



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:35 PM UTC

PDB ID : 3P4S / pdb_00003p4s
Title : Crystal structure of Menaquinol:fumarate oxidoreductase in complex with a 3-nitropropionate adduct
Authors : Tomasiak, T.M.; Archuleta, T.L.; Andrell, J.; Luna-Chavez, C.; Davis, T.A.; Sarwar, M.; Ham, A.J.; McDonald, W.H.; Yankowskaya, V.; Stern, H.A.; Johnston, J.N.; Maklashina, E.; Cecchini, G.; Iverson, T.M.
Deposited on : 2010-10-07
Resolution : 3.10 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](#) ①) were used in the production of this report:

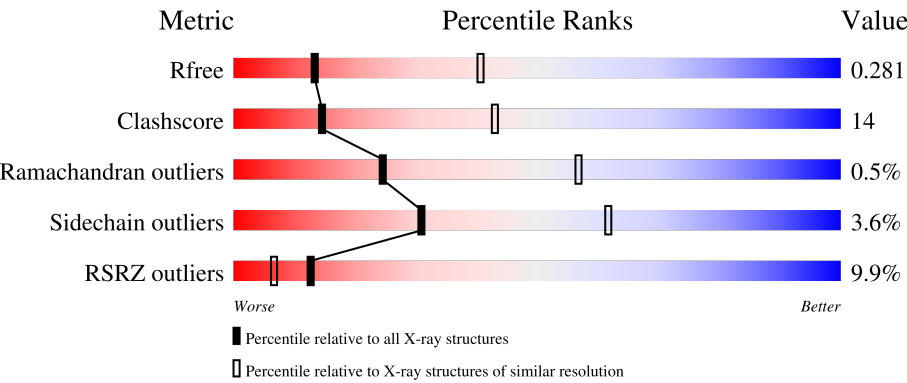
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

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

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	577	82% 17% .
1	M	577	31% 58% 38% 5%
2	B	243	2% 84% 16% .
2	N	243	7% 70% 28% .
3	C	130	85% 13% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	O	130	
4	D	119	
4	P	119	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	FES	N	244	-	-	X	-
8	F3S	B	245	-	-	X	-
8	F3S	N	245	-	-	X	-
9	SF4	B	246	-	-	X	-
9	SF4	N	246	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 16792 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 Fumarate reductase flavoprotein subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			
1	M	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			

- Molecule 2 is a protein called Fumarate reductase iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			
2	N	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			

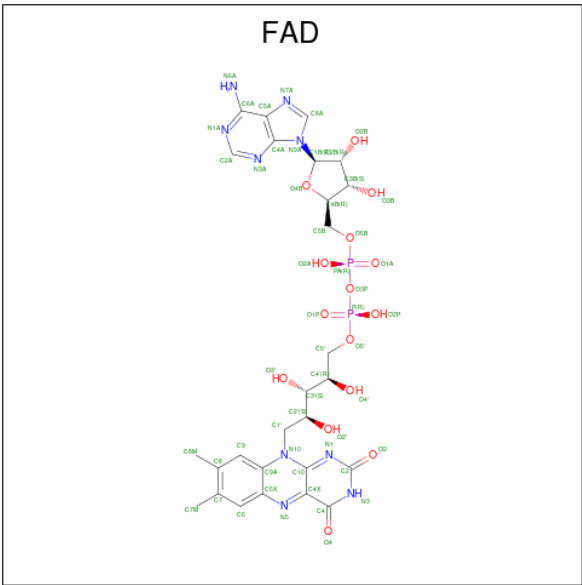
- Molecule 3 is a protein called Fumarate reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			
3	O	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			

- Molecule 4 is a protein called Fumarate reductase subunit D.

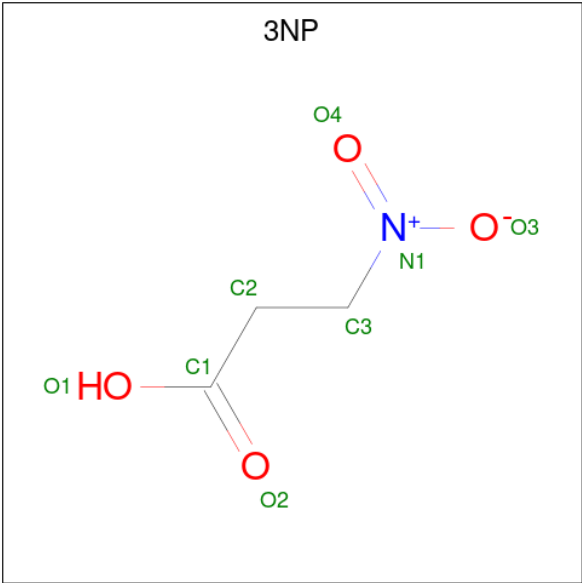
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			
4	P	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 6 is 3-NITROPROPANOIC ACID (CCD ID: 3NP) (formula: C₃H₅NO₄).



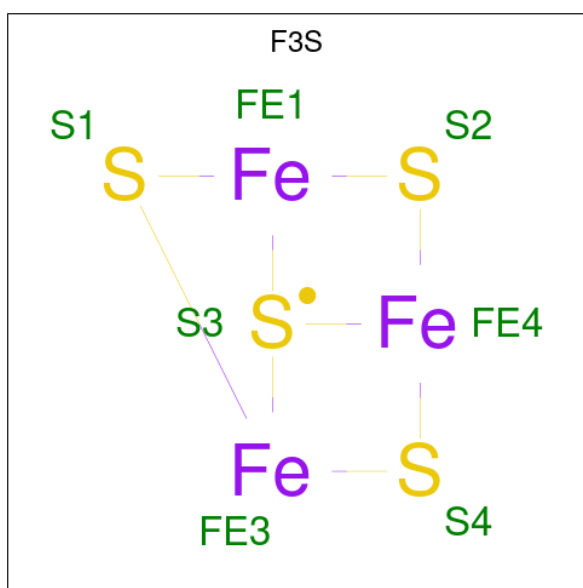
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			6	3	1	2		

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



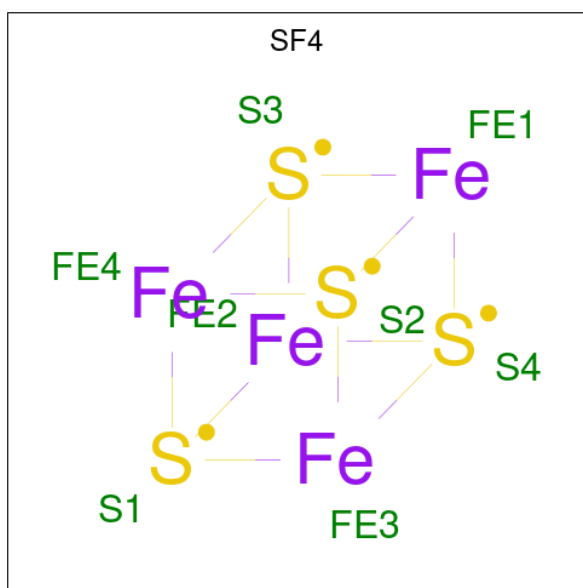
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			4	2	2		
7	N	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 8 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe₃S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		
8	N	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).

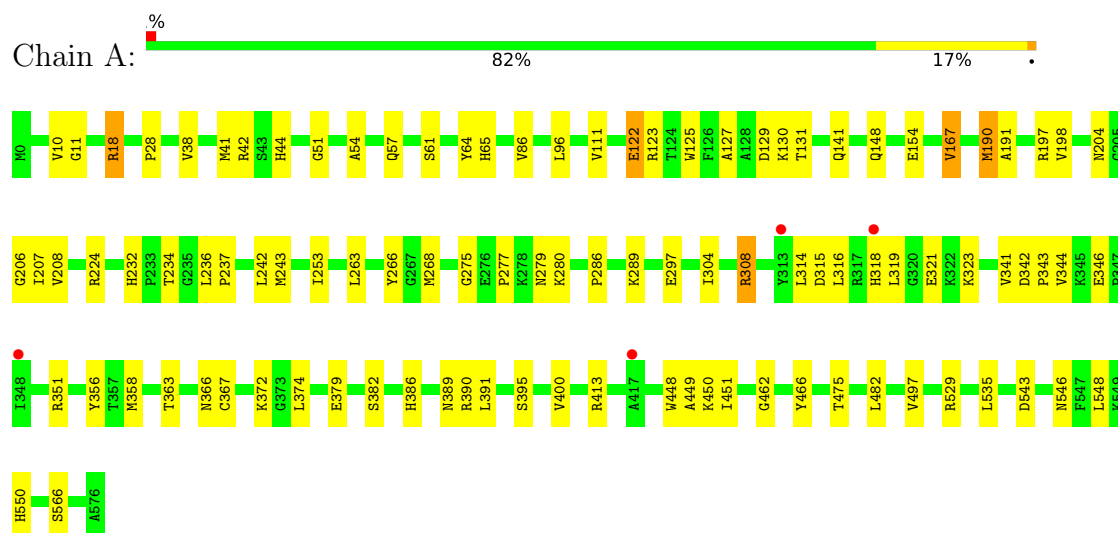


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		
9	N	1	Total	Fe	S	0	0
			8	4	4		

