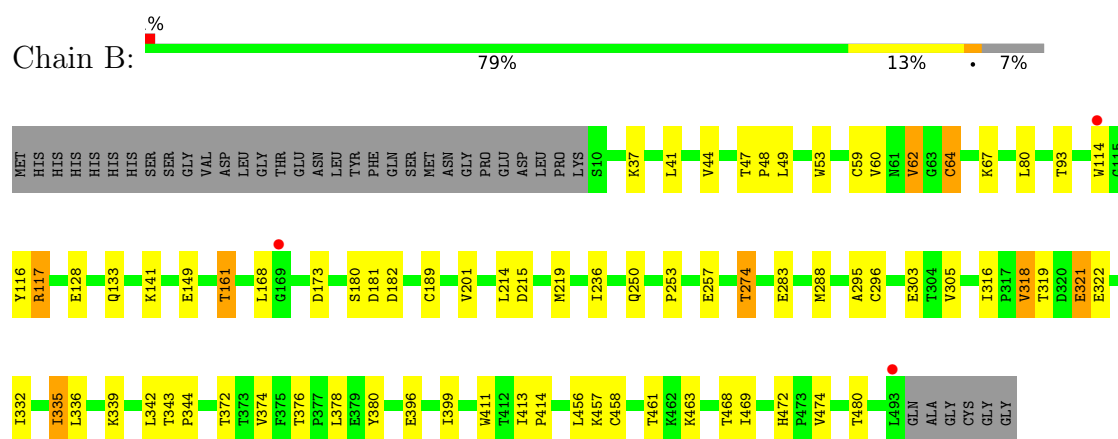
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

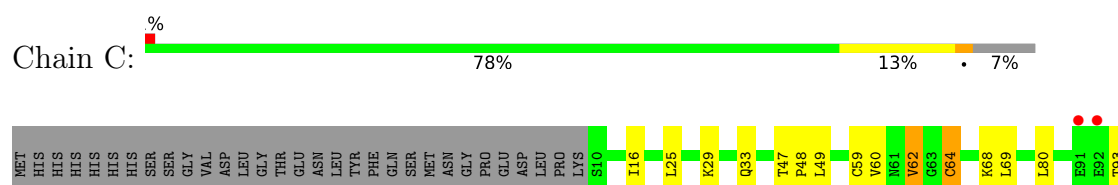
• Molecule 1: THIOREDOXIN REDUCTASE 1



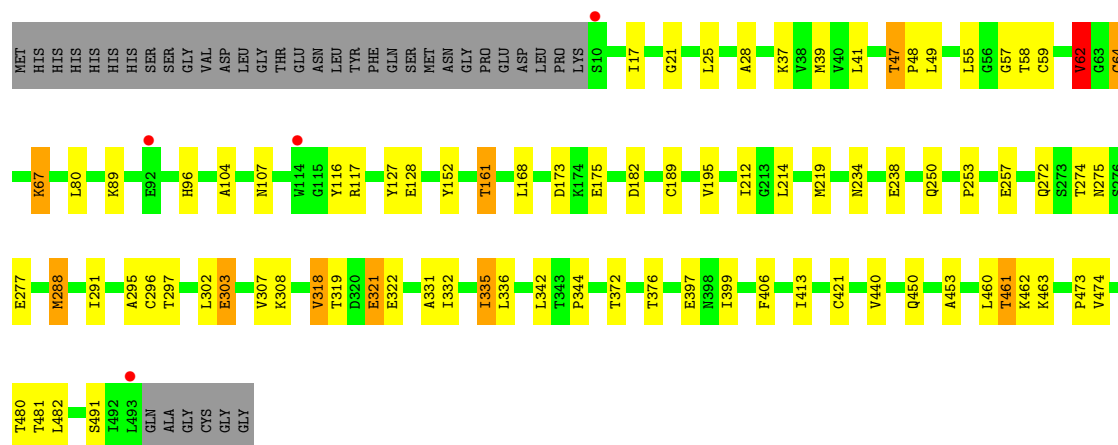
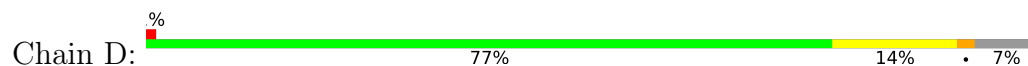
• Molecule 1: THIOREDOXIN REDUCTASE 1



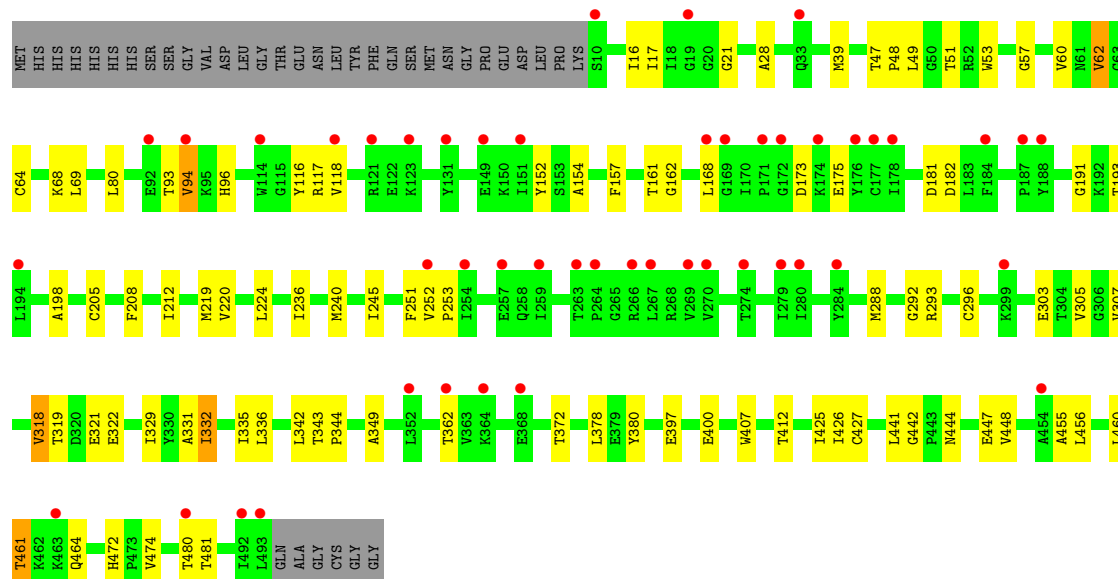
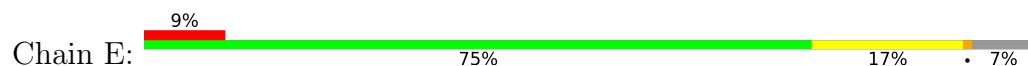
• Molecule 1: THIOREDOXIN REDUCTASE 1



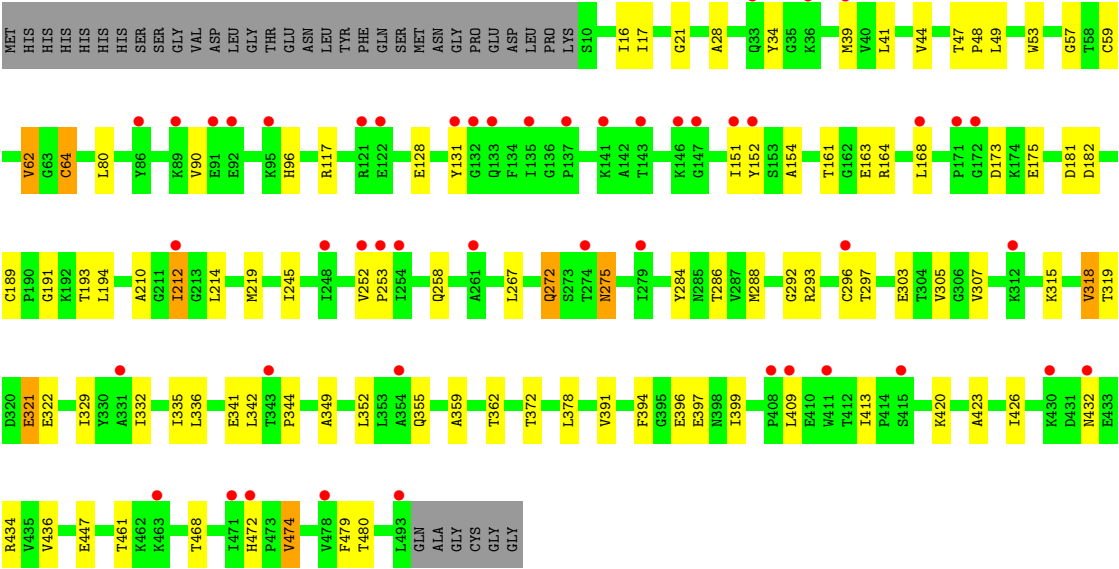
- Molecule 1: THIOREDOXIN REDUCTASE 1



- Molecule 1: THIOREDOXIN REDUCTASE 1



- Molecule 1: THIOREDOXIN REDUCTASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.76Å 149.65Å 146.79Å 90.00° 91.96° 90.00°	Depositor
Resolution (Å)	149.07 – 2.70 149.07 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.0 (149.07-2.70) 95.0 (149.07-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.203 , 0.248 (Not available) , 0.258	Depositor DCC
R_{free} test set	5025 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.001 for -h,-l,-k 0.000 for -h,l,k 0.036 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	22479	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.72	0/3761	0.83	0/5104
1	B	0.71	0/3777	0.80	0/5128
1	C	0.72	0/3776	0.83	0/5123
1	D	0.72	0/3766	0.81	0/5110
1	E	0.56	0/3649	0.74	0/4973
1	F	0.56	0/3698	0.73	0/5034
All	All	0.67	0/22427	0.79	0/30472

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3687	0	3635	64	0
1	B	3698	0	3638	56	0
1	C	3702	0	3655	61	0
1	D	3692	0	3644	64	0
1	E	3576	0	3397	80	0
1	F	3624	0	3509	78	0
2	A	53	0	31	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	53	0	31	3	0
2	C	53	0	31	2	0
2	D	53	0	31	1	0
2	E	33	0	18	2	0
2	F	27	0	11	2	0
3	A	52	0	0	1	0
3	B	53	0	0	0	0
3	C	57	0	0	1	0
3	D	59	0	0	0	0
3	E	1	0	0	0	0
3	F	6	0	0	0	0
All	All	22479	0	21631	374	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 9.

All (374) 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:E:342:LEU:HD11	1:E:372:THR:HG22	1.45	0.95
1:A:480:THR:HG21	3:A:2050:HOH:O	1.67	0.93
1:D:47:THR:HG22	1:D:49:LEU:H	1.34	0.93
1:F:332:ILE:HD11	1:F:349:ALA:CB	1.99	0.92
1:A:47:THR:HG22	1:A:49:LEU:H	1.35	0.91
1:D:219:MET:HE3	1:D:253:PRO:HD3	1.52	0.91
1:E:332:ILE:HD11	1:E:349:ALA:HB1	1.51	0.90
1:C:342:LEU:HD11	1:C:372:THR:HG22	1.55	0.87
1:B:47:THR:HG22	1:B:49:LEU:H	1.43	0.84
1:D:168:LEU:HD23	1:D:291:ILE:HD13	1.58	0.83
1:C:47:THR:HG22	1:C:49:LEU:H	1.42	0.82
1:C:80:LEU:HD23	1:D:80:LEU:CD2	2.08	0.82
1:E:161:THR:HG22	1:E:296:CYS:HB2	1.61	0.82
1:F:219:MET:HE1	1:F:253:PRO:CD	2.08	0.82
1:F:332:ILE:HD11	1:F:349:ALA:HB1	1.59	0.81
1:F:322:GLU:HG2	1:F:332:ILE:HD13	1.61	0.81
1:F:297:THR:HG23	1:F:335:ILE:HD12	1.63	0.80
1:F:342:LEU:HD11	1:F:372:THR:HG22	1.64	0.78
1:A:80:LEU:HD23	1:B:80:LEU:HD23	1.65	0.78
1:C:161:THR:HG21	1:C:296:CYS:O	1.84	0.78
1:D:161:THR:HG22	1:D:335:ILE:HG13	1.66	0.77
1:B:168:LEU:O	1:B:173:ASP:OD2	2.03	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:MET:HE2	1:A:253:PRO:HD3	1.68	0.75
1:C:161:THR:HG23	1:C:296:CYS:HB2	1.66	0.75
1:D:47:THR:HG22	1:D:49:LEU:N	2.01	0.74
1:F:219:MET:HE1	1:F:253:PRO:HD3	1.67	0.74
1:F:210:ALA:HB2	1:F:245:ILE:HD11	1.70	0.73
1:D:41:LEU:HD23	1:D:128:GLU:HB3	1.71	0.73
1:E:80:LEU:HD22	1:F:80:LEU:HD23	1.69	0.72
1:C:62:VAL:O	1:C:62:VAL:CG1	2.37	0.72
1:F:62:VAL:O	1:F:62:VAL:CG1	2.38	0.71
1:F:468:THR:O	1:F:480:THR:HG23	1.91	0.71
1:C:80:LEU:HD23	1:D:80:LEU:HD23	1.72	0.70
1:E:161:THR:HG23	2:E:600:FAD:N7A	2.06	0.70
1:D:62:VAL:O	1:D:62:VAL:HG13	1.91	0.70
1:B:62:VAL:CG1	1:B:62:VAL:O	2.39	0.70
1:C:59:CYS:HG	1:C:64:CYS:HG	0.73	0.70
1:A:47:THR:HG22	1:A:49:LEU:N	2.06	0.70
1:E:62:VAL:CG1	1:E:62:VAL:O	2.41	0.69
1:A:62:VAL:CG2	1:A:181:ASP:HA	2.23	0.69
1:C:47:THR:HG21	1:C:182:ASP:OD1	1.93	0.69
1:C:62:VAL:O	1:C:62:VAL:HG13	1.92	0.69
1:A:219:MET:CE	1:A:253:PRO:HD3	2.24	0.68
1:F:161:THR:HG22	1:F:335:ILE:HG13	1.75	0.68
1:D:219:MET:HE3	1:D:253:PRO:CD	2.24	0.68
1:A:161:THR:HG21	1:A:296:CYS:O	1.93	0.67
1:A:212:ILE:HG22	1:A:212:ILE:O	1.93	0.67
1:B:342:LEU:HD11	1:B:372:THR:HG22	1.75	0.67
1:D:47:THR:HG21	1:D:182:ASP:OD1	1.95	0.67
1:C:198:ALA:HB2	1:C:220:VAL:HG13	1.76	0.66
1:B:342:LEU:HD11	1:B:372:THR:CG2	2.24	0.66
1:E:219:MET:HE1	1:E:253:PRO:CD	2.25	0.66
1:D:342:LEU:HD11	1:D:372:THR:CG2	2.24	0.66
1:B:161:THR:HG21	1:B:296:CYS:O	1.95	0.66
1:B:374:VAL:HG12	1:B:376:THR:HG23	1.76	0.66
1:A:80:LEU:HD23	1:B:80:LEU:CD2	2.26	0.66
1:A:256:VAL:HG22	1:A:269:VAL:HG22	1.79	0.65
1:C:342:LEU:CD1	1:C:372:THR:HG22	2.26	0.65
1:A:96:HIS:ND1	1:A:212:ILE:HG23	2.12	0.65
1:E:322:GLU:HG2	1:E:332:ILE:HD12	1.79	0.65
1:F:219:MET:CE	1:F:253:PRO:HD3	2.27	0.65
1:A:161:THR:HG23	1:A:296:CYS:HB2	1.79	0.64
1:F:332:ILE:CD1	1:F:349:ALA:HB1	2.25	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:62:VAL:HG11	1:F:181:ASP:OD1	1.98	0.64
1:B:62:VAL:O	1:B:62:VAL:HG13	1.97	0.64
1:E:378:LEU:HD11	1:E:442:GLY:HA2	1.79	0.64
1:B:468:THR:O	1:B:480:THR:HG23	1.98	0.63
1:F:258:GLN:HA	1:F:267:LEU:HD23	1.81	0.63
1:B:59:CYS:HG	1:B:64:CYS:HG	0.70	0.63
1:E:80:LEU:CD2	1:F:80:LEU:HD23	2.28	0.63
1:D:297:THR:HG23	1:D:335:ILE:HD12	1.80	0.62
1:B:161:THR:HG23	1:B:296:CYS:HB2	1.80	0.62
1:D:219:MET:CE	1:D:253:PRO:HG3	2.29	0.62
1:D:62:VAL:O	1:D:62:VAL:CG1	2.47	0.62
1:E:305:VAL:HG21	1:E:329:ILE:HD11	1.81	0.62
1:F:342:LEU:HD11	1:F:372:THR:CG2	2.27	0.62
1:F:342:LEU:CD1	1:F:372:THR:HG22	2.29	0.61
1:E:161:THR:HG23	2:E:600:FAD:C8A	2.30	0.61
1:F:96:HIS:CD2	1:F:212:ILE:HD12	2.35	0.61
1:C:80:LEU:HD23	1:D:80:LEU:HD22	1.80	0.61
1:E:198:ALA:HB2	1:E:220:VAL:HG13	1.82	0.61
1:F:62:VAL:O	1:F:62:VAL:HG13	1.99	0.61
1:A:69:LEU:HD13	1:B:413:ILE:HD11	1.82	0.61
1:E:47:THR:HG21	1:E:182:ASP:OD1	2.00	0.60
1:E:47:THR:HG23	1:E:48:PRO:HD2	1.83	0.60
1:E:455:ALA:HB1	1:E:460:LEU:HD22	1.83	0.60
1:D:168:LEU:CD2	1:D:291:ILE:HD13	2.32	0.59
1:F:168:LEU:O	1:F:173:ASP:OD2	2.21	0.59
1:E:47:THR:HG22	1:E:49:LEU:H	1.67	0.59
1:B:161:THR:HG22	1:B:335:ILE:HG13	1.84	0.59
1:C:219:MET:CE	1:C:253:PRO:HG3	2.32	0.59
1:A:64:CYS:SG	2:A:600:FAD:C10	2.90	0.59
1:A:62:VAL:HG22	1:A:181:ASP:HA	1.84	0.59
1:D:480:THR:HG22	1:D:481:THR:HG23	1.85	0.59
1:F:191:GLY:O	1:F:193:THR:HG23	2.03	0.59
1:A:212:ILE:O	1:A:212:ILE:CG2	2.50	0.58
1:A:168:LEU:O	1:A:173:ASP:OD2	2.21	0.58
1:F:47:THR:HG21	1:F:182:ASP:OD1	2.04	0.58
1:A:41:LEU:HD23	1:A:128:GLU:HB3	1.86	0.58
1:D:17:ILE:HD12	1:D:28:ALA:HB2	1.86	0.58
1:B:180:SER:N	1:B:288:MET:HE3	2.18	0.58
1:D:342:LEU:HD11	1:D:372:THR:HG22	1.87	0.57
1:E:474:VAL:HG13	1:F:447:GLU:CD	2.29	0.57
1:D:295:ALA:HB1	1:D:335:ILE:CD1	2.34	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:161:THR:HG21	1:F:296:CYS:O	2.04	0.57
1:F:210:ALA:HB2	1:F:245:ILE:CD1	2.35	0.57
1:C:219:MET:CE	1:C:253:PRO:HD3	2.35	0.57
1:C:342:LEU:HD11	1:C:372:THR:CG2	2.30	0.57
1:E:191:GLY:O	1:E:193:THR:HG23	2.05	0.57
1:E:212:ILE:O	1:E:212:ILE:HG22	2.02	0.57
1:D:195:VAL:HG22	1:D:288:MET:HE2	1.85	0.56
1:A:219:MET:CE	1:A:253:PRO:CD	2.82	0.56
1:C:219:MET:HE1	1:C:253:PRO:HG3	1.88	0.56
1:E:342:LEU:CD1	1:E:372:THR:HG22	2.27	0.56
1:A:161:THR:HG22	1:A:335:ILE:HG13	1.86	0.56
1:C:219:MET:CE	1:C:253:PRO:CD	2.83	0.56
1:A:47:THR:HG21	1:A:182:ASP:OD1	2.04	0.56
1:D:55:LEU:HD13	1:D:127:TYR:CE1	2.41	0.56
1:C:16:ILE:HG13	1:C:154:ALA:HB2	1.86	0.56
1:D:39:MET:HE1	1:D:152:TYR:CD1	2.41	0.56
1:E:53:TRP:CZ3	1:E:62:VAL:HG21	2.41	0.56
1:F:315:LYS:NZ	1:F:341:GLU:OE2	2.39	0.56
1:F:394:PHE:HB2	1:F:399:ILE:HD11	1.87	0.55
1:B:250:GLN:HB3	1:B:274:THR:HG22	1.89	0.55
1:D:96:HIS:ND1	1:D:212:ILE:HG23	2.22	0.55
1:B:318:VAL:HG13	1:B:319:THR:O	2.06	0.55
1:C:47:THR:HG22	1:C:49:LEU:N	2.19	0.55
1:A:480:THR:HG22	1:A:481:THR:HG23	1.89	0.54
1:B:161:THR:HG22	1:B:335:ILE:CG1	2.37	0.54
1:D:47:THR:HG23	1:D:48:PRO:HD2	1.89	0.54
1:E:318:VAL:HG13	1:E:319:THR:O	2.07	0.54
1:E:219:MET:HE1	1:E:253:PRO:HD3	1.88	0.54
1:F:305:VAL:HG13	1:F:307:VAL:HG23	1.89	0.54
1:E:461:THR:HG22	1:E:464:GLN:H	1.73	0.54
1:F:332:ILE:HD11	1:F:349:ALA:HB3	1.88	0.54
1:A:47:THR:HG23	1:A:48:PRO:HD2	1.89	0.54
1:B:316:ILE:HD12	1:B:335:ILE:CG2	2.37	0.54
1:F:275:ASN:OD1	1:F:275:ASN:N	2.39	0.54
1:B:62:VAL:HG11	1:B:181:ASP:OD1	2.08	0.53
1:E:80:LEU:HD22	1:F:80:LEU:CD2	2.36	0.53
1:C:161:THR:CG2	1:C:296:CYS:O	2.54	0.53
1:A:25:LEU:HD13	1:A:116:TYR:CD1	2.43	0.53
1:F:96:HIS:CG	1:F:212:ILE:HD12	2.43	0.53
1:C:461:THR:HG22	1:C:463:LYS:N	2.24	0.53
1:E:318:VAL:HG22	1:E:322:GLU:C	2.34	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:240:MET:HE2	1:E:245:ILE:HD13	1.91	0.53
1:E:472:HIS:HB2	1:F:344:PRO:HG3	1.90	0.53
1:E:305:VAL:HG13	1:E:307:VAL:HG23	1.89	0.52
1:B:47:THR:HG21	1:B:182:ASP:OD1	2.09	0.52
1:D:58:THR:HG23	1:D:62:VAL:HG12	1.91	0.52
1:E:331:ALA:C	1:E:336:LEU:HD11	2.34	0.52
1:A:62:VAL:HG21	1:A:181:ASP:HA	1.90	0.52
1:B:322:GLU:HG2	1:B:332:ILE:HG22	1.92	0.52
1:A:39:MET:HE1	1:A:152:TYR:CD1	2.44	0.52
1:A:319:THR:C	1:A:321:GLU:H	2.18	0.52
1:C:69:LEU:HD22	1:D:413:ILE:HD12	1.92	0.52
1:B:295:ALA:HB1	1:B:335:ILE:HD12	1.92	0.52
1:D:161:THR:HG21	1:D:296:CYS:O	2.09	0.52
1:E:332:ILE:HD11	1:E:349:ALA:CB	2.31	0.52
1:A:59:CYS:CB	1:A:64:CYS:HG	2.23	0.51
1:E:219:MET:HE1	1:E:253:PRO:N	2.24	0.51
1:F:332:ILE:CD1	1:F:349:ALA:CB	2.80	0.51
1:A:472:HIS:HB2	1:B:344:PRO:HG3	1.93	0.51
1:C:168:LEU:O	1:C:173:ASP:OD2	2.28	0.51
1:F:210:ALA:CB	1:F:245:ILE:HD11	2.38	0.51
1:F:318:VAL:HG22	1:F:322:GLU:C	2.36	0.51
1:D:322:GLU:HG2	1:D:332:ILE:HG22	1.93	0.51
1:E:480:THR:HG22	1:E:481:THR:HG23	1.92	0.51
1:B:47:THR:HG23	1:B:48:PRO:HD2	1.92	0.51
1:B:374:VAL:CG1	1:B:376:THR:HG23	2.41	0.51
1:A:318:VAL:HG22	1:A:322:GLU:C	2.36	0.50
1:F:219:MET:HE1	1:F:253:PRO:N	2.26	0.50
1:A:322:GLU:HG2	1:A:332:ILE:HG22	1.93	0.50
1:A:461:THR:HG22	1:A:463:LYS:N	2.26	0.50
1:E:344:PRO:HG3	1:F:472:HIS:HB2	1.93	0.50
1:A:342:LEU:HD11	1:A:372:THR:CG2	2.41	0.50
1:D:219:MET:HE1	1:D:253:PRO:HG3	1.91	0.50
1:D:234:ASN:O	1:D:238:GLU:HG3	2.11	0.50
1:E:16:ILE:CD1	1:E:154:ALA:HB2	2.42	0.50
1:B:316:ILE:HD12	1:B:335:ILE:HG21	1.94	0.50
1:E:62:VAL:O	1:E:62:VAL:HG12	2.12	0.49
1:F:47:THR:HG21	1:F:182:ASP:OD2	2.12	0.49
1:A:295:ALA:HB1	1:A:335:ILE:CD1	2.41	0.49
1:B:336:LEU:HD23	1:B:339:LYS:HG3	1.94	0.49
1:E:17:ILE:HD12	1:E:28:ALA:HB2	1.94	0.49
1:E:96:HIS:CE1	1:E:212:ILE:HD12	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:305:VAL:HG21	1:F:329:ILE:HD11	1.93	0.49
1:E:447:GLU:CD	1:F:474:VAL:HG13	2.38	0.49
1:F:47:THR:HG21	1:F:182:ASP:CG	2.37	0.49
1:A:318:VAL:HG13	1:A:319:THR:O	2.13	0.49
1:A:435:VAL:O	1:A:456:LEU:HD22	2.13	0.49