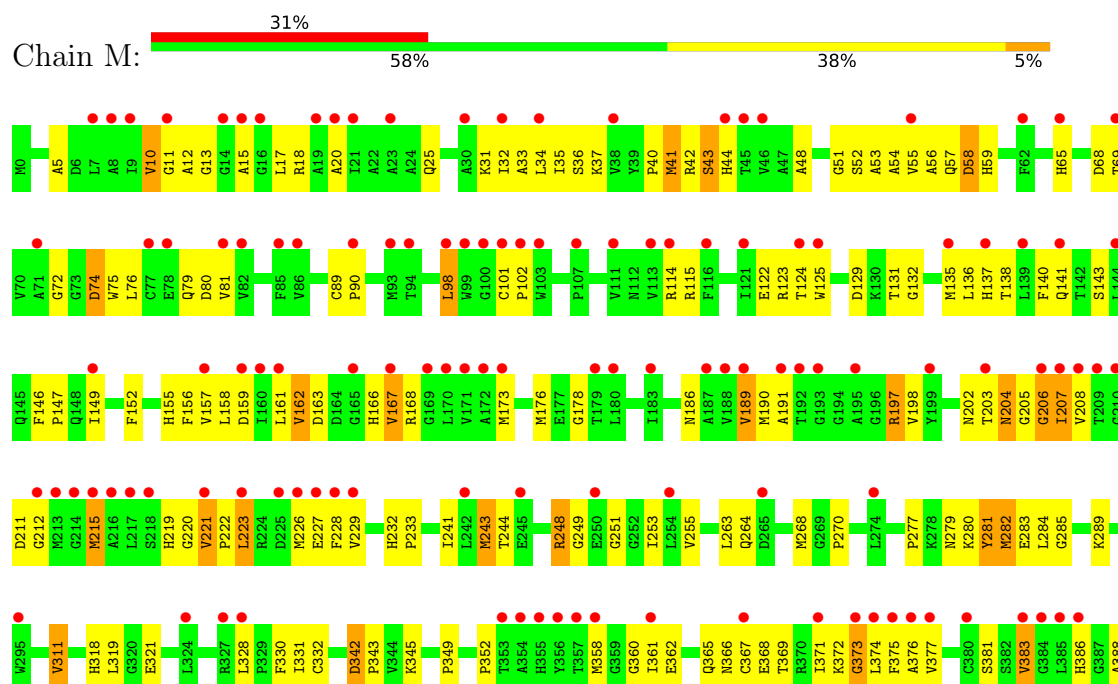
3 Residue-property plots

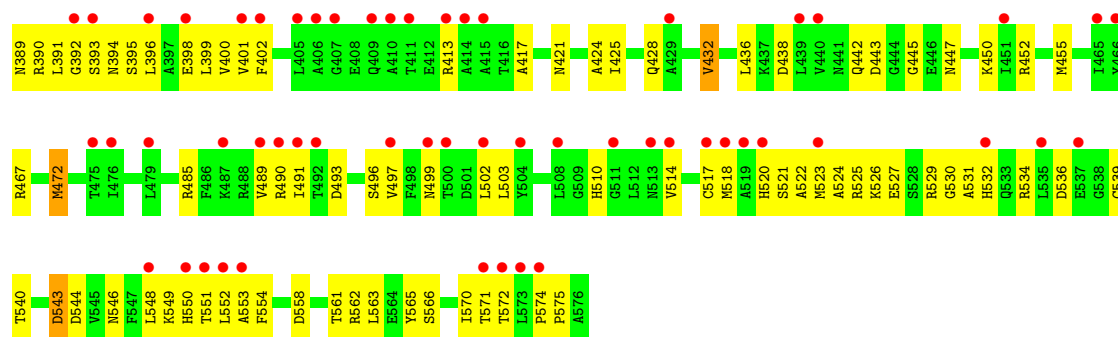
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

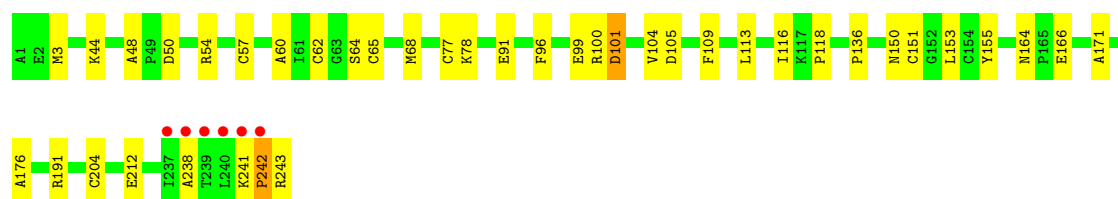
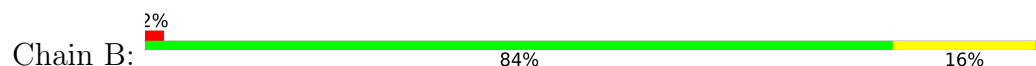


• Molecule 1: Fumarate reductase flavoprotein subunit

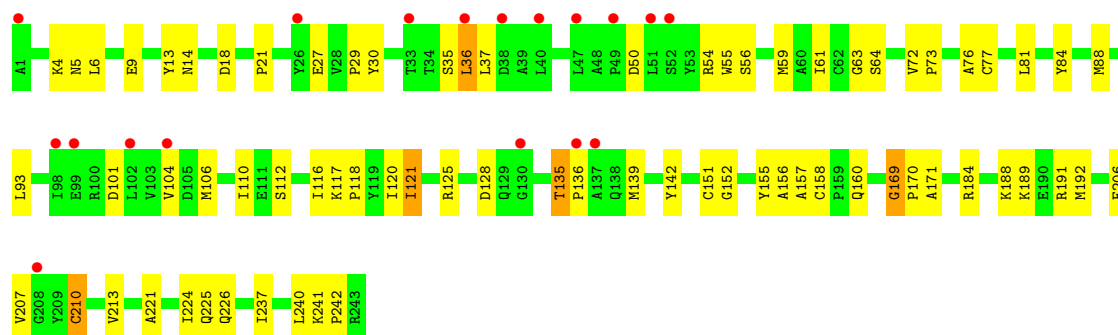




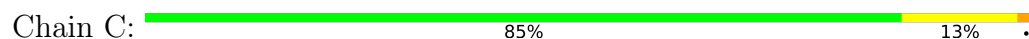
• Molecule 2: Fumarate reductase iron-sulfur subunit



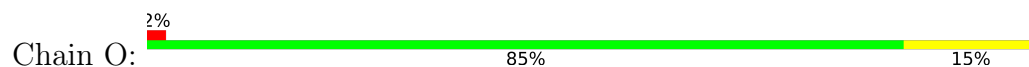
• Molecule 2: Fumarate reductase iron-sulfur subunit



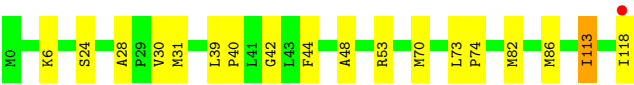
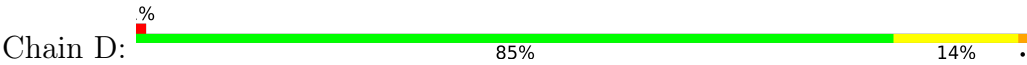
• Molecule 3: Fumarate reductase subunit C



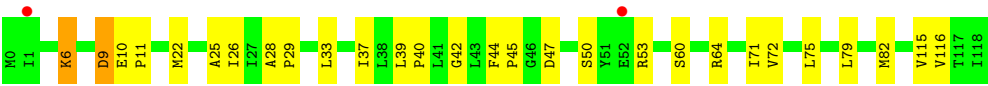
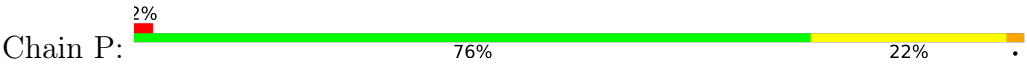
• Molecule 3: Fumarate reductase subunit C



• Molecule 4: Fumarate reductase subunit D



● Molecule 4: Fumarate reductase subunit D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.06Å 139.01Å 276.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.10 40.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	93.5 (40.00-3.10) 92.8 (40.00-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.255 , 0.279 0.254 , 0.281	Depositor DCC
R_{free} test set	1254 reflections (1.82%)	wwPDB-VP
Wilson B-factor (Å ²)	73.8	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	16792	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FES, SF4, F3S, FAD, 3NP

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	0.43	0/4541	0.83	1/6139 (0.0%)
1	M	0.48	0/4541	0.86	4/6139 (0.1%)
2	B	0.44	0/1931	0.82	0/2617
2	N	0.46	0/1931	0.83	2/2617 (0.1%)
3	C	0.42	0/1094	0.80	0/1496
3	O	0.46	0/1094	0.82	0/1496
4	D	0.43	0/956	0.87	0/1303
4	P	0.46	0/956	0.87	0/1303
All	All	0.45	0/17044	0.84	7/23110 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	342	ASP	CA-C-N	5.99	126.15	119.32
1	M	342	ASP	C-N-CA	5.99	126.15	119.32
1	A	351	ARG	N-CA-C	5.68	113.13	108.07
1	M	25	GLN	N-CA-C	5.58	117.22	111.03
1	M	204	ASN	N-CA-C	5.32	118.00	110.50
2	N	169	GLY	CA-C-N	5.30	126.46	119.84
2	N	169	GLY	C-N-CA	5.30	126.46	119.84

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	4449	0	4333	79	0
1	M	4449	0	4335	248	0
2	B	1888	0	1839	41	0
2	N	1888	0	1839	60	0
3	C	1058	0	1108	13	0
3	O	1058	0	1108	21	0
4	D	926	0	971	11	0
4	P	926	0	971	20	0
5	A	53	0	31	5	0
5	M	53	0	31	19	0
6	A	6	0	2	0	0
7	B	4	0	0	0	0
7	N	4	0	0	2	0
8	B	7	0	0	3	0
8	N	7	0	0	5	0
9	B	8	0	0	3	0
9	N	8	0	0	2	0
All	All	16792	0	16568	468	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 (468) 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:M:44:HIS:NE2	5:M:601:FAD:HM82	1.29	1.46
1:M:211:ASP:OD1	1:M:510:HIS:CD2	2.04	1.11
2:B:151:CYS:SG	9:B:246:SF4:FE1	1.46	1.06
1:M:115:ARG:HG2	1:M:122:GLU:HB3	1.38	1.03
1:M:219:HIS:HD2	1:M:371:ILE:HD13	1.18	1.02
1:M:227:GLU:HB2	1:M:522:ALA:HB2	1.42	1.02
1:M:219:HIS:CD2	1:M:371:ILE:HD13	1.98	0.98
1:M:129:ASP:OD2	1:M:330:PHE:HB2	1.62	0.98
1:M:44:HIS:NE2	5:M:601:FAD:C8M	2.26	0.98
1:M:158:LEU:HD13	1:M:436:LEU:HG	1.51	0.93
1:M:394:ASN:HB3	5:M:601:FAD:O2	1.67	0.93
2:N:210:CYS:SG	8:N:245:F3S:FE3	1.60	0.92
2:N:5:ASN:HA	2:N:30:TYR:CD2	2.05	0.92
2:B:136:PRO:HB2	3:C:100:ASP:OD2	1.71	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:15:ALA:HB2	1:M:399:LEU:HD22	1.55	0.88
4:D:113:ILE:HG23	4:D:118:ILE:HD11	1.57	0.87
1:M:219:HIS:HD2	1:M:371:ILE:CD1	1.87	0.86
2:N:5:ASN:OD1	2:N:29:PRO:HA	1.75	0.86
2:B:96:PHE:HB3	2:B:104:VAL:CG1	2.07	0.85
1:M:211:ASP:OD1	1:M:510:HIS:HD2	1.60	0.84
1:M:53:ALA:H	1:M:394:ASN:HB2	1.44	0.83
2:B:204:CYS:SG	8:B:245:F3S:FE1	1.70	0.83
1:M:390:ARG:HD2	1:M:395:SER:HB2	1.60	0.83
1:M:11:GLY:HA2	5:M:601:FAD:H1B	1.60	0.82
1:A:286:PRO:HG2	1:A:289:LYS:HG3	1.61	0.82
1:M:12:ALA:HB3	5:M:601:FAD:HO3A	1.44	0.82
1:A:390:ARG:HH11	1:A:395:SER:HB2	1.45	0.82
1:M:421:ASN:O	1:M:425:ILE:HG12	1.78	0.82
1:M:253:ILE:HA	1:M:283:GLU:HG2	1.61	0.81
1:M:202:ASN:ND2	1:M:204:ASN:HB2	1.96	0.81
1:M:221:VAL:CG2	1:M:371:ILE:HD12	2.11	0.81
2:N:35:SER:HB3	2:N:77:CYS:HA	1.62	0.81
1:M:12:ALA:HB3	5:M:601:FAD:O3B	1.80	0.80
2:N:5:ASN:HA	2:N:30:TYR:HD2	1.42	0.80
1:M:129:ASP:HB2	1:M:328:LEU:HA	1.64	0.80
1:M:221:VAL:HG23	1:M:371:ILE:HD12	1.64	0.80
2:B:204:CYS:HG	8:B:245:F3S:FE1	0.53	0.79
2:N:210:CYS:HG	8:N:245:F3S:FE3	0.50	0.79
1:M:12:ALA:CA	5:M:601:FAD:O3B	2.30	0.79
1:M:227:GLU:CB	1:M:522:ALA:HB2	2.13	0.79
1:M:12:ALA:N	5:M:601:FAD:O3B	2.15	0.79
1:M:205:GLY:HA3	2:N:56:SER:O	1.83	0.78
1:M:11:GLY:HA2	5:M:601:FAD:C1B	2.13	0.78
1:M:219:HIS:CD2	1:M:371:ILE:CD1	2.66	0.78
1:M:65:HIS:CD2	1:M:123:ARG:HD2	2.20	0.77
1:M:383:VAL:HG13	1:M:402:PHE:HE2	1.49	0.77
2:B:65:CYS:SG	2:B:77:CYS:HB2	2.25	0.76
2:B:96:PHE:HB3	2:B:104:VAL:HG11	1.67	0.76
1:M:372:LYS:O	1:M:413:ARG:HG2	1.84	0.76
2:B:151:CYS:HG	9:B:246:SF4:FE1	1.00	0.76
3:O:87:PHE:CD1	3:O:112:LEU:HB3	2.21	0.75
1:M:211:ASP:HA	1:M:510:HIS:HB2	1.67	0.75
1:A:279:ASN:O	1:A:280:LYS:HG2	1.85	0.75
1:M:521:SER:OG	1:M:551:THR:HB	1.85	0.75
3:C:33:VAL:HB	3:C:34:PRO:HD3	1.69	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:227:GLU:HB2	1:M:522:ALA:CB	2.16	0.74
1:A:18:ARG:HG2	1:A:400:VAL:HA	1.70	0.74
1:M:413:ARG:O	1:M:417:ALA:HB2	1.87	0.74
1:M:48:ALA:HB3	1:M:132:GLY:HA3	1.70	0.73
1:M:472:MET:HE1	1:M:523:MET:CG	2.19	0.73
1:M:79:GLN:HB3	1:M:571:THR:HG22	1.69	0.73
2:N:210:CYS:SG	8:N:245:F3S:S1	2.87	0.73
1:M:57:GLN:O	1:M:58:ASP:HB2	1.86	0.72
1:M:168:ARG:HG3	1:M:425:ILE:HG13	1.71	0.72
1:M:53:ALA:HB3	1:M:394:ASN:H	1.55	0.72
3:O:83:THR:O	3:O:87:PHE:CD2	2.44	0.71
1:M:229:VAL:O	1:M:531:ALA:HB1	1.91	0.71
2:N:221:ALA:O	2:N:225:GLN:HG2	1.91	0.71
1:A:390:ARG:HH11	1:A:395:SER:CB	2.03	0.71
1:M:191:ALA:HB2	1:M:377:VAL:HG13	1.71	0.71
1:M:226:MET:HG3	1:M:517:CYS:HB3	1.72	0.71
3:O:83:THR:O	3:O:87:PHE:HD2	1.74	0.70
1:A:390:ARG:NH1	1:A:395:SER:CB	2.54	0.70
1:M:114:ARG:HH12	1:M:328:LEU:HD21	1.57	0.70
1:M:115:ARG:CG	1:M:122:GLU:HB3	2.18	0.69
3:O:33:VAL:HB	3:O:34:PRO:HD3	1.74	0.69
1:M:159:ASP:HB3	1:M:432:VAL:HG23	1.74	0.69
3:O:31:THR:HG21	3:O:82:HIS:HB2	1.74	0.69
1:A:390:ARG:NH1	1:A:395:SER:HB2	2.08	0.69
1:M:80:ASP:HB3	1:M:365:GLN:OE1	1.93	0.69
1:M:161:LEU:O	1:M:167:VAL:HG23	1.91	0.68
1:M:251:GLY:HA2	1:M:277:PRO:HG2	1.74	0.68
1:M:12:ALA:CB	5:M:601:FAD:O3B	2.40	0.68
1:M:163:ASP:HB2	1:M:425:ILE:HD11	1.75	0.68
1:M:55:VAL:HB	1:M:90:PRO:HG3	1.76	0.68
1:M:114:ARG:O	1:M:124:THR:HB	1.93	0.68
1:M:20:ALA:HB2	1:M:34:LEU:HD11	1.76	0.67
1:M:20:ALA:CB	1:M:34:LEU:HD11	2.24	0.67
2:N:37:LEU:HD22	2:N:77:CYS:HA	1.76	0.67
2:N:112:SER:O	2:N:116:ILE:HG12	1.95	0.67
1:M:5:ALA:HA	1:M:31:LYS:HD2	1.76	0.66
1:M:42:ARG:O	1:M:43:SER:HB2	1.93	0.66
7:N:244:FES:FE2	7:N:244:FES:S1	1.86	0.66
3:C:91:PRO:HB2	3:C:105:PRO:HB3	1.76	0.66
1:M:159:ASP:HB3	1:M:432:VAL:CG2	2.24	0.66
1:A:386:HIS:ND1	1:A:390:ARG:HG3	2.10	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:HIS:NE2	5:A:601:FAD:C8M	2.59	0.66
2:B:96:PHE:CB	2:B:104:VAL:HG11	2.25	0.65
1:M:280:LYS:HA	1:M:285:GLY:HA2	1.76	0.65
3:O:87:PHE:CE1	3:O:112:LEU:HB3	2.31	0.65
2:B:96:PHE:HB3	2:B:104:VAL:HG13	1.77	0.65
1:A:65:HIS:ND1	1:A:86:VAL:HG12	2.12	0.65
2:N:81:LEU:HG	2:N:88:MET:HE1	1.77	0.65
1:M:264:GLN:HE22	1:M:270:PRO:HA	1.61	0.65
2:N:151:CYS:SG	9:N:246:SF4:FE1	1.90	0.64
1:M:493:ASP:OD2	2:N:50:ASP:HA	1.98	0.64
1:M:472:MET:HE1	1:M:523:MET:HG2	1.78	0.63
3:O:87:PHE:CD1	3:O:112:LEU:CB	2.81	0.63
1:A:44:HIS:NE2	5:A:601:FAD:HM83	2.14	0.63
1:A:42:ARG:HG2	2:B:64:SER:HB3	1.80	0.63
1:M:543:ASP:HB3	1:M:546:ASN:HB2	1.80	0.62
1:M:472:MET:HE1	1:M:523:MET:HG3	1.81	0.62
1:M:227:GLU:HA	1:M:518:MET:O	1.99	0.62
1:M:68:ASP:O	1:M:391:LEU:CD2	2.47	0.62
2:N:14:ASN:H	2:N:18:ASP:HB2	1.64	0.62
2:B:151:CYS:SG	9:B:246:SF4:S2	2.97	0.62
1:M:140:PHE:O	1:M:143:SER:HB3	1.99	0.62
1:M:398:GLU:O	1:M:402:PHE:HB3	1.99	0.62
2:B:44:LYS:HA	2:B:48:ALA:O	2.00	0.62
4:P:6:LYS:H	4:P:6:LYS:HD3	1.64	0.62
1:M:208:VAL:O	1:M:208:VAL:HG12	1.99	0.61
1:M:526:LYS:HB3	1:M:539:CYS:SG	2.40	0.61
1:M:342:ASP:HB3	1:M:345:LYS:HB3	1.81	0.61
1:A:141:GLN:HB3	2:B:118:PRO:O	2.01	0.61
2:N:63:GLY:N	7:N:244:FES:S1	2.69	0.61
1:M:162:VAL:CG2	1:M:219:HIS:HE1	2.13	0.61
1:M:221:VAL:HG11	1:M:369:THR:HB	1.82	0.61
1:A:315:ASP:HB3	1:A:318:HIS:HE1	1.64	0.61
1:M:233:PRO:HG2	1:M:248:ARG:HH22	1.66	0.61
1:M:101:CYS:HB2	1:M:138:THR:HG21	1.83	0.60
1:M:12:ALA:C	5:M:601:FAD:O3B	2.44	0.60
1:M:452:ARG:HA	1:M:455:MET:HE2	1.82	0.60
3:O:87:PHE:HD1	3:O:112:LEU:CB	2.15	0.60
3:O:87:PHE:HD1	3:O:112:LEU:HB2	1.67	0.60
2:N:37:LEU:HD12	2:N:55:TRP:HB2	1.84	0.60
1:M:98:LEU:HD11	2:N:125:ARG:HD3	1.84	0.59
3:C:90:ALA:N	3:C:91:PRO:HD2	2.17	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:48:ALA:O	4:D:53:ARG:HD3	2.02	0.59
1:A:129:ASP:OD1	1:A:130:LYS:HG2	2.01	0.59
1:M:215:MET:HG3	1:M:510:HIS:CE1	2.37	0.59
1:A:51:GLY:HA2	1:A:131:THR:HG21	1.83	0.59
1:M:72:GLY:CA	1:M:391:LEU:HD21	2.33	0.59
1:M:72:GLY:HA3	1:M:391:LEU:HD21	1.84	0.59
1:M:51:GLY:O	5:M:601:FAD:N3	2.31	0.59
1:M:52:SER:O	1:M:125:TRP:HB2	2.03	0.58
1:A:390:ARG:NH1	1:A:395:SER:HB3	2.17	0.58
1:A:167:VAL:HG21	1:A:374:LEU:HB2	1.85	0.58
1:A:253:ILE:O	1:A:314:LEU:HA	2.03	0.58
2:B:155:TYR:HE1	2:B:171:ALA:HB3	1.68	0.58
1:M:54:ALA:O	1:M:123:ARG:O	2.22	0.58
1:M:211:ASP:HA	1:M:510:HIS:CB	2.33	0.58
1:M:162:VAL:HB	1:M:219:HIS:CE1	2.39	0.58
1:A:372:LYS:HE3	1:A:413:ARG:HD2	1.86	0.57
1:M:166:HIS:NE2	1:M:373:GLY:CA	2.67	0.57
2:N:5:ASN:CA	2:N:30:TYR:CD2	2.86	0.57
1:M:68:ASP:O	1:M:391:LEU:HD22	2.05	0.57
2:N:116:ILE:O	2:N:191:ARG:HG2	2.04	0.57
1:M:361:ILE:HB	1:M:376:ALA:HB3	1.85	0.57
4:P:64:ARG:HH21	4:P:116:VAL:HA	1.70	0.57
1:M:178:GLY:HA3	1:M:496:SER:O	2.05	0.56
1:A:358:MET:HE3	1:A:389:ASN:HA	1.87	0.56
2:B:241:LYS:N	2:B:242:PRO:HD2	2.20	0.56
1:M:311:VAL:HG11	1:M:349:PRO:HB3	1.85	0.56
2:N:152:GLY:N	9:N:246:SF4:S4	2.72	0.56
1:M:31:LYS:HE2	1:M:33:ALA:HB2	1.86	0.56
1:M:226:MET:HB2	1:M:517:CYS:O	2.06	0.56
1:M:383:VAL:HG13	1:M:402:PHE:CE2	2.35	0.56
1:A:341:VAL:HA	1:A:346:GLU:OE2	2.06	0.56
2:N:84:TYR:HB2	2:N:88:MET:HE2	1.87	0.55
2:N:188:LYS:HB3	2:N:192:MET:HE2	1.88	0.55
1:A:315:ASP:HB3	1:A:318:HIS:CE1	2.42	0.55
1:M:544:ASP:O	1:M:548:LEU:HB2	2.06	0.55
2:N:158:CYS:HB2	8:N:245:F3S:S4	2.45	0.55
1:A:57:GLN:NE2	1:A:122:GLU:OE2	2.33	0.55
2:N:155:TYR:CE2	2:N:169:GLY:HA3	2.41	0.55
1:M:12:ALA:CB	5:M:601:FAD:HO3A	2.15	0.55
1:M:101:CYS:C	2:N:184:ARG:HH22	2.15	0.55
1:A:28:PRO:HA	1:A:148:GLN:HE21	1.70	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:232:HIS:O	1:M:352:PRO:HA	2.07	0.55
1:M:263:LEU:HB2	1:M:282:MET:SD	2.47	0.55
1:M:123:ARG:O	1:M:125:TRP:CD1	2.60	0.55
1:A:197:ARG:HD2	1:A:206:GLY:HA2	1.89	0.54
1:M:115:ARG:HG2	1:M:122:GLU:CB	2.25	0.54
2:B:60:ALA:N	2:B:77:CYS:SG	2.81	0.54
3:C:106:GLU:HB2	3:C:107:PRO:HD3	1.90	0.54
1:M:211:ASP:O	1:M:510:HIS:CG	2.60	0.54
1:M:221:VAL:HG22	1:M:371:ILE:HD12	1.89	0.54
1:M:166:HIS:NE2	1:M:373:GLY:HA3	2.23	0.54
1:A:341:VAL:HG13	1:A:346:GLU:HG3	1.90	0.54
1:M:18:ARG:HG2	1:M:400:VAL:HA	1.88	0.54
1:A:224:ARG:NH2	1:A:382:SER:O	2.39	0.54
2:B:116:ILE:HD11	2:B:118:PRO:HB3	1.88	0.54
1:A:263:LEU:O	1:A:268:MET:HB2	2.08	0.54
1:M:226:MET:CB	1:M:518:MET:HA	2.37	0.54
2:N:5:ASN:CG	2:N:29:PRO:HA	2.31	0.54
1:A:122:GLU:H	1:A:122:GLU:CD	2.16	0.54
1:M:443:ASP:HA	1:M:490:ARG:HG2	1.90	0.53
1:A:316:LEU:HA	1:A:319:LEU:HD23	1.91	0.53
4:P:79:LEU:HD23	4:P:82:MET:HE2	1.91	0.53
1:M:102:PRO:HB2	2:N:139:MET:HE3	1.90	0.53
1:M:166:HIS:CD2	1:M:373:GLY:HA3	2.43	0.53
1:A:253:ILE:HG12	1:A:318:HIS:CE1	2.44	0.53
1:M:467:ARG:O	1:M:534:ARG:HA	2.08	0.53
1:A:342:ASP:C	1:A:344:VAL:H	2.17	0.53
1:M:12:ALA:H	5:M:601:FAD:H1B	1.74	0.53
1:A:44:HIS:NE2	5:A:601:FAD:HM81	2.23	0.53
2:N:37:LEU:HD22	2:N:77:CYS:CA	2.39	0.53
1:A:315:ASP:C	1:A:318:HIS:CE1	2.87	0.52
1:M:57:GLN:O	1:M:58:ASP:CB	2.56	0.52
1:M:226:MET:HB3	1:M:518:MET:HA	1.90	0.52
1:A:61:SER:HB3	1:A:64:TYR:CD1	2.44	0.52
3:C:120:THR:HG23	4:D:30:VAL:HB	1.91	0.52
2:B:65:CYS:SG	2:B:77:CYS:CB	2.97	0.52
1:M:36:SER:HA	5:M:601:FAD:N3A	2.24	0.52
1:M:222:PRO:HB3	1:M:552:LEU:HB3	1.89	0.52
1:M:445:GLY:H	1:M:490:ARG:HG3	1.74	0.52
2:N:206:PHE:CE1	2:N:225:GLN:HG3	2.44	0.52
2:N:210:CYS:SG	8:N:245:F3S:S4	3.07	0.52
4:D:42:GLY:HA2	4:D:44:PHE:CE2	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:525:ARG:HG2	1:M:527:GLU:HG2	1.91	0.52
1:M:553:ALA:HB1	1:M:561:THR:CG2	2.40	0.52
1:A:11:GLY:HA2	5:A:601:FAD:H1B	1.91	0.52
2:N:5:ASN:HB2	2:N:27:GLU:HG2	1.92	0.52
1:M:13:GLY:N	5:M:601:FAD:H4B	2.25	0.52
1:M:42:ARG:O	1:M:43:SER:CB	2.58	0.52
3:O:83:THR:HG23	3:O:87:PHE:CE2	2.44	0.52
2:B:212:GLU:HG3	3:C:21:PHE:CE1	2.45	0.51
2:N:35:SER:HB2	2:N:37:LEU:HD23	1.92	0.51
3:O:90:ALA:N	3:O:91:PRO:HD2	2.25	0.51
4:P:10:GLU:N	4:P:11:PRO:HD2	2.26	0.51
3:O:71:ILE:HA	3:O:74:ILE:HD12	1.93	0.51
1:M:72:GLY:H	1:M:391:LEU:HD21	1.75	0.51
1:A:236:LEU:HD21	1:A:243:MET:HE3	1.92	0.51
1:M:524:ALA:CB	1:M:565:TYR:OH	2.59	0.51