1:C:318:VAL:HG13	1:C:319:THR:O	2.12	0.49
1:F:17:ILE:HD12	1:F:28:ALA:HB2	1.94	0.49
1:A:39:MET:HE1	1:A:152:TYR:CG	2.48	0.49
1:E:16:ILE:HD12	1:E:154:ALA:HB2	1.94	0.49
1:D:319:THR:C	1:D:321:GLU:H	2.20	0.49
1:E:94:VAL:HG11	1:F:90:VAL:HG22	1.94	0.49
1:E:292:GLY:C	1:E:293:ARG:HG2	2.38	0.49
1:C:161:THR:HG22	1:C:335:ILE:HG12	1.95	0.49
1:E:162:GLY:N	1:E:335:ILE:HD11	2.28	0.49
1:F:47:THR:HG22	1:F:49:LEU:H	1.77	0.49
1:F:194:LEU:HD13	1:F:284:TYR:CZ	2.48	0.49
1:C:60:VAL:HG21	1:C:116:TYR:HE2	1.78	0.48
1:C:413:ILE:HD13	1:D:104:ALA:HB1	1.94	0.48
1:D:302:LEU:HD22	1:D:307:VAL:HB	1.96	0.48
1:E:205:CYS:HA	1:E:208:PHE:CE2	2.47	0.48
1:E:425:ILE:HD12	1:E:427:CYS:SG	2.53	0.48
1:C:47:THR:HG23	1:C:48:PRO:HD2	1.94	0.48
1:B:342:LEU:CD1	1:B:372:THR:HG22	2.43	0.48
1:A:406:PHE:CZ	1:A:421:CYS:HB3	2.48	0.48
1:C:319:THR:C	1:C:321:GLU:H	2.22	0.48
1:E:62:VAL:HG11	1:E:181:ASP:OD1	2.14	0.48
1:C:62:VAL:HG11	1:C:181:ASP:OD1	2.14	0.48
1:C:68:LYS:HE2	3:C:2007:HOH:O	2.14	0.48
1:E:62:VAL:O	1:E:62:VAL:HG13	2.12	0.48
1:F:319:THR:C	1:F:321:GLU:H	2.22	0.48
1:A:297:THR:HG23	1:A:335:ILE:HD12	1.95	0.48
1:E:461:THR:HG22	1:E:464:GLN:HG3	1.96	0.48
1:F:193:THR:HG22	1:F:286:THR:HB	1.96	0.48
1:F:391:VAL:HG13	1:F:396:GLU:CA	2.43	0.48
1:F:434:ARG:HH11	1:F:461:THR:HG22	1.79	0.48
1:E:236:ILE:HD11	1:E:380:TYR:HB2	1.96	0.47
1:E:426:ILE:N	1:E:426:ILE:HD12	2.29	0.47
1:A:70:MET:HE1	1:A:102:ILE:CD1	2.44	0.47
1:C:201:VAL:HG22	2:C:600:FAD:HM73	1.97	0.47
1:F:219:MET:HE1	1:F:253:PRO:CG	2.44	0.47
1:C:162:GLY:O	1:C:335:ILE:HD11	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:69:LEU:HD22	1:F:413:ILE:HD12	1.97	0.47
1:E:96:HIS:ND1	1:E:212:ILE:HG23	2.30	0.47
1:C:366:ASP:OD2	1:C:457:LYS:HE3	2.15	0.47
1:D:25:LEU:HD13	1:D:116:TYR:CD1	2.49	0.47
1:D:440:VAL:HG13	1:D:440:VAL:O	2.14	0.47
1:B:114[B]:TRP:CD1	1:C:114:TRP:CD1	3.02	0.47
1:C:205:CYS:HA	1:C:208:PHE:CE2	2.50	0.47
1:F:16:ILE:HG13	1:F:154:ALA:HB2	1.97	0.47
1:F:212:ILE:O	1:F:212:ILE:CG2	2.62	0.47
1:D:168:LEU:O	1:D:173:ASP:OD2	2.33	0.46
1:E:154:ALA:HB3	1:E:157:PHE:CE1	2.50	0.46
1:A:44:VAL:HG11	1:A:53:TRP:CE2	2.50	0.46
1:B:319:THR:C	1:B:321:GLU:H	2.22	0.46
1:A:258:GLN:OE1	1:A:261:ALA:HB2	2.15	0.46
1:A:447:GLU:CD	1:B:474:VAL:HG13	2.41	0.46
1:F:34:TYR:CE2	1:F:359:ALA:HB2	2.50	0.46
1:D:406:PHE:CZ	1:D:421:CYS:HB3	2.50	0.46
1:F:164:ARG:HG2	1:F:296:CYS:SG	2.56	0.46
1:A:342:LEU:HD11	1:A:372:THR:HG23	1.97	0.46
1:B:41:LEU:HD23	1:B:128:GLU:HB2	1.97	0.46
1:C:458:CYS:SG	1:D:460:LEU:HD12	2.56	0.46
1:E:60:VAL:HG21	1:E:116:TYR:HE2	1.81	0.46
1:A:450:GLN:O	1:A:453:ALA:HB3	2.16	0.46
1:F:47:THR:HG23	1:F:48:PRO:HD2	1.98	0.46
1:C:413:ILE:HD13	1:D:104:ALA:CB	2.46	0.46
1:E:461:THR:CG2	1:E:464:GLN:H	2.29	0.46
1:D:461:THR:HG22	1:D:463:LYS:N	2.30	0.45
1:E:240:MET:HB3	1:E:245:ILE:HD12	1.98	0.45
1:C:25:LEU:O	1:C:29:LYS:HD3	2.16	0.45
1:D:39:MET:HE1	1:D:152:TYR:CG	2.51	0.45
1:E:303:GLU:CD	1:E:303:GLU:H	2.24	0.45
1:D:342:LEU:CD1	1:D:372:THR:HG22	2.46	0.45
1:E:219:MET:CE	1:E:253:PRO:HD3	2.44	0.45
1:E:319:THR:C	1:E:321:GLU:H	2.24	0.45
1:F:352:LEU:HD23	1:F:355:GLN:NE2	2.30	0.45
1:B:461:THR:HG22	1:B:463:LYS:H	1.82	0.45
1:B:201:VAL:HG22	2:B:600:FAD:C7M	2.46	0.45
1:E:305:VAL:CG2	1:E:329:ILE:HD11	2.47	0.45
1:B:201:VAL:HG13	2:B:600:FAD:HM73	1.98	0.45
1:C:162:GLY:O	1:C:335:ILE:CD1	2.65	0.45
1:C:201:VAL:HG22	2:C:600:FAD:C7M	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:460:LEU:HD12	1:E:461:THR:H	1.82	0.45
1:C:447:GLU:CD	1:D:474:VAL:HG13	2.41	0.45
1:D:64:CYS:SG	2:D:600:FAD:C10	3.05	0.45
1:F:44:VAL:HG11	1:F:53:TRP:CE2	2.52	0.45
1:C:318:VAL:HG22	1:C:322:GLU:C	2.42	0.45
1:A:344:PRO:HB2	1:B:469:ILE:CG2	2.47	0.44
1:C:387:GLU:HA	1:C:426:ILE:HD13	1.99	0.44
1:B:114[A]:TRP:CZ3	1:C:118:VAL:HG21	2.52	0.44
1:F:391:VAL:HG13	1:F:396:GLU:HA	2.00	0.44
1:B:44:VAL:HG11	1:B:53:TRP:CE2	2.52	0.44
1:E:305:VAL:HG22	1:E:305:VAL:O	2.18	0.44
1:B:141:LYS:NZ	1:B:149:GLU:OE2	2.45	0.44
1:F:272:GLN:HE21	1:F:272:GLN:HB3	1.61	0.44
1:B:318:VAL:HG22	1:B:322:GLU:C	2.42	0.44
1:B:461:THR:HG22	1:B:463:LYS:N	2.32	0.44
1:C:119:ALA:O	1:C:123:LYS:HG3	2.18	0.44
1:D:462:LYS:NZ	1:D:482:LEU:O	2.48	0.44
1:E:47:THR:HG21	1:E:182:ASP:CG	2.42	0.44
1:B:215:ASP:OD1	1:B:215:ASP:C	2.61	0.44
1:D:250:GLN:HB3	1:D:274:THR:OG1	2.17	0.44
1:E:68:LYS:HG2	1:F:409:LEU:HD23	2.00	0.44
1:F:41:LEU:HD23	1:F:128:GLU:HB3	1.99	0.44
1:A:344:PRO:HG3	1:B:472:HIS:HB2	2.00	0.43
1:D:318:VAL:HG22	1:D:322:GLU:C	2.42	0.43
1:C:219:MET:HE1	1:C:253:PRO:CG	2.48	0.43
1:F:292:GLY:C	1:F:293:ARG:HG2	2.43	0.43
1:B:180:SER:CA	1:B:288:MET:HE3	2.49	0.43
1:D:21:GLY:HA2	1:D:57:GLY:HA3	2.00	0.43
1:D:189:CYS:SG	1:D:214:LEU:HD21	2.57	0.43
1:A:480:THR:HG22	1:A:481:THR:CG2	2.48	0.43
1:C:219:MET:CE	1:C:253:PRO:CG	2.96	0.43
1:A:41:LEU:CD2	1:A:128:GLU:HB3	2.48	0.43
1:D:59:CYS:CB	1:D:64:CYS:HG	2.31	0.43
1:E:219:MET:HE3	1:E:251:PHE:O	2.19	0.43
1:E:168:LEU:O	1:E:173:ASP:OD2	2.37	0.43
1:A:59:CYS:SG	1:A:64:CYS:SG	3.06	0.42
1:C:236:ILE:HG21	1:C:376:THR:HG21	2.00	0.42
1:C:461:THR:CG2	1:C:462:LYS:N	2.81	0.42
1:D:480:THR:HG22	1:D:481:THR:CG2	2.48	0.42
1:B:47:THR:HG22	1:B:49:LEU:N	2.22	0.42
1:C:472:HIS:HB2	1:D:344:PRO:HG3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:195:VAL:HG22	1:D:288:MET:CE	2.50	0.42
1:C:254:ILE:HD13	1:C:272:GLN:HB2	2.02	0.42
1:D:331:ALA:C	1:D:336:LEU:HD11	2.45	0.42
1:F:423:ALA:HB1	1:F:479:PHE:CE1	2.54	0.42
1:A:58:THR:HA	1:A:62:VAL:HG12	2.01	0.42
1:B:114[B]:TRP:CZ2	1:B:117:ARG:NH1	2.88	0.42
1:E:322:GLU:HG2	1:E:332:ILE:CD1	2.49	0.42
1:F:59:CYS:CB	1:F:64:CYS:HG	2.30	0.42
1:A:96:HIS:CE1	1:A:212:ILE:HD13	2.55	0.42
1:B:219:MET:HE2	1:B:253:PRO:HD3	2.01	0.42
1:F:39:MET:HE1	1:F:152:TYR:CG	2.54	0.42
1:F:131:TYR:CE1	2:F:600:FAD:N6A	2.88	0.41
1:B:189:CYS:SG	1:B:214:LEU:HD21	2.60	0.41
1:E:161:THR:HG22	1:E:296:CYS:CB	2.41	0.41
1:A:219:MET:HE1	1:A:253:PRO:N	2.36	0.41
1:F:426:ILE:HD12	1:F:426:ILE:N	2.36	0.41
1:F:426:ILE:HG22	1:F:436:VAL:HG22	2.01	0.41
1:C:198:ALA:HB1	1:C:224:LEU:HA	2.02	0.41
1:C:331:ALA:O	1:C:336:LEU:HD11	2.20	0.41
1:D:67:LYS:C	1:D:67:LYS:HD2	2.46	0.41
1:E:212:ILE:O	1:E:212:ILE:CG2	2.68	0.41
1:A:461:THR:HG22	1:A:463:LYS:H	1.85	0.41
1:B:201:VAL:HG22	2:B:600:FAD:HM73	2.01	0.41
1:C:335:ILE:HA	1:C:335:ILE:HD12	1.70	0.41
1:E:198:ALA:HB1	1:E:224:LEU:HA	2.03	0.41
1:F:21:GLY:HA2	1:F:57:GLY:HA3	2.02	0.41
1:C:158:LEU:HD11	1:C:332:ILE:HG23	2.02	0.41
1:E:47:THR:CG2	1:E:48:PRO:HD2	2.49	0.41
1:E:407:TRP:CZ2	1:E:412:THR:HA	2.56	0.41
1:A:462:LYS:NZ	1:A:482:LEU:O	2.44	0.41
1:B:236:ILE:HD11	1:B:380:TYR:HB2	2.03	0.41
1:C:102:ILE:N	1:C:102:ILE:HD13	2.36	0.41
1:C:399:ILE:HA	1:C:399:ILE:HD12	1.86	0.41
1:D:47:THR:CG2	1:D:49:LEU:H	2.18	0.41
1:E:21:GLY:HA2	1:E:57:GLY:HA3	2.03	0.41
1:E:444:ASN:O	1:E:448:VAL:HG23	2.21	0.41
1:F:219:MET:HE3	1:F:252:VAL:HA	2.02	0.41
1:A:231:ASP:O	1:A:235:LYS:HG3	2.20	0.41
1:A:239:HIS:CE1	1:A:378:LEU:HB2	2.56	0.41
1:A:376:THR:O	1:A:377:PRO:C	2.62	0.41
1:B:60:VAL:HG21	1:B:116:TYR:HE2	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:480:THR:HG22	1:E:481:THR:CG2	2.50	0.41
1:F:394:PHE:HB2	1:F:399:ILE:CD1	2.50	0.41
1:A:212:ILE:HD13	1:A:212:ILE:HG21	1.81	0.41
1:D:212:ILE:O	1:D:212:ILE:HG22	2.21	0.41
1:F:189:CYS:SG	1:F:214:LEU:HD21	2.60	0.41
1:D:297:THR:CG2	1:D:335:ILE:HD12	2.49	0.40
1:D:450:GLN:O	1:D:453:ALA:HB3	2.21	0.40
1:B:411:TRP:C	1:B:414:PRO:HD2	2.47	0.40
1:C:219:MET:HE2	1:C:253:PRO:HG3	2.02	0.40
1:E:53:TRP:CH2	1:E:62:VAL:HG21	2.56	0.40
1:F:378:LEU:HA	1:F:378:LEU:HD12	1.85	0.40
1:D:295:ALA:HB1	1:D:335:ILE:HD12	2.01	0.40
1:D:303:GLU:H	1:D:303:GLU:CD	2.29	0.40
1:D:319:THR:C	1:D:321:GLU:N	2.79	0.40
1:E:378:LEU:HD23	1:E:441:LEU:HD21	2.03	0.40
1:A:319:THR:C	1:A:321:GLU:N	2.78	0.40
1:B:236:ILE:HG21	1:B:376:THR:HG21	2.03	0.40
1:F:57:GLY:HA2	2:F:600:FAD:O3B	2.21	0.40
1:A:161:THR:CG2	1:A:296:CYS:O	2.67	0.40
1:A:219:MET:HE2	1:A:253:PRO:CD	2.43	0.40
1:A:460:LEU:HD12	1:B:458:CYS:SG	2.61	0.40
1:C:302:LEU:HD22	1:C:307:VAL:HB	2.04	0.40
1:E:39:MET:HE1	1:E:152:TYR:CG	2.57	0.40
1:E:161:THR:HG21	1:E:296:CYS:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	482/521 (92%)	467 (97%)	13 (3%)	2 (0%)	30 54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	483/521 (93%)	468 (97%)	15 (3%)	0	100	100
1	C	482/521 (92%)	466 (97%)	16 (3%)	0	100	100
1	D	482/521 (92%)	464 (96%)	16 (3%)	2 (0%)	30	54
1	E	482/521 (92%)	466 (97%)	16 (3%)	0	100	100
1	F	482/521 (92%)	468 (97%)	14 (3%)	0	100	100
All	All	2893/3126 (92%)	2799 (97%)	90 (3%)	4 (0%)	48	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	VAL
1	D	62	VAL
1	A	473	PRO
1	D	473	PRO