1:M:53:ALA:N	1:M:394:ASN:HB2	2.21	0.50
1:M:173:MET:HE3	1:M:178:GLY:HA2	1.92	0.50
1:M:166:HIS:NE2	1:M:373:GLY:HA2	2.25	0.50
4:P:39:LEU:HB3	4:P:40:PRO:HD3	1.91	0.50
1:A:266:TYR:OH	1:A:297:GLU:HG2	2.11	0.50
1:A:386:HIS:CE1	1:A:390:ARG:HG3	2.46	0.50
1:M:42:ARG:CZ	2:N:64:SER:HA	2.41	0.50
1:A:41:MET:HE2	2:B:150:ASN:HD22	1.76	0.50
4:D:42:GLY:HA2	4:D:44:PHE:HE2	1.76	0.50
1:M:166:HIS:HE1	1:M:186:ASN:C	2.20	0.50
1:M:279:ASN:O	1:M:280:LYS:HG2	2.11	0.50
3:O:87:PHE:HE2	4:P:25:ALA:HB1	1.76	0.50
4:P:42:GLY:HA2	4:P:44:PHE:CE2	2.47	0.50
1:A:167:VAL:CG2	1:A:374:LEU:HB2	2.42	0.50
1:M:10:VAL:HG13	5:M:601:FAD:C2A	2.42	0.49
1:M:69:THR:HA	1:M:391:LEU:HD22	1.94	0.49
1:M:162:VAL:HG13	1:M:428:GLN:HE22	1.77	0.49
1:M:249:GLY:HA2	1:M:284:LEU:HD21	1.93	0.49
2:N:5:ASN:CA	2:N:30:TYR:CE2	2.96	0.49
1:A:232:HIS:CD2	1:A:234:THR:H	2.31	0.49
4:D:73:LEU:HB2	4:D:74:PRO:HD3	1.94	0.49
1:M:123:ARG:O	1:M:125:TRP:HD1	1.94	0.49
1:M:251:GLY:O	1:M:318:HIS:NE2	2.45	0.49
1:M:447:ASN:HB3	1:M:450:LYS:HG2	1.93	0.49
2:N:120:ILE:C	2:N:121:ILE:HG13	2.37	0.49
1:M:76:LEU:HD12	1:M:529:ARG:HD3	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:162:VAL:HB	1:M:219:HIS:HE1	1.76	0.49
4:P:60:SER:O	4:P:64:ARG:HG3	2.13	0.49
1:A:204:ASN:N	1:A:204:ASN:HD22	2.11	0.49
1:M:52:SER:HA	1:M:394:ASN:HB2	1.94	0.49
1:M:268:MET:CE	1:M:289:LYS:HB3	2.42	0.49
1:M:372:LYS:O	1:M:413:ARG:CG	2.59	0.49
2:N:13:TYR:HB2	2:N:21:PRO:HB3	1.93	0.49
1:A:466:TYR:CD2	1:A:535:LEU:HD21	2.48	0.49
1:M:41:MET:HA	1:M:136:LEU:HD11	1.95	0.49
2:N:36:LEU:HB3	2:N:76:ALA:HB1	1.95	0.49
1:M:383:VAL:CG1	1:M:402:PHE:HE2	2.23	0.48
1:M:72:GLY:N	1:M:391:LEU:HD21	2.29	0.48
1:M:10:VAL:HG21	1:M:157:VAL:HG21	1.95	0.48
1:M:141:GLN:HB3	2:N:118:PRO:O	2.14	0.48
3:O:43:ILE:HD11	4:P:71:ILE:HG21	1.94	0.48
1:A:316:LEU:O	1:A:319:LEU:HB2	2.12	0.48
1:M:168:ARG:HG3	1:M:425:ILE:CG1	2.40	0.48
1:M:562:ARG:HG2	1:M:563:LEU:H	1.78	0.48
1:A:315:ASP:O	1:A:318:HIS:CE1	2.66	0.48
1:A:462:GLY:HA3	1:A:475:THR:OG1	2.13	0.48
2:N:241:LYS:H	2:N:242:PRO:HD2	1.78	0.48
1:A:356:TYR:CE2	1:A:390:ARG:HD3	2.49	0.48
2:B:116:ILE:HD13	2:B:176:ALA:HA	1.94	0.48
2:B:238:ALA:HA	2:B:241:LYS:HB2	1.94	0.48
1:A:315:ASP:C	1:A:318:HIS:HE1	2.22	0.48
2:B:241:LYS:O	2:B:243:ARG:HG2	2.14	0.47
3:C:33:VAL:HA	4:D:82:MET:CE	2.44	0.47
1:M:369:THR:OG1	1:M:374:LEU:O	2.25	0.47
1:M:53:ALA:H	1:M:394:ASN:CB	2.21	0.47
1:M:72:GLY:HA3	1:M:391:LEU:CD2	2.43	0.47
1:M:389:ASN:ND2	1:M:530:GLY:HA2	2.29	0.47
1:A:275:GLY:O	1:A:277:PRO:HD3	2.13	0.47
1:M:226:MET:HB2	1:M:517:CYS:C	2.39	0.47
1:M:438:ASP:O	1:M:442:GLN:HB2	2.13	0.47
1:M:570:ILE:HG12	1:M:575:PRO:HG3	1.96	0.47
4:D:6:LYS:HA	4:P:6:LYS:HG2	1.96	0.47
1:M:76:LEU:CD1	1:M:525:ARG:NH1	2.78	0.47
1:M:135:MET:HE1	1:M:396:LEU:HB3	1.96	0.47
1:M:189:VAL:HA	1:M:375:PHE:HB2	1.97	0.47
1:M:226:MET:HB3	1:M:518:MET:HG2	1.96	0.47
2:N:93:LEU:HG	2:N:156:ALA:HB2	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:22:MET:O	4:P:26:ILE:HD12	2.15	0.47
1:M:102:PRO:HB3	2:N:142:TYR:OH	2.15	0.47
1:M:152:PHE:N	1:M:152:PHE:CD1	2.83	0.47
1:M:243:MET:HE3	1:M:243:MET:HA	1.97	0.47
1:M:386:HIS:ND1	1:M:390:ARG:HG3	2.30	0.47
1:M:562:ARG:HG2	1:M:563:LEU:N	2.30	0.47
3:O:87:PHE:CE2	4:P:25:ALA:HB1	2.49	0.47
1:M:522:ALA:HB1	1:M:532:HIS:CE1	2.50	0.47
1:M:553:ALA:HB1	1:M:561:THR:HG21	1.97	0.46
1:M:221:VAL:CG1	1:M:369:THR:HB	2.46	0.46
1:M:398:GLU:O	1:M:402:PHE:CB	2.62	0.46
1:M:226:MET:C	1:M:518:MET:HA	2.40	0.46
3:O:128:LEU:HD22	4:P:45:PRO:HD2	1.98	0.46
4:P:33:LEU:HA	4:P:37:ILE:HD12	1.97	0.46
1:A:10:VAL:HB	1:A:190:MET:CE	2.45	0.46
2:B:78:LYS:O	2:B:78:LYS:HG2	2.14	0.46
1:M:520:HIS:HB3	1:M:563:LEU:HD21	1.96	0.46
2:N:210:CYS:SG	2:N:221:ALA:HB2	2.55	0.46
1:A:232:HIS:HD2	1:A:234:THR:H	1.64	0.46
2:B:57:CYS:HB3	2:B:62:CYS:HB3	1.97	0.46
2:B:100:ARG:O	2:B:101:ASP:C	2.58	0.46
1:M:42:ARG:HD2	2:N:64:SER:OG	2.15	0.46
1:M:65:HIS:HD2	1:M:123:ARG:HH11	1.64	0.46
1:M:226:MET:HE3	1:M:518:MET:HG2	1.97	0.46
1:A:96:LEU:HD11	1:A:400:VAL:HG11	1.97	0.46
1:M:125:TRP:CD1	1:M:125:TRP:N	2.83	0.46
2:B:109:PHE:HE2	2:B:113:LEU:HD12	1.80	0.46
1:M:20:ALA:HB1	1:M:34:LEU:HD11	1.96	0.46
1:M:244:THR:CG2	1:M:331:ILE:HD11	2.46	0.46
1:M:366:ASN:O	1:M:367:CYS:HB2	2.15	0.46
2:B:204:CYS:SG	8:B:245:F3S:S1	3.13	0.46
1:M:75:TRP:CD1	1:M:575:PRO:HA	2.50	0.46
1:M:44:HIS:HB2	1:M:208:VAL:HG21	1.98	0.46
2:B:164:ASN:OD1	2:B:164:ASN:C	2.58	0.46
1:M:53:ALA:HB3	1:M:393:SER:HA	1.98	0.46
1:M:263:LEU:HD13	1:M:283:GLU:H	1.81	0.46
1:M:13:GLY:O	1:M:17:LEU:HG	2.16	0.45
1:M:215:MET:HG3	1:M:510:HIS:HE1	1.81	0.45
2:N:207:VAL:HG22	3:O:25:TYR:CZ	2.51	0.45
4:P:9:ASP:OD2	4:P:9:ASP:N	2.50	0.45
1:A:197:ARG:HB2	1:A:208:VAL:O	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:54:ARG:NH2	2:N:104:VAL:O	2.49	0.45
1:M:56:ALA:HB2	1:M:123:ARG:HA	1.98	0.45
2:B:50:ASP:O	2:B:100:ARG:NH2	2.48	0.45
1:A:122:GLU:OE2	1:A:122:GLU:N	2.50	0.45
1:A:237:PRO:O	1:A:308:ARG:HD2	2.16	0.45
1:A:356:TYR:CE1	1:A:379:GLU:HG3	2.51	0.45
1:M:168:ARG:HG3	1:M:425:ILE:CD1	2.46	0.45
1:M:156:PHE:O	1:M:173:MET:N	2.41	0.45
1:M:550:HIS:HB2	1:M:566:SER:HB2	1.99	0.45
1:M:12:ALA:HA	1:M:17:LEU:HD21	1.99	0.45
1:M:33:ALA:HB1	1:M:152:PHE:CE1	2.52	0.45
1:M:76:LEU:HD11	1:M:525:ARG:NH1	2.31	0.45
1:M:212:GLY:O	1:M:215:MET:HB2	2.17	0.45
1:A:232:HIS:CE1	1:A:242:LEU:HD11	2.52	0.44
2:N:6:LEU:N	2:N:30:TYR:CE2	2.85	0.44
1:A:363:THR:HB	1:A:367:CYS:HA	1.99	0.44
1:M:51:GLY:HA2	1:M:131:THR:HG21	2.00	0.44
2:B:164:ASN:OD1	2:B:166:GLU:N	2.50	0.44
5:A:601:FAD:H9	5:A:601:FAD:H1'1	1.81	0.44
1:M:89:CYS:SG	1:M:401:VAL:HG21	2.58	0.44
1:M:197:ARG:HA	1:M:202:ASN:HD21	1.82	0.44
1:M:536:ASP:O	1:M:540:THR:HG23	2.17	0.44
1:M:37:LYS:HA	1:M:155:HIS:H	1.81	0.44
1:M:571:THR:HG23	1:M:572:THR:N	2.33	0.44
1:A:127:ALA:HB3	1:A:131:THR:HA	2.00	0.44
1:A:529:ARG:NH2	1:A:548:LEU:HD13	2.32	0.44
1:M:228:PHE:HB3	1:M:358:MET:HE3	2.00	0.44
1:M:510:HIS:O	1:M:514:VAL:HG23	2.18	0.44
1:M:34:LEU:HD13	1:M:149:ILE:HG23	1.99	0.44
1:M:115:ARG:HE	1:M:279:ASN:HD22	1.66	0.44
1:M:248:ARG:H	1:M:248:ARG:HG2	1.57	0.44
3:C:50:LYS:HE2	3:C:50:LYS:HA	1.99	0.43
1:M:10:VAL:HG13	5:M:601:FAD:N1A	2.32	0.43
1:M:383:VAL:CG1	1:M:402:PHE:CE2	3.00	0.43
1:M:207:ILE:HG13	1:M:208:VAL:HG23	2.01	0.43
2:N:157:ALA:HB2	2:N:213:VAL:HG21	2.00	0.43
4:P:72:VAL:O	4:P:75:LEU:HB2	2.19	0.43
1:A:550:HIS:HB2	1:A:566:SER:OG	2.18	0.43
4:D:39:LEU:HB3	4:D:40:PRO:HD3	1.99	0.43
1:M:369:THR:HG21	1:M:375:PHE:HA	2.00	0.43
1:A:125:TRP:CD1	1:A:125:TRP:N	2.87	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:74:ASP:OD1	1:M:74:ASP:N	2.52	0.43
2:N:4:LYS:C	2:N:5:ASN:OD1	2.62	0.43
3:C:106:GLU:CD	3:C:106:GLU:H	2.26	0.43
1:M:162:VAL:CB	1:M:219:HIS:HE1	2.31	0.43
2:N:155:TYR:HE1	2:N:171:ALA:HB3	1.84	0.43
2:N:158:CYS:SG	2:N:160:GLN:HB2	2.59	0.43
3:O:33:VAL:HB	3:O:34:PRO:CD	2.47	0.43
1:A:54:ALA:HB3	1:A:125:TRP:NE1	2.33	0.43
1:M:176:MET:O	1:M:497:VAL:HG13	2.19	0.43
2:B:99:GLU:OE2	3:C:4:ARG:NH1	2.52	0.42
1:M:219:HIS:CD2	1:M:371:ILE:HD11	2.53	0.42
1:A:42:ARG:NH2	2:B:150:ASN:O	2.51	0.42
2:B:65:CYS:SG	2:B:77:CYS:N	2.82	0.42
1:M:81:VAL:HG11	1:M:383:VAL:HB	2.01	0.42
5:M:601:FAD:H9	5:M:601:FAD:H1'1	1.75	0.42
1:A:57:GLN:NE2	1:A:122:GLU:O	2.52	0.42
1:A:304:ILE:HD12	1:A:304:ILE:H	1.84	0.42
3:C:49:LEU:HB2	3:C:56:TRP:CE3	2.54	0.42
1:M:282:MET:C	1:M:284:LEU:H	2.27	0.42
1:M:421:ASN:ND2	1:M:424:ALA:HB3	2.34	0.42
1:M:12:ALA:HB1	1:M:40:PRO:HA	2.00	0.42
1:M:368:GLU:HG3	1:M:375:PHE:CE2	2.55	0.42
1:M:499:ASN:O	1:M:503:LEU:HG	2.20	0.42
4:P:47:ASP:HB2	4:P:50:SER:HB3	2.01	0.42
1:A:11:GLY:HA3	1:A:191:ALA:O	2.20	0.42
1:M:159:ASP:OD2	1:M:432:VAL:HB	2.19	0.42
1:M:428:GLN:O	1:M:432:VAL:HG12	2.19	0.42
2:B:104:VAL:CG1	2:B:105:ASP:N	2.82	0.42
1:M:281:TYR:O	1:M:282:MET:CB	2.68	0.42
2:N:6:LEU:N	2:N:30:TYR:CD2	2.86	0.42
2:N:135:THR:HG22	2:N:136:PRO:HD2	2.02	0.42
3:O:28:ARG:HG3	3:O:85:THR:HG21	2.00	0.42
1:M:228:PHE:CZ	1:M:388:ALA:HA	2.55	0.42
2:N:188:LYS:H	2:N:188:LYS:HG3	1.63	0.42
1:A:154:GLU:OE2	2:B:54:ARG:NE	2.53	0.42
2:B:68:MET:HB2	2:B:91:GLU:HB2	2.02	0.42
1:M:491:ILE:HD13	1:M:502:LEU:HD12	2.01	0.42
2:N:117:LYS:N	2:N:118:PRO:HD3	2.34	0.42
1:A:497:VAL:O	2:B:100:ARG:NH1	2.53	0.42
1:M:574:PRO:HA	1:M:575:PRO:HD3	1.92	0.42
4:P:37:ILE:C	4:P:40:PRO:HD2	2.45	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ALA:O	1:A:123:ARG:O	2.38	0.41
4:D:24:SER:O	4:D:28:ALA:HB3	2.19	0.41
1:M:377:VAL:HG23	1:M:402:PHE:CD1	2.55	0.41
2:N:59:MET:HE2	2:N:61:ILE:HG21	2.02	0.41
3:O:19:LEU:HB2	3:O:20:PRO:HD2	2.02	0.41
1:A:366:ASN:O	1:A:367:CYS:HB2	2.21	0.41
1:M:361:ILE:H	1:M:381:SER:HA	1.85	0.41
1:M:553:ALA:HA	1:M:562:ARG:O	2.20	0.41
2:N:170:PRO:HA	2:N:224:ILE:HD11	2.03	0.41
3:C:63:LEU:HA	3:C:68:ILE:HG21	2.03	0.41
1:M:43:SER:OG	1:M:44:HIS:N	2.53	0.41
1:M:53:ALA:HA	1:M:124:THR:HA	2.03	0.41
1:M:268:MET:HE1	1:M:289:LYS:HB3	2.00	0.41
2:B:241:LYS:N	2:B:242:PRO:CD	2.84	0.41
1:M:98:LEU:CD1	2:N:125:ARG:HD3	2.49	0.41
1:M:198:VAL:HA	1:M:455:MET:HE3	2.02	0.41
1:M:525:ARG:NH2	1:M:549:LYS:O	2.54	0.41
1:A:543:ASP:OD2	1:A:546:ASN:HB2	2.21	0.41
1:M:485:ARG:O	1:M:489:VAL:HG23	2.20	0.41
1:M:554:PHE:O	1:M:561:THR:HA	2.21	0.41
1:M:76:LEU:HD13	1:M:525:ARG:HH12	1.86	0.41
1:M:146:PHE:HA	1:M:147:PRO:HD3	1.90	0.41
1:M:232:HIS:HA	1:M:233:PRO:HD2	1.90	0.41
1:M:524:ALA:HB1	1:M:565:TYR:OH	2.21	0.41
4:P:28:ALA:N	4:P:29:PRO:HD2	2.36	0.41
1:A:38:VAL:HG11	1:A:207:ILE:HG21	2.03	0.41
1:A:450:LYS:HA	1:A:450:LYS:HD3	1.85	0.41
1:A:451:ILE:HG23	1:A:482:LEU:HD22	2.02	0.41
1:M:197:ARG:HD2	1:M:206:GLY:HA2	2.03	0.41
1:M:223:LEU:HD23	1:M:360:GLY:HA2	2.03	0.41
1:A:448:TRP:CG	1:A:449:ALA:N	2.88	0.41
2:B:241:LYS:O	2:B:243:ARG:N	2.53	0.41
4:D:31:MET:HG3	4:D:70:MET:SD	2.61	0.41
3:O:130:TRP:O	4:P:53:ARG:NH2	2.54	0.41
1:M:166:HIS:CE1	1:M:186:ASN:O	2.74	0.40
1:M:332:CYS:HA	1:M:343:PRO:HG2	2.02	0.40
1:M:395:SER:O	1:M:398:GLU:HB3	2.22	0.40
1:M:524:ALA:HB3	1:M:565:TYR:OH	2.20	0.40
2:N:72:VAL:HA	2:N:73:PRO:HD3	1.92	0.40
1:M:41:MET:HB2	1:M:137:HIS:CE1	2.56	0.40
1:M:472:MET:HE2	1:M:472:MET:HB3	1.89	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:LEU:HD12	1:A:323:LYS:HD3	2.02	0.40
1:M:53:ALA:CB	1:M:392:GLY:O	2.69	0.40
2:N:106:MET:O	2:N:110:ILE:HG12	2.22	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	575/577 (100%)	562 (98%)	12 (2%)	1 (0%)	43	73
1	M	575/577 (100%)	542 (94%)	27 (5%)	6 (1%)	12	41
2	B	241/243 (99%)	224 (93%)	15 (6%)	2 (1%)	16	47
2	N	241/243 (99%)	230 (95%)	9 (4%)	2 (1%)	16	47
3	C	128/130 (98%)	126 (98%)	2 (2%)	0	100	100
3	O	128/130 (98%)	126 (98%)	2 (2%)	0	100	100
4	D	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
4	P	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
All	All	2122/2138 (99%)	2034 (96%)	77 (4%)	11 (0%)	24	57