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	379/428 (89%)	351 (93%)	28 (7%)	13	32
1	B	380/428 (89%)	358 (94%)	22 (6%)	18	42
1	C	383/428 (90%)	356 (93%)	27 (7%)	14	34
1	D	382/428 (89%)	357 (94%)	25 (6%)	15	37
1	E	350/428 (82%)	332 (95%)	18 (5%)	21	48
1	F	367/428 (86%)	348 (95%)	19 (5%)	21	47
All	All	2241/2568 (87%)	2102 (94%)	139 (6%)	16	39

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	62	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	64	CYS
1	A	89	LYS
1	A	100	ARG
1	A	107	ASN
1	A	117	ARG
1	A	161	THR
1	A	175	GLU
1	A	274	THR
1	A	275	ASN
1	A	277	GLU
1	A	288	MET
1	A	303	GLU
1	A	305	VAL
1	A	318	VAL
1	A	321	GLU
1	A	335	ILE
1	A	336	LEU
1	A	343	THR
1	A	356	ARG
1	A	361	SER
1	A	376	THR
1	A	389	LYS
1	A	397	GLU
1	A	399	ILE
1	A	461	THR
1	A	474	VAL
1	B	37	LYS
1	B	62	VAL
1	B	64	CYS
1	B	67	LYS
1	B	93	THR
1	B	117	ARG
1	B	133	GLN
1	B	161	THR
1	B	257	GLU
1	B	274	THR
1	B	283	GLU
1	B	303	GLU
1	B	305	VAL
1	B	318	VAL
1	B	321	GLU
1	B	335	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	343	THR
1	B	378	LEU
1	B	396	GLU
1	B	399	ILE
1	B	456	LEU
1	B	457	LYS
1	C	33	GLN
1	C	62	VAL
1	C	64	CYS
1	C	93	THR
1	C	102	ILE
1	C	121	ARG
1	C	161	THR
1	C	175	GLU
1	C	275	ASN
1	C	303	GLU
1	C	318	VAL
1	C	321	GLU
1	C	335	ILE
1	C	336	LEU
1	C	343	THR
1	C	356	ARG
1	C	376	THR
1	C	389	LYS
1	C	396	GLU
1	C	399	ILE
1	C	413	ILE
1	C	420	LYS
1	C	456	LEU
1	C	461	THR
1	C	474	VAL
1	C	487	ARG
1	C	491	SER
1	D	37	LYS
1	D	47	THR
1	D	62	VAL
1	D	64	CYS
1	D	67	LYS
1	D	89	LYS
1	D	107	ASN
1	D	117	ARG
1	D	161	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	175	GLU
1	D	257	GLU
1	D	272	GLN
1	D	275	ASN
1	D	277	GLU
1	D	288	MET
1	D	303	GLU
1	D	308	LYS
1	D	318	VAL
1	D	321	GLU
1	D	335	ILE
1	D	376	THR
1	D	397	GLU
1	D	399	ILE
1	D	461	THR
1	D	491	SER
1	E	51	THR
1	E	62	VAL
1	E	64	CYS
1	E	93	THR
1	E	94	VAL
1	E	117	ARG
1	E	118	VAL
1	E	175	GLU
1	E	252	VAL
1	E	288	MET
1	E	318	VAL
1	E	332	ILE
1	E	343	THR
1	E	362	THR
1	E	397	GLU
1	E	400	GLU
1	E	456	LEU
1	E	461	THR
1	F	62	VAL
1	F	64	CYS
1	F	117	ARG
1	F	151	ILE
1	F	163	GLU
1	F	175	GLU
1	F	212	ILE
1	F	272	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	275	ASN
1	F	288	MET
1	F	303	GLU
1	F	318	VAL
1	F	321	GLU
1	F	336	LEU
1	F	362	THR
1	F	397	GLU
1	F	420	LYS
1	F	432	ASN
1	F	474	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	GLN
1	A	113	ASN
1	A	129	ASN
1	A	239	HIS
1	A	275	ASN
1	B	81	GLN
1	B	419	ASN
1	C	107	ASN
1	C	275	ASN
1	D	106	GLN
1	D	113	ASN
1	D	275	ASN
1	E	239	HIS
1	E	275	ASN
1	E	419	ASN
1	F	108	HIS
1	F	129	ASN
1	F	272	GLN
1	F	355	GLN
1	F	419	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	FAD	D	600	-	58,58,58	1.30	6 (10%)	85,89,89	1.61	14 (16%)
2	FAD	A	600	-	58,58,58	1.34	6 (10%)	85,89,89	1.60	17 (20%)
2	FAD	B	600	-	58,58,58	1.42	7 (12%)	85,89,89	1.58	15 (17%)
2	FAD	F	600	-	28,29,58	1.18	5 (17%)	43,45,89	2.13	11 (25%)
2	FAD	C	600	-	58,58,58	1.28	7 (12%)	85,89,89	1.58	15 (17%)
2	FAD	E	600	-	35,35,58	1.20	6 (17%)	50,53,89	1.67	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	D	600	-	-	9/34/50/50	0/6/6/6
2	FAD	A	600	-	-	2/34/50/50	0/6/6/6
2	FAD	B	600	-	-	12/34/50/50	0/6/6/6
2	FAD	F	600	-	-	3/16/32/50	0/3/3/6
2	FAD	C	600	-	-	9/34/50/50	0/6/6/6
2	FAD	E	600	-	-	8/26/42/50	0/3/3/6