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	43	SER
1	M	58	ASP
1	M	282	MET
2	N	189	LYS
2	B	101	ASP
1	M	373	GLY
2	N	101	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	206	GLY
2	B	242	PRO
1	M	220	GLY
1	A	343	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	460/460 (100%)	451 (98%)	9 (2%)	48	72
1	M	460/460 (100%)	429 (93%)	31 (7%)	15	43
2	B	205/205 (100%)	202 (98%)	3 (2%)	57	75
2	N	205/205 (100%)	196 (96%)	9 (4%)	25	56
3	C	111/111 (100%)	106 (96%)	5 (4%)	24	56
3	O	111/111 (100%)	110 (99%)	1 (1%)	70	80
4	D	97/97 (100%)	95 (98%)	2 (2%)	47	71
4	P	97/97 (100%)	94 (97%)	3 (3%)	35	64
All	All	1746/1746 (100%)	1683 (96%)	63 (4%)	31	62

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ARG
1	A	111	VAL
1	A	122	GLU
1	A	167	VAL
1	A	190	MET
1	A	198	VAL
1	A	308	ARG
1	A	321	GLU
1	A	391	LEU
2	B	3	MET
2	B	153	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	191	ARG
3	C	12	THR
3	C	24	PHE
3	C	49	LEU
3	C	50	LYS
3	C	73	LEU
4	D	86	MET
4	D	113	ILE
1	M	10	VAL
1	M	32	ILE
1	M	35	ILE
1	M	41	MET
1	M	59	HIS
1	M	74	ASP
1	M	98	LEU
1	M	162	VAL
1	M	167	VAL
1	M	189	VAL
1	M	190	MET
1	M	197	ARG
1	M	203	THR
1	M	207	ILE
1	M	215	MET
1	M	221	VAL
1	M	223	LEU
1	M	241	ILE
1	M	243	MET
1	M	248	ARG
1	M	255	VAL
1	M	281	TYR
1	M	311	VAL
1	M	319	LEU
1	M	321	GLU
1	M	362	GLU
1	M	383	VAL
1	M	432	VAL
1	M	472	MET
1	M	543	ASP
1	M	558	ASP
2	N	9	GLU
2	N	36	LEU
2	N	121	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	N	128	ASP
2	N	135	THR
2	N	210	CYS
2	N	226	GLN
2	N	237	ILE
2	N	240	LEU
3	O	99	LYS
4	P	6	LYS
4	P	9	ASP
4	P	115	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	95	GLN
1	A	141	GLN
1	A	204	ASN
1	A	230	GLN
1	A	232	HIS
1	A	279	ASN
1	A	296	HIS
1	A	318	HIS
1	A	366	ASN
2	B	134	GLN
2	B	150	ASN
2	B	186	HIS
2	B	194	GLN
3	C	72	ASN
4	D	83	HIS
1	M	27	ASN
1	M	134	HIS
1	M	137	HIS
1	M	150	GLN
1	M	166	HIS
1	M	202	ASN
1	M	219	HIS
1	M	232	HIS
1	M	258	ASN
1	M	264	GLN
1	M	292	GLN
1	M	296	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	510	HIS
2	N	95	ASN
2	N	198	GLN
2	N	225	GLN
4	P	80	HIS
4	P	83	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

9 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	$\# Z > 2$
8	F3S	N	245	2	0,9,9	-	-	-		
5	FAD	M	601	-	58,58,58	1.20	8 (13%)	85,89,89	1.72	18 (21%)
6	3NP	A	602	-	5,5,7	0.98	0	5,5,8	1.52	0
9	SF4	B	246	2	0,12,12	-	-	-		
7	FES	B	244	2	0,4,4	-	-	-		
9	SF4	N	246	2	0,12,12	-	-	-		
8	F3S	B	245	2	0,9,9	-	-	-		
7	FES	N	244	2	0,4,4	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FAD	A	601	-	58,58,58	1.01	5 (8%)	85,89,89	1.63	16 (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
8	F3S	N	245	2	-	-	0/3/3/3
5	FAD	M	601	-	-	15/34/50/50	0/6/6/6
6	3NP	A	602	-	-	2/3/3/5	-
9	SF4	B	246	2	-	-	0/6/5/5
7	FES	B	244	2	-	-	0/1/1/1
9	SF4	N	246	2	-	-	0/6/5/5
8	F3S	B	245	2	-	-	0/3/3/3
7	FES	N	244	2	-	-	0/1/1/1
5	FAD	A	601	-	-	7/34/50/50	0/6/6/6

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	601	FAD	C2B-C1B	-2.92	1.44	1.53
5	M	601	FAD	P-O3P	2.63	1.62	1.59
5	A	601	FAD	C4X-N5	2.44	1.36	1.30
5	M	601	FAD	O2B-C2B	-2.38	1.37	1.43
5	M	601	FAD	C5X-N5	-2.34	1.35	1.39
5	A	601	FAD	P-O3P	2.26	1.61	1.59
5	M	601	FAD	C4X-N5	2.22	1.35	1.30
5	M	601	FAD	C10-N10	2.18	1.42	1.37
5	A	601	FAD	C10-N10	2.14	1.42	1.37
5	M	601	FAD	PA-O3P	2.10	1.61	1.59
5	M	601	FAD	C5A-N7A	-2.06	1.35	1.39
5	A	601	FAD	C8A-N7A	2.03	1.35	1.31
5	A	601	FAD	C5A-N7A	-2.00	1.35	1.39

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	601	FAD	C5A-C4A-N3A	-5.88	118.62	126.72
5	A	601	FAD	C5A-C4A-N3A	-5.30	119.41	126.72
5	M	601	FAD	N3A-C2A-N1A	-5.13	120.82	128.58