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	FAD	P-O3P	5.01	1.64	1.59
2	D	600	FAD	P-O3P	4.58	1.64	1.59
2	A	600	FAD	P-O3P	4.28	1.64	1.59
2	B	600	FAD	C4X-N5	4.06	1.39	1.30
2	C	600	FAD	C4X-N5	3.99	1.39	1.30
2	A	600	FAD	C4X-N5	3.82	1.39	1.30
2	D	600	FAD	C4X-N5	3.78	1.38	1.30
2	C	600	FAD	P-O3P	3.65	1.63	1.59
2	A	600	FAD	C10-N1	3.63	1.40	1.33
2	D	600	FAD	C10-N1	3.37	1.40	1.33
2	B	600	FAD	C5A-N7A	-3.35	1.33	1.39
2	B	600	FAD	PA-O3P	3.20	1.62	1.59
2	A	600	FAD	C5A-N7A	-3.19	1.33	1.39
2	C	600	FAD	C10-N1	3.16	1.39	1.33
2	B	600	FAD	C10-N1	3.13	1.39	1.33
2	C	600	FAD	C2A-N1A	3.05	1.39	1.33
2	B	600	FAD	C2A-N1A	2.84	1.39	1.33
2	A	600	FAD	C2A-N1A	2.80	1.38	1.33
2	D	600	FAD	C2A-N1A	2.71	1.38	1.33
2	E	600	FAD	C2A-N1A	2.69	1.38	1.33
2	C	600	FAD	C2A-N3A	2.67	1.38	1.33
2	E	600	FAD	P-O3P	2.64	1.62	1.59
2	F	600	FAD	C2A-N1A	2.55	1.38	1.33
2	E	600	FAD	PA-O3P	2.52	1.62	1.59
2	B	600	FAD	C2A-N3A	2.51	1.38	1.33
2	F	600	FAD	C2A-N3A	2.51	1.38	1.33
2	A	600	FAD	C2A-N3A	2.45	1.38	1.33
2	E	600	FAD	C2A-N3A	2.44	1.38	1.33
2	D	600	FAD	C5A-N7A	-2.41	1.34	1.39
2	F	600	FAD	PA-O3P	2.31	1.62	1.59
2	F	600	FAD	C5A-N7A	-2.26	1.35	1.39
2	C	600	FAD	C8A-N7A	2.19	1.35	1.31
2	E	600	FAD	C8A-N7A	2.18	1.35	1.31
2	E	600	FAD	C5A-N7A	-2.14	1.35	1.39
2	C	600	FAD	C5A-N7A	-2.08	1.35	1.39
2	F	600	FAD	C8A-N7A	2.04	1.35	1.31
2	D	600	FAD	C2A-N3A	2.01	1.37	1.33

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	600	FAD	N3A-C2A-N1A	-6.04	119.44	128.58

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	600	FAD	N3A-C2A-N1A	-5.86	119.71	128.58
2	E	600	FAD	N3A-C2A-N1A	-5.84	119.74	128.58
2	B	600	FAD	N3A-C2A-N1A	-5.84	119.75	128.58
2	D	600	FAD	N3A-C2A-N1A	-5.75	119.87	128.58
2	A	600	FAD	N3A-C2A-N1A	-5.36	120.46	128.58
2	F	600	FAD	O3B-C3B-C4B	5.24	126.12	111.08
2	D	600	FAD	N9A-C8A-N7A	-4.75	107.20	113.94
2	A	600	FAD	N9A-C8A-N7A	-4.66	107.32	113.94
2	F	600	FAD	C5A-C4A-N3A	-4.57	120.43	126.72
2	A	600	FAD	C5A-N7A-C8A	4.38	110.33	103.45
2	A	600	FAD	C5A-C4A-N3A	-4.35	120.73	126.72
2	D	600	FAD	C5A-N7A-C8A	4.28	110.17	103.45
2	C	600	FAD	N9A-C8A-N7A	-4.27	107.88	113.94
2	E	600	FAD	C5A-C4A-N3A	-4.18	120.96	126.72
2	E	600	FAD	N9A-C8A-N7A	-4.18	108.00	113.94
2	B	600	FAD	C5A-N7A-C8A	4.08	109.86	103.45
2	F	600	FAD	N9A-C8A-N7A	-4.07	108.16	113.94
2	C	600	FAD	C5A-N7A-C8A	3.95	109.65	103.45
2	B	600	FAD	N9A-C8A-N7A	-3.94	108.34	113.94
2	D	600	FAD	C5A-C4A-N3A	-3.84	121.43	126.72
2	B	600	FAD	C5A-C4A-N3A	-3.84	121.44	126.72
2	C	600	FAD	C5A-C4A-N3A	-3.76	121.54	126.72
2	F	600	FAD	C5A-N7A-C8A	3.66	109.20	103.45
2	E	600	FAD	C5A-N7A-C8A	3.57	109.07	103.45
2	F	600	FAD	C2A-N3A-C4A	3.50	120.39	111.83
2	F	600	FAD	O3B-C3B-C2B	3.48	122.98	111.82
2	C	600	FAD	C4A-C5A-N7A	-3.39	106.70	110.58
2	B	600	FAD	C4A-C5A-N7A	-3.39	106.71	110.58
2	E	600	FAD	C2A-N3A-C4A	3.29	119.86	111.83
2	A	600	FAD	C4-N3-C2	-3.27	119.83	125.64
2	D	600	FAD	C4A-C5A-N7A	-3.25	106.87	110.58
2	C	600	FAD	C2A-N3A-C4A	3.20	119.64	111.83
2	D	600	FAD	C2A-N3A-C4A	3.13	119.49	111.83
2	A	600	FAD	C2A-N3A-C4A	3.13	119.47	111.83
2	F	600	FAD	C2B-C3B-C4B	3.12	108.64	102.61
2	A	600	FAD	N3A-C4A-N9A	3.02	132.30	127.17
2	B	600	FAD	C2A-N3A-C4A	3.01	119.19	111.83
2	B	600	FAD	C4-N3-C2	-2.97	120.37	125.64
2	F	600	FAD	N3A-C4A-N9A	2.95	132.19	127.17
2	D	600	FAD	C4-N3-C2	-2.94	120.42	125.64
2	C	600	FAD	C4-N3-C2	-2.88	120.52	125.64
2	A	600	FAD	C4X-C4-N3	2.83	120.45	113.25

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	FAD	C4A-C5A-N7A	-2.82	107.35	110.58
2	D	600	FAD	C4X-C4-N3	2.79	120.37	113.25
2	B	600	FAD	C4X-C10-N10	2.78	120.46	116.48
2	E	600	FAD	N3A-C4A-N9A	2.72	131.79	127.17
2	B	600	FAD	C4X-C4-N3	2.70	120.13	113.25
2	D	600	FAD	O4-C4-C4X	-2.70	119.42	126.53
2	C	600	FAD	C4X-C4-N3	2.66	120.03	113.25
2	F	600	FAD	C4A-C5A-N7A	-2.61	107.60	110.58
2	C	600	FAD	C9A-C5X-N5	-2.54	119.75	122.45
2	A	600	FAD	O4-C4-C4X	-2.54	119.84	126.53
2	A	600	FAD	C6A-C5A-C4A	2.53	120.63	117.18
2	E	600	FAD	O2A-PA-O3P	2.53	114.10	107.27
2	C	600	FAD	C5X-C9A-N10	2.51	120.24	117.97
2	B	600	FAD	C6A-C5A-C4A	2.49	120.57	117.18
2	B	600	FAD	C10-C4X-N5	-2.48	119.75	124.81
2	E	600	FAD	C4A-C5A-N7A	-2.47	107.76	110.58
2	D	600	FAD	C4A-N9A-C8A	2.47	108.33	105.74
2	D	600	FAD	C4X-C10-N10	2.42	119.95	116.48
2	A	600	FAD	C4X-C10-N1	-2.40	118.71	124.59
2	C	600	FAD	C4X-C10-N10	2.37	119.88	116.48
2	A	600	FAD	C4X-C10-N10	2.34	119.84	116.48
2	D	600	FAD	N3A-C4A-N9A	2.34	131.15	127.17
2	B	600	FAD	C5A-C4A-N9A	2.31	108.33	105.81
2	B	600	FAD	C4-C4X-N5	2.26	121.32	118.21
2	C	600	FAD	C5A-C4A-N9A	2.25	108.26	105.81
2	B	600	FAD	O2A-PA-O3P	2.22	113.28	107.27
2	D	600	FAD	C10-C4X-N5	-2.20	120.32	124.81
2	A	600	FAD	C4A-N9A-C8A	2.20	108.04	105.74
2	A	600	FAD	C9A-C5X-N5	-2.16	120.17	122.45
2	C	600	FAD	C10-C4X-N5	-2.13	120.45	124.81
2	F	600	FAD	O2A-PA-O3P	2.13	113.02	107.27
2	A	600	FAD	C10-C4X-N5	-2.12	120.47	124.81
2	A	600	FAD	C5X-C9A-N10	2.11	119.87	117.97
2	B	600	FAD	O4-C4-C4X	-2.08	121.03	126.53
2	C	600	FAD	O4-C4-C4X	-2.08	121.04	126.53
2	E	600	FAD	C4A-N9A-C8A	2.08	107.92	105.74
2	D	600	FAD	C9A-C5X-N5	-2.04	120.29	122.45
2	C	600	FAD	O2A-PA-O3P	2.02	112.73	107.27

There are no chirality outliers.

All (43) torsion outliers are listed below:

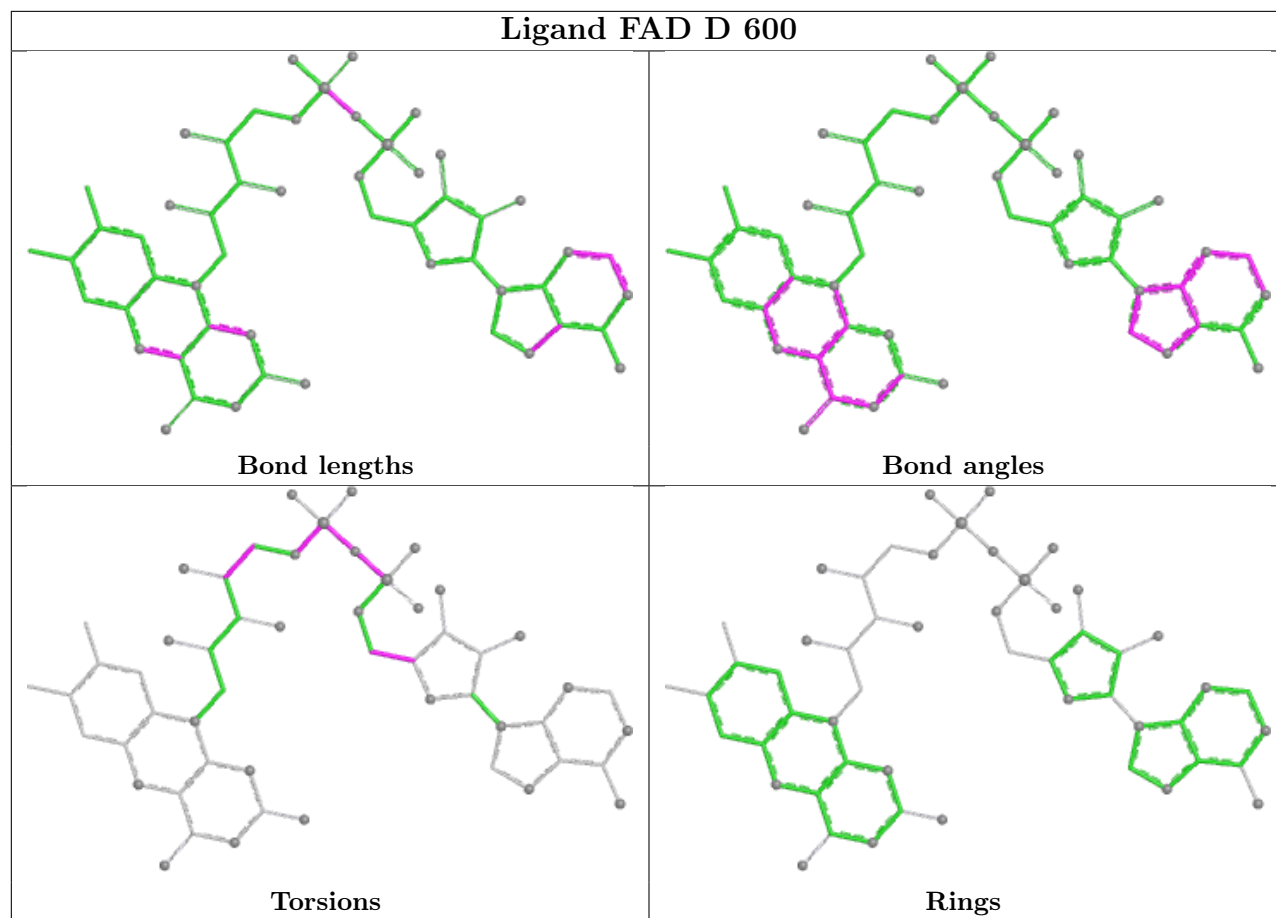
Mol	Chain	Res	Type	Atoms
2	B	600	FAD	O4'-C4'-C5'-O5'
2	B	600	FAD	C5'-O5'-P-O1P
2	B	600	FAD	C5'-O5'-P-O2P
2	B	600	FAD	C5'-O5'-P-O3P
2	C	600	FAD	C5B-O5B-PA-O1A
2	C	600	FAD	O4'-C4'-C5'-O5'
2	C	600	FAD	C5'-O5'-P-O1P
2	C	600	FAD	C5'-O5'-P-O2P
2	C	600	FAD	C5'-O5'-P-O3P
2	D	600	FAD	O4'-C4'-C5'-O5'
2	D	600	FAD	C5'-O5'-P-O2P
2	D	600	FAD	C5'-O5'-P-O3P
2	E	600	FAD	O4'-C4'-C5'-O5'
2	E	600	FAD	C5'-O5'-P-O1P
2	E	600	FAD	C5'-O5'-P-O3P
2	E	600	FAD	PA-O3P-P-O5'
2	F	600	FAD	PA-O3P-P-O5'
2	A	600	FAD	O4B-C4B-C5B-O5B
2	A	600	FAD	C3B-C4B-C5B-O5B
2	D	600	FAD	C3'-C4'-C5'-O5'
2	C	600	FAD	PA-O3P-P-O5'
2	D	600	FAD	PA-O3P-P-O5'
2	B	600	FAD	C2B-C1B-N9A-C8A
2	B	600	FAD	P-O3P-PA-O2A
2	D	600	FAD	P-O3P-PA-O2A
2	C	600	FAD	C5B-O5B-PA-O3P
2	D	600	FAD	C5'-O5'-P-O1P
2	E	600	FAD	C5'-O5'-P-O2P
2	B	600	FAD	O4B-C4B-C5B-O5B
2	D	600	FAD	O4B-C4B-C5B-O5B
2	E	600	FAD	O4B-C4B-C5B-O5B
2	B	600	FAD	PA-O3P-P-O5'
2	B	600	FAD	C3'-C4'-C5'-O5'
2	C	600	FAD	C3'-C4'-C5'-O5'
2	B	600	FAD	P-O3P-PA-O1A
2	D	600	FAD	P-O3P-PA-O1A
2	E	600	FAD	PA-O3P-P-O1P
2	F	600	FAD	PA-O3P-P-O1P
2	B	600	FAD	C3B-C4B-C5B-O5B
2	B	600	FAD	O4B-C1B-N9A-C8A
2	F	600	FAD	C2B-C1B-N9A-C8A
2	E	600	FAD	C2'-C3'-C4'-C5'
2	C	600	FAD	PA-O3P-P-O2P

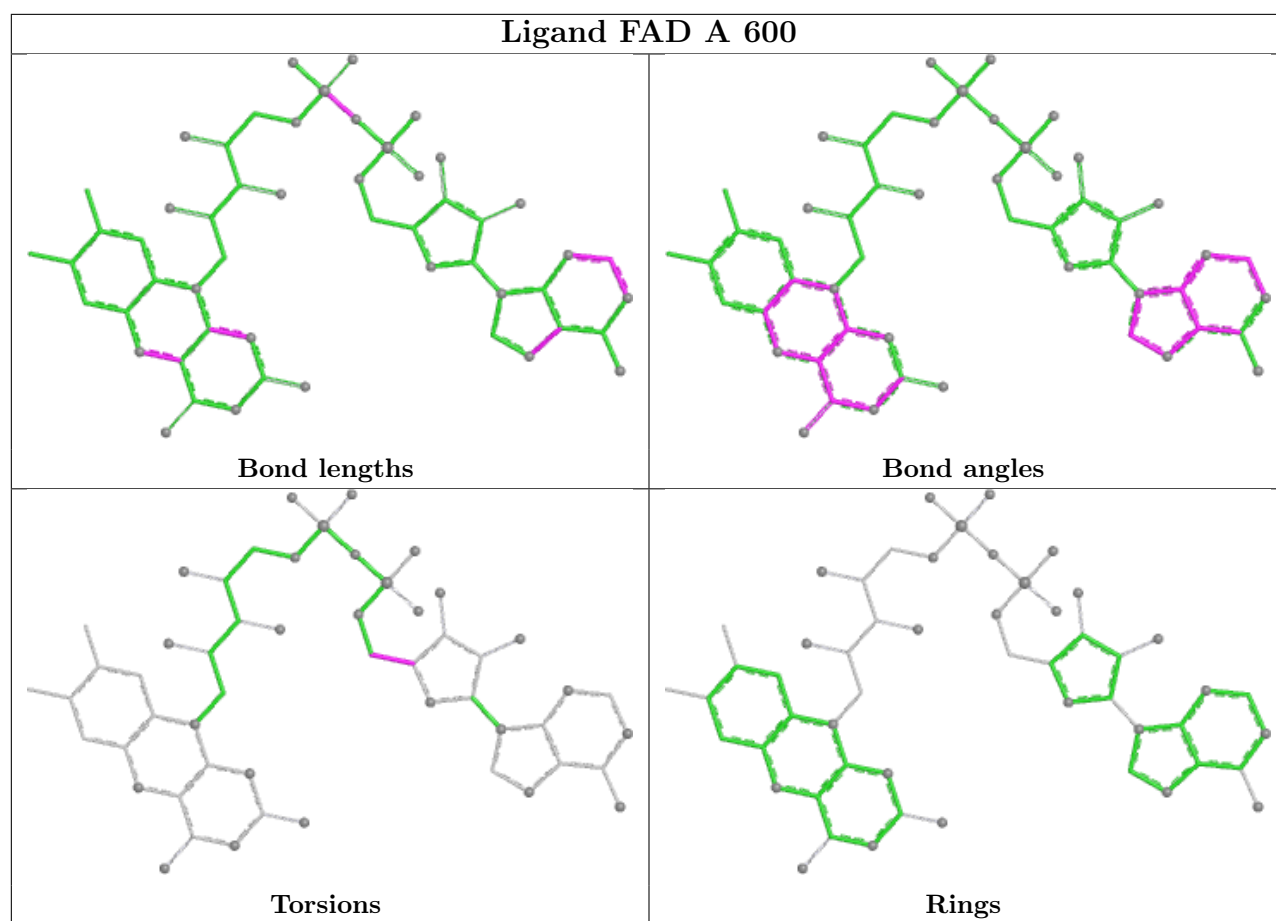
There are no ring outliers.