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	601	FAD	N3A-C2A-N1A	-5.07	120.90	128.58
5	M	601	FAD	C5B-C4B-C3B	4.30	130.69	115.21
5	M	601	FAD	N3A-C4A-N9A	4.00	133.97	127.17
5	M	601	FAD	C2A-N3A-C4A	3.88	121.31	111.83
5	A	601	FAD	N9A-C8A-N7A	-3.78	108.58	113.94
5	A	601	FAD	C2A-N3A-C4A	3.68	120.83	111.83
5	A	601	FAD	N3A-C4A-N9A	3.52	133.15	127.17
5	A	601	FAD	C4-N3-C2	-3.32	119.75	125.64
5	M	601	FAD	N9A-C8A-N7A	-3.22	109.36	113.94
5	A	601	FAD	C4A-N9A-C8A	2.89	108.77	105.74
5	M	601	FAD	O2B-C2B-C1B	-2.84	100.32	110.10
5	M	601	FAD	C4-N3-C2	-2.82	120.63	125.64
5	A	601	FAD	O4-C4-C4X	-2.81	119.10	126.53
5	A	601	FAD	C4A-C5A-N7A	-2.80	107.38	110.58
5	A	601	FAD	C5A-N7A-C8A	2.79	107.84	103.45
5	A	601	FAD	C4X-C4-N3	2.71	120.16	113.25
5	M	601	FAD	C5X-C9A-N10	2.71	120.42	117.97
5	M	601	FAD	C4A-C5A-N7A	-2.69	107.51	110.58
5	M	601	FAD	C5A-N7A-C8A	2.66	107.63	103.45
5	M	601	FAD	C9A-N10-C10	-2.65	116.72	120.75
5	M	601	FAD	C4X-C10-N10	2.57	120.17	116.48
5	M	601	FAD	C1'-C2'-C3'	2.54	116.54	109.66
5	M	601	FAD	C4X-C4-N3	2.36	119.27	113.25
5	A	601	FAD	O2-C2-N1	-2.35	117.89	121.80
5	M	601	FAD	O4-C4-C4X	-2.26	120.56	126.53
5	M	601	FAD	C4A-N9A-C8A	2.23	108.08	105.74
5	A	601	FAD	C4X-C10-N10	2.22	119.65	116.48
5	A	601	FAD	O4B-C1B-N9A	2.19	112.30	108.09
5	A	601	FAD	C4X-C10-N1	-2.16	119.29	124.59
5	M	601	FAD	C4X-C10-N1	-2.16	119.30	124.59
5	A	601	FAD	C10-C4X-N5	-2.00	120.71	124.81

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	FAD	C5B-O5B-PA-O1A
5	A	601	FAD	C5B-O5B-PA-O3P
5	A	601	FAD	O4B-C4B-C5B-O5B
5	A	601	FAD	N10-C1'-C2'-O2'
5	A	601	FAD	N10-C1'-C2'-C3'
5	M	601	FAD	C5B-O5B-PA-O1A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	M	601	FAD	C5B-O5B-PA-O2A
5	M	601	FAD	C5B-O5B-PA-O3P
5	M	601	FAD	P-O3P-PA-O5B
5	M	601	FAD	N10-C1'-C2'-O2'
5	M	601	FAD	N10-C1'-C2'-C3'
5	M	601	FAD	C5'-O5'-P-O1P
5	A	601	FAD	C3B-C4B-C5B-O5B
6	A	602	3NP	O1-C1-C2-C3
5	M	601	FAD	C2'-C3'-C4'-O4'
6	A	602	3NP	O2-C1-C2-C3
5	M	601	FAD	O4B-C4B-C5B-O5B
5	M	601	FAD	C2'-C3'-C4'-C5'
5	M	601	FAD	O3'-C3'-C4'-O4'
5	A	601	FAD	C5B-O5B-PA-O2A
5	M	601	FAD	C5'-O5'-P-O3P
5	M	601	FAD	O3'-C3'-C4'-C5'
5	M	601	FAD	C1'-C2'-C3'-O3'
5	M	601	FAD	O2'-C2'-C3'-O3'

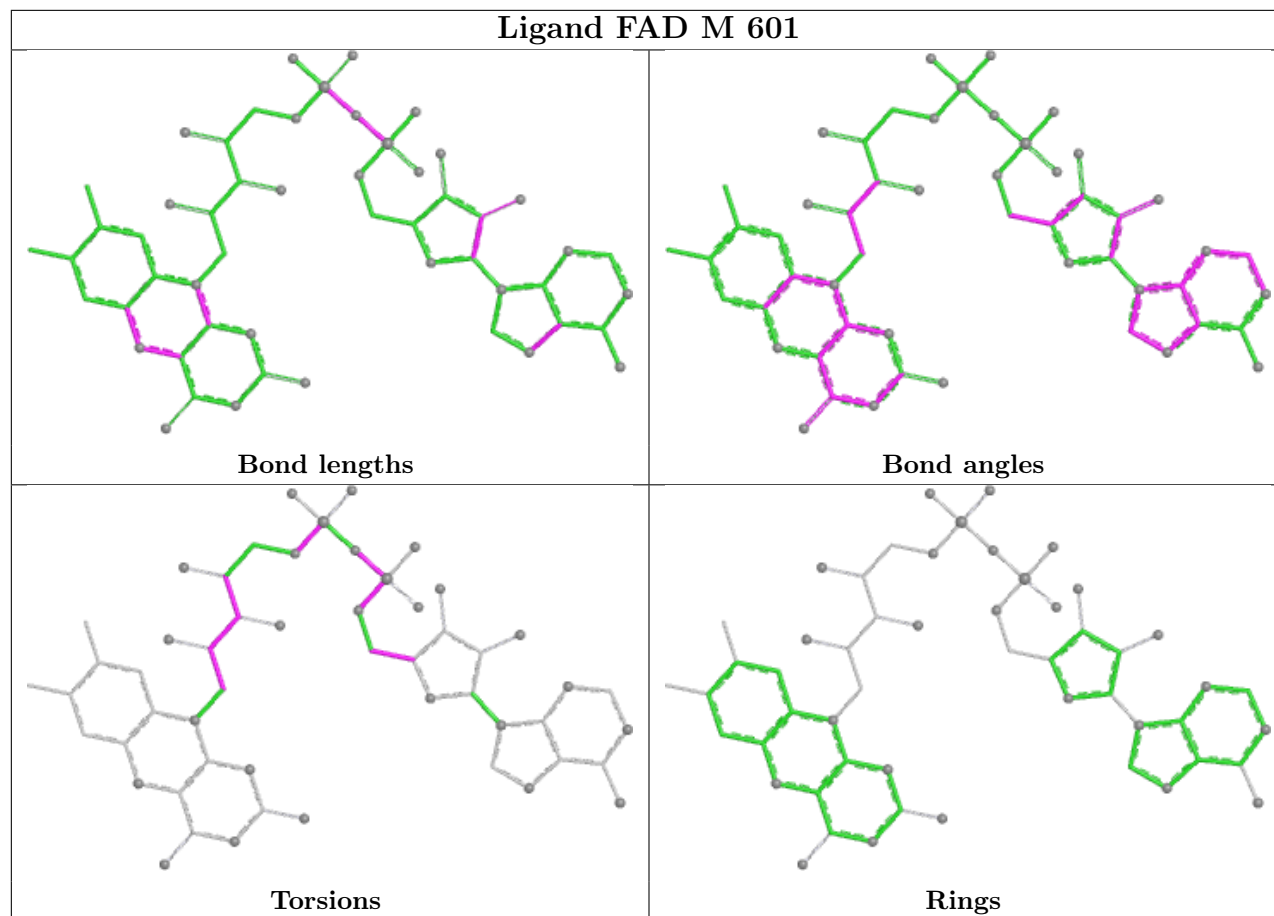
There are no ring outliers.

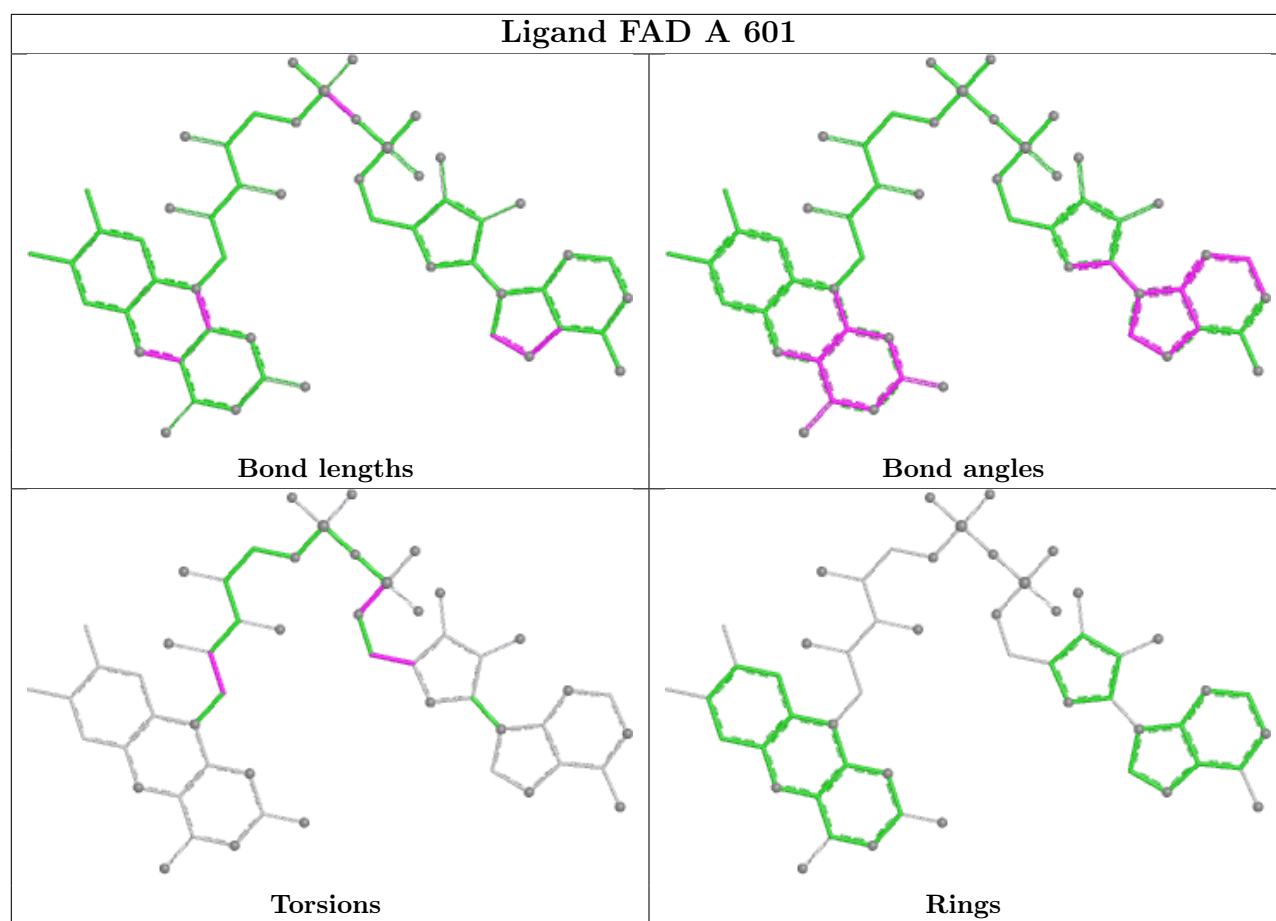
7 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	N	245	F3S	5	0
5	M	601	FAD	19	0
9	B	246	SF4	3	0
9	N	246	SF4	2	0
8	B	245	F3S	3	0
7	N	244	FES	2	0
5	A	601	FAD	5	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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	577/577 (100%)	-0.17	4 (0%) 84 68	42, 56, 89, 117	0
1	M	577/577 (100%)	1.64	178 (30%) 1 1	87, 137, 155, 180	0
2	B	243/243 (100%)	0.00	6 (2%) 58 37	41, 60, 86, 314	0
2	N	243/243 (100%)	0.87	18 (7%) 20 11	76, 113, 151, 159	0
3	C	130/130 (100%)	-0.08	0 100 100	61, 73, 102, 131	0
3	O	130/130 (100%)	0.08	2 (1%) 72 52	59, 85, 144, 150	0
4	D	119/119 (100%)	-0.05	1 (0%) 82 65	61, 72, 95, 122	0
4	P	119/119 (100%)	0.11	2 (1%) 69 48	67, 80, 122, 156	0
All	All	2138/2138 (100%)	0.50	211 (9%) 13 7	41, 82, 150, 314	0