6 monomers are involved in 11 short contacts:

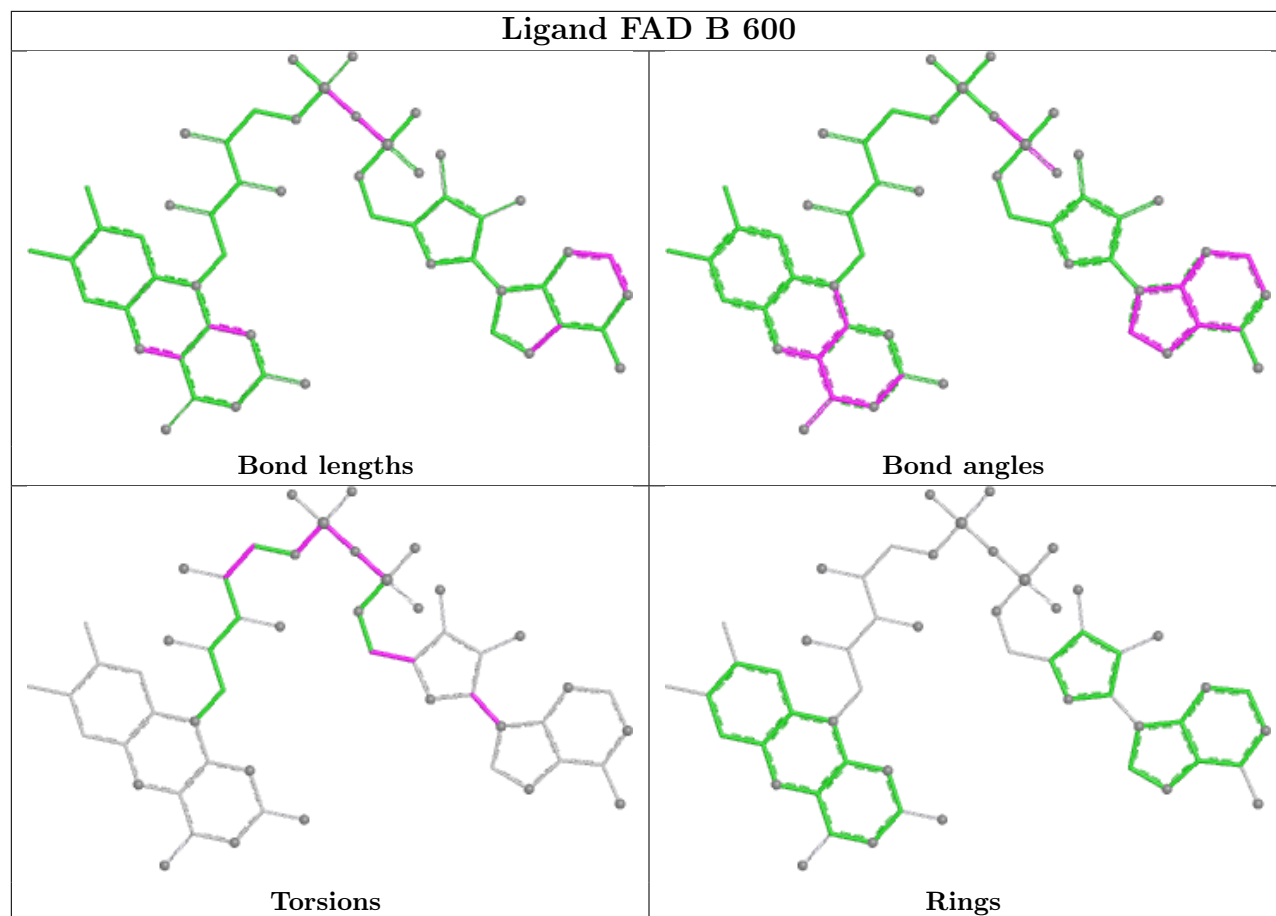
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	600	FAD	1	0
2	A	600	FAD	1	0
2	B	600	FAD	3	0
2	F	600	FAD	2	0
2	C	600	FAD	2	0
2	E	600	FAD	2	0

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.

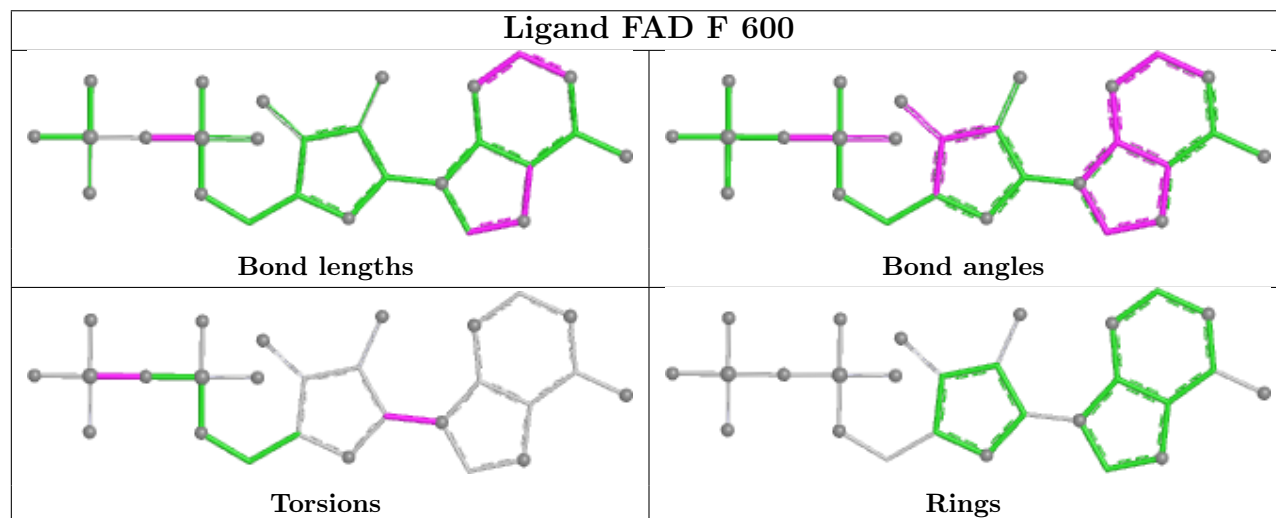


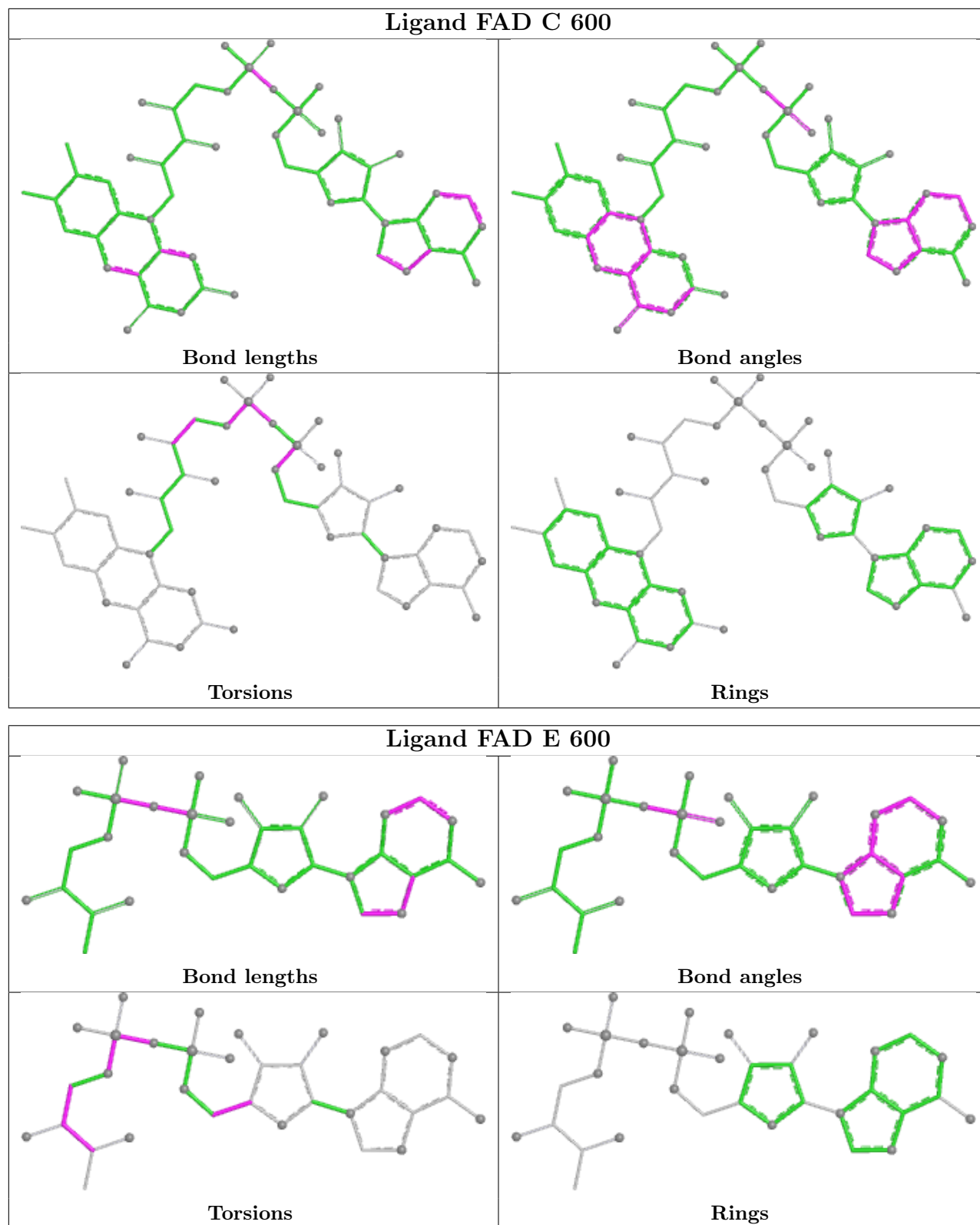


Ligand FAD B 600



Ligand FAD F 600





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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	484/521 (92%)	-0.04	3 (0%)	85 85	27, 36, 44, 53	0
1	B	484/521 (92%)	-0.10	3 (0%)	85 85	19, 35, 44, 52	1 (0%)
1	C	484/521 (92%)	-0.06	3 (0%)	85 85	25, 35, 43, 53	0
1	D	484/521 (92%)	-0.11	4 (0%)	82 81	25, 35, 43, 52	0
1	E	484/521 (92%)	1.04	48 (9%)	13 10	52, 62, 68, 71	0
1	F	484/521 (92%)	1.03	48 (9%)	13 10	50, 62, 67, 71	0
All	All	2904/3126 (92%)	0.29	109 (3%)	44 40	19, 38, 66, 71	1 (0%)

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	114[A]	TRP	4.8
1	E	92	GLU	4.1
1	F	92	GLU	3.8
1	E	279	ILE	3.7
1	E	174	LYS	3.6
1	E	33	GLN	3.5
1	F	137	PRO	3.4
1	E	168	LEU	3.2
1	E	266	ARG	3.2
1	E	280	ILE	3.2
1	F	135	ILE	3.2
1	E	368	GLU	3.0
1	E	121	ARG	3.0
1	E	176	TYR	2.9
1	F	168	LEU	2.9
1	F	493	LEU	2.9
1	D	92	GLU	2.9
1	E	493	LEU	2.9
1	E	269	VAL	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	257	GLU	2.8
1	E	114	TRP	2.8
1	E	252	VAL	2.8
1	F	253	PRO	2.7
1	F	89	LYS	2.7
1	F	172	GLY	2.7
1	D	493	LEU	2.7
1	E	194	LEU	2.6
1	F	478	VAL	2.6
1	F	409	LEU	2.6
1	F	132	GLY	2.6
1	E	264	PRO	2.6
1	F	254	ILE	2.6
1	E	463	LYS	2.6
1	E	454	ALA	2.5
1	E	94	VAL	2.5
1	E	362	THR	2.5
1	E	254	ILE	2.5
1	E	188	TYR	2.5
1	A	169	GLY	2.5
1	C	169	GLY	2.5
1	E	352	LEU	2.5
1	F	131	TYR	2.5
1	F	33	GLN	2.5
1	E	274	THR	2.4
1	F	91	GLU	2.4
1	E	171	PRO	2.4
1	E	131	TYR	2.4
1	F	354	ALA	2.4
1	A	92	GLU	2.4
1	F	261	ALA	2.4
1	F	312	LYS	2.4
1	A	493	LEU	2.4
1	E	10	SER	2.4
1	E	169	GLY	2.4
1	F	279	ILE	2.3
1	F	463	LYS	2.3
1	F	408	PRO	2.3
1	E	492	ILE	2.3
1	E	480	THR	2.3
1	C	92	GLU	2.3
1	E	177	CYS	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	146	LYS	2.3
1	E	263	THR	2.3
1	F	152	TYR	2.2
1	F	171	PRO	2.2
1	F	252	VAL	2.2
1	F	141	LYS	2.2
1	F	296	CYS	2.2
1	F	143	THR	2.2
1	F	95	LYS	2.2
1	E	284	TYR	2.2
1	D	10	SER	2.2
1	E	270	VAL	2.2
1	F	212	ILE	2.2
1	F	411	TRP	2.2
1	F	122	GLU	2.2
1	F	274	THR	2.2
1	B	169	GLY	2.2
1	F	133	GLN	2.1
1	F	430	LYS	2.1
1	B	493	LEU	2.1
1	F	415	SER	2.1
1	F	121	ARG	2.1
1	E	123	LYS	2.1
1	F	86	TYR	2.1
1	E	172	GLY	2.1
1	E	151	ILE	2.1
1	E	259	ILE	2.1
1	F	471	ILE	2.1
1	F	472	HIS	2.1
1	C	91	GLU	2.1
1	F	343	THR	2.1
1	E	267	LEU	2.1
1	F	151	ILE	2.1
1	F	248	ILE	2.1
1	E	184	PHE	2.1
1	D	114	TRP	2.1
1	E	299	LYS	2.1
1	E	364	LYS	2.1
1	F	39	MET	2.1
1	F	432	ASN	2.1
1	F	147	GLY	2.1
1	E	178	ILE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	149	GLU	2.0
1	E	187	PRO	2.0
1	E	19	GLY	2.0
1	F	36	LYS	2.0
1	F	331	ALA	2.0
1	E	118	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

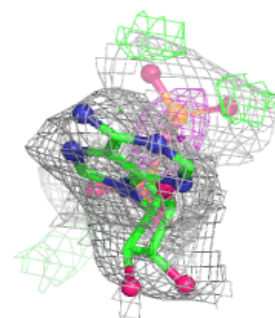
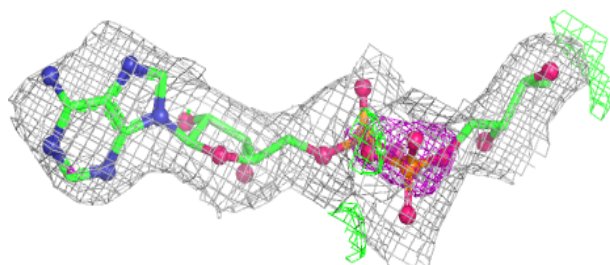
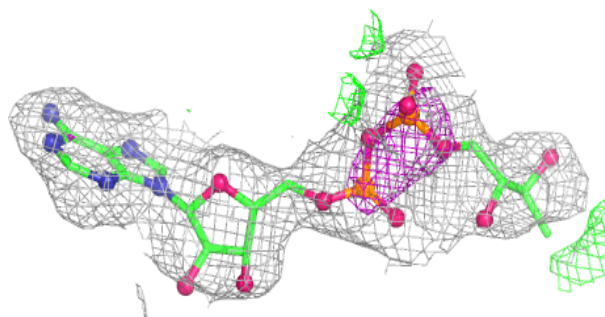
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FAD	E	600	33/53	0.78	0.16	77,78,82,83	0
2	FAD	F	600	27/53	0.80	0.15	73,76,77,78	0
2	FAD	C	600	53/53	0.92	0.12	32,51,71,71	0
2	FAD	D	600	53/53	0.92	0.13	32,55,77,77	0
2	FAD	A	600	53/53	0.93	0.12	34,55,75,75	0
2	FAD	B	600	53/53	0.93	0.13	27,53,75,75	0

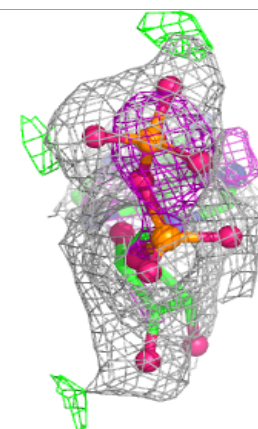
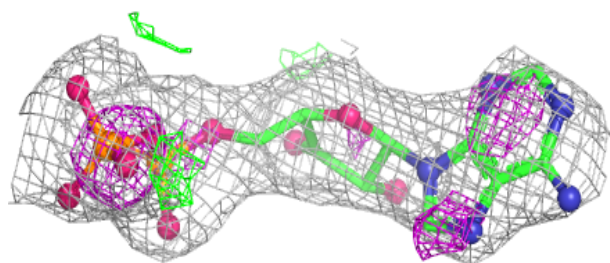
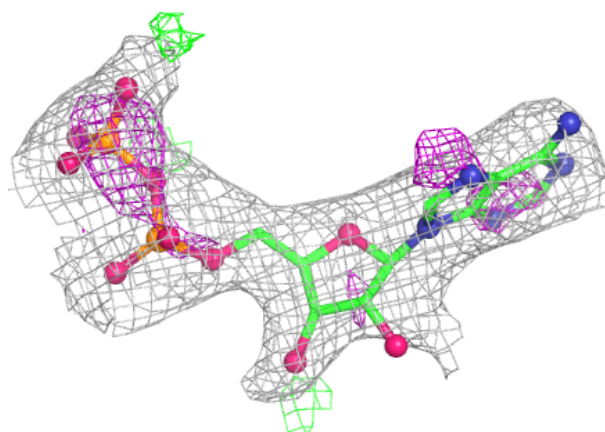
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FAD E 600:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

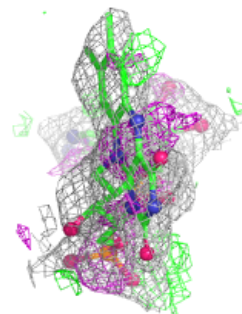
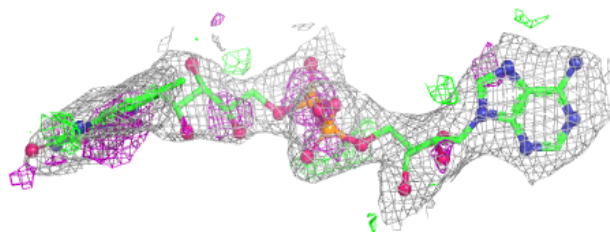
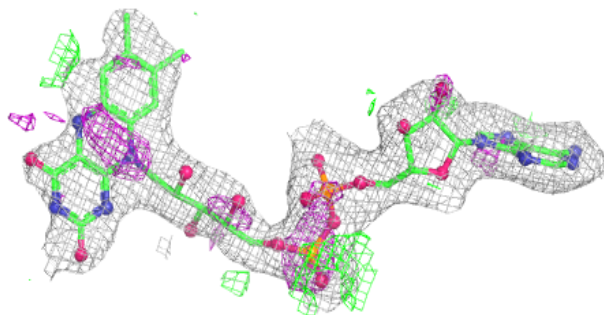
**Electron density around FAD F 600:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

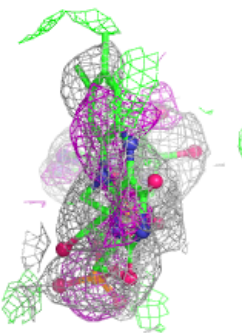
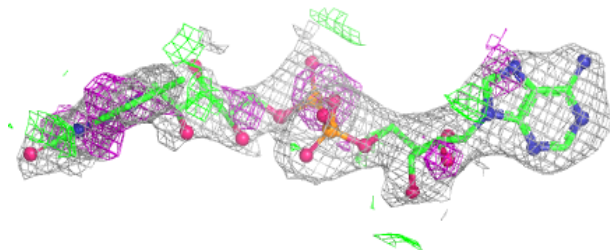
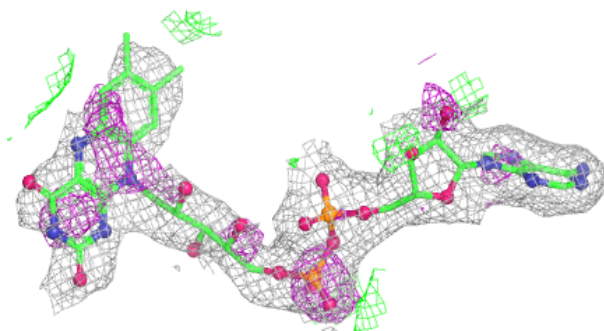


Electron density around FAD C 600:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

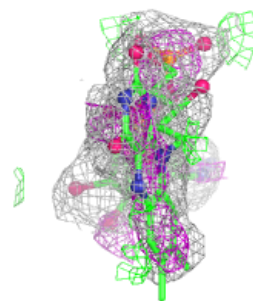
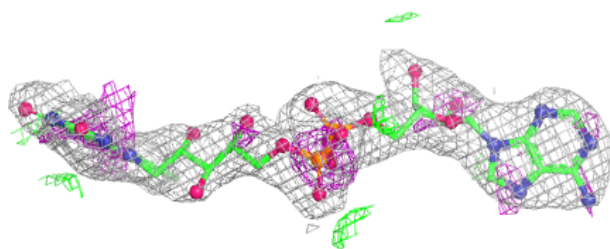
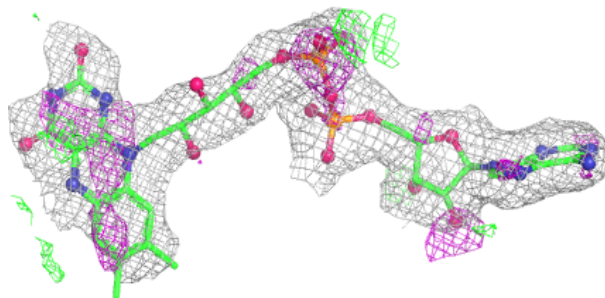
**Electron density around FAD D 600:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

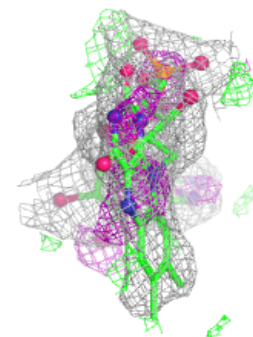
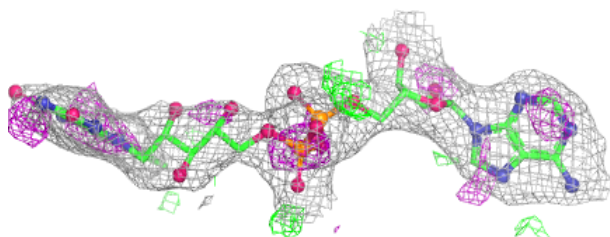
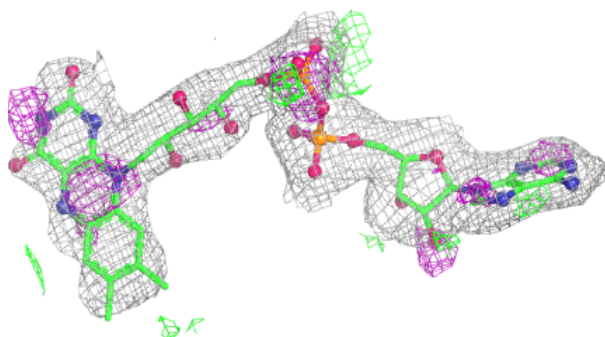


Electron density around FAD A 600:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around FAD B 600:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.