All (211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	393	SER	9.4
1	M	188	VAL	7.7
2	B	240	LEU	6.9
1	M	189	VAL	6.9
1	M	385	LEU	6.6
1	M	229	VAL	6.4
1	M	376	ALA	6.3
1	M	476	ILE	6.2
2	B	237	ILE	6.1
1	M	367	CYS	6.1
1	M	465	ILE	6.1
1	M	411	THR	5.9
2	B	239	THR	5.7
1	M	386	HIS	5.5
2	N	98	ILE	5.5
1	M	172	ALA	5.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	216	ALA	5.4
1	M	225	ASP	5.4
1	M	218	SER	5.3
1	M	373	GLY	5.2
1	M	223	LEU	5.1
1	M	100	GLY	4.8
1	M	217	LEU	4.8
1	M	9	ILE	4.7
1	M	8	ALA	4.6
2	B	242	PRO	4.6
1	M	77	CYS	4.6
1	M	55	VAL	4.6
1	M	227	GLU	4.5
1	M	212	GLY	4.5
1	M	514	VAL	4.4
1	M	375	PHE	4.4
2	N	33	THR	4.4
1	M	32	ILE	4.3
1	M	203	THR	4.2
1	M	374	LEU	4.1
1	M	295	TRP	4.1
1	M	111	VAL	4.0
1	M	169	GLY	4.0
1	M	157	VAL	4.0
1	M	392	GLY	3.9
1	M	489	VAL	3.9
1	M	65	HIS	3.9
1	M	171	VAL	3.8
1	M	139	LEU	3.8
1	M	46	VAL	3.8
1	M	85	PHE	3.8
1	M	406	ALA	3.8
1	M	215	MET	3.7
2	N	208	GLY	3.7
1	M	195	ALA	3.7
1	M	207	ILE	3.7
1	M	479	LEU	3.6
1	M	401	VAL	3.6
1	M	102	PRO	3.5
1	M	410	ALA	3.5
1	M	475	THR	3.5
1	M	170	LEU	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	107	PRO	3.5
1	M	492	THR	3.5
1	M	228	PHE	3.4
1	M	513	ASN	3.4
1	M	361	ILE	3.4
1	M	99	TRP	3.4
1	M	213	MET	3.3
1	M	254	LEU	3.3
1	M	383	VAL	3.3
1	M	354	ALA	3.2
1	M	500	THR	3.2
1	M	116	PHE	3.2
1	M	571	THR	3.2
1	M	19	ALA	3.2
1	M	160	ILE	3.1
1	M	209	THR	3.1
1	M	137	HIS	3.1
1	M	550	HIS	3.1
1	M	384	GLY	3.0
1	M	511	GLY	3.0
1	M	221	VAL	3.0
1	M	210	GLY	3.0
1	M	377	VAL	3.0
1	M	93	MET	3.0
1	M	7	LEU	2.9
2	N	47	LEU	2.9
2	B	238	ALA	2.9
1	M	101	CYS	2.9
2	N	52	SER	2.9
1	M	86	VAL	2.9
1	M	535	LEU	2.9
1	M	167	VAL	2.8
1	M	573	LEU	2.8
1	M	520	HIS	2.8
1	M	121	ILE	2.8
2	N	26	TYR	2.8
1	M	81	VAL	2.8
1	M	439	LEU	2.8
1	M	103	TRP	2.8
1	M	187	ALA	2.8
1	M	553	ALA	2.8
2	N	40	LEU	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	N	130	GLY	2.7
1	M	192	THR	2.7
1	M	518	MET	2.7
2	N	38	ASP	2.7
1	M	183	ILE	2.7
1	M	14	GLY	2.7
1	M	407	GLY	2.7
4	P	52	GLU	2.7
1	A	313	TYR	2.7
1	M	519	ALA	2.7
1	M	165	GLY	2.6
1	M	179	THR	2.6
1	M	125	TRP	2.6
1	M	226	MET	2.6
1	M	324	LEU	2.6
1	M	552	LEU	2.6
1	M	38	VAL	2.6
1	M	532	HIS	2.6
1	M	90	PRO	2.6
2	N	102	LEU	2.5
1	M	491	ILE	2.5
2	N	136	PRO	2.5
1	M	517	CYS	2.5
2	N	36	LEU	2.5
1	M	502	LEU	2.5
1	M	574	PRO	2.5
1	M	11	GLY	2.5
1	M	30	ALA	2.5
1	M	71	ALA	2.5
2	N	137	ALA	2.5
1	M	62	PHE	2.5
1	M	82	VAL	2.5
1	M	537	GLU	2.4
1	M	199	TYR	2.4
1	M	440	VAL	2.4
1	M	15	ALA	2.4
1	M	451	ILE	2.4
1	M	402	PHE	2.4
1	M	242	LEU	2.4
1	M	274	LEU	2.4
1	M	45	THR	2.4
1	M	356	TYR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	173	MET	2.4
2	N	1	ALA	2.4
1	M	413	ARG	2.4
1	M	124	THR	2.3
1	M	415	ALA	2.3
1	M	490	ARG	2.3
1	M	398	GLU	2.3
1	M	44	HIS	2.3
1	M	523	MET	2.3
1	M	34	LEU	2.3
1	M	371	ILE	2.3
1	M	508	LEU	2.3
1	M	327	ARG	2.3
1	A	348	ILE	2.3
1	M	21	ILE	2.3
1	M	20	ALA	2.3
1	M	429	ALA	2.3
1	M	161	LEU	2.3
1	M	396	LEU	2.3
1	M	466	TYR	2.3
1	M	214	GLY	2.2
1	M	98	LEU	2.2
1	M	208	VAL	2.2
1	M	499	ASN	2.2
1	M	380	CYS	2.2
1	M	497	VAL	2.2
1	M	78	GLU	2.2
2	B	241	LYS	2.2
1	M	141	GLN	2.2
1	M	191	ALA	2.2
1	M	409	GLN	2.2
1	M	144	LEU	2.2
1	M	245	GLU	2.2
1	M	414	ALA	2.2
3	O	93	ALA	2.2
1	M	504	TYR	2.2
1	M	548	LEU	2.2
1	M	572	THR	2.1
1	M	149	ILE	2.1
1	M	328	LEU	2.1
1	M	405	LEU	2.1
1	M	355	HIS	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	358	MET	2.1
1	M	265	ASP	2.1
1	M	487	LYS	2.1
2	N	51	LEU	2.1
1	M	193	GLY	2.1
1	M	159	ASP	2.1
1	A	417	ALA	2.1
1	M	23	ALA	2.1
2	N	99	GLU	2.1
2	N	104	VAL	2.1
1	M	114	ARG	2.1
4	D	118	ILE	2.1
1	M	551	THR	2.1
1	M	16	GLY	2.1
3	O	6	PRO	2.1
4	P	1	ILE	2.0
1	M	69	THR	2.0
1	M	353	THR	2.0
1	M	357	THR	2.0
1	A	318	HIS	2.0
1	M	135	MET	2.0
1	M	94	THR	2.0
1	M	206	GLY	2.0
2	N	49	PRO	2.0
1	M	113	VAL	2.0
1	M	250	GLU	2.0
1	M	180	LEU	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.

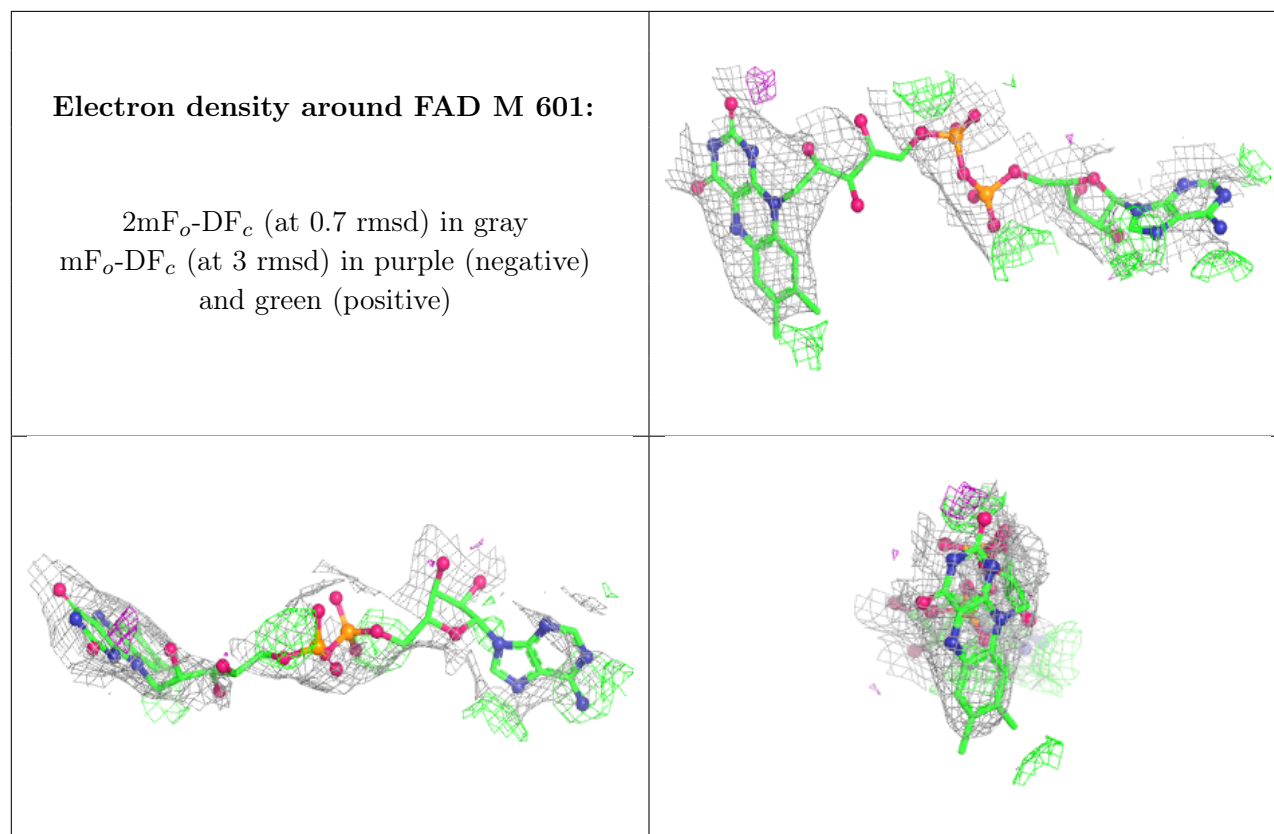
6.4 Ligands [i](#)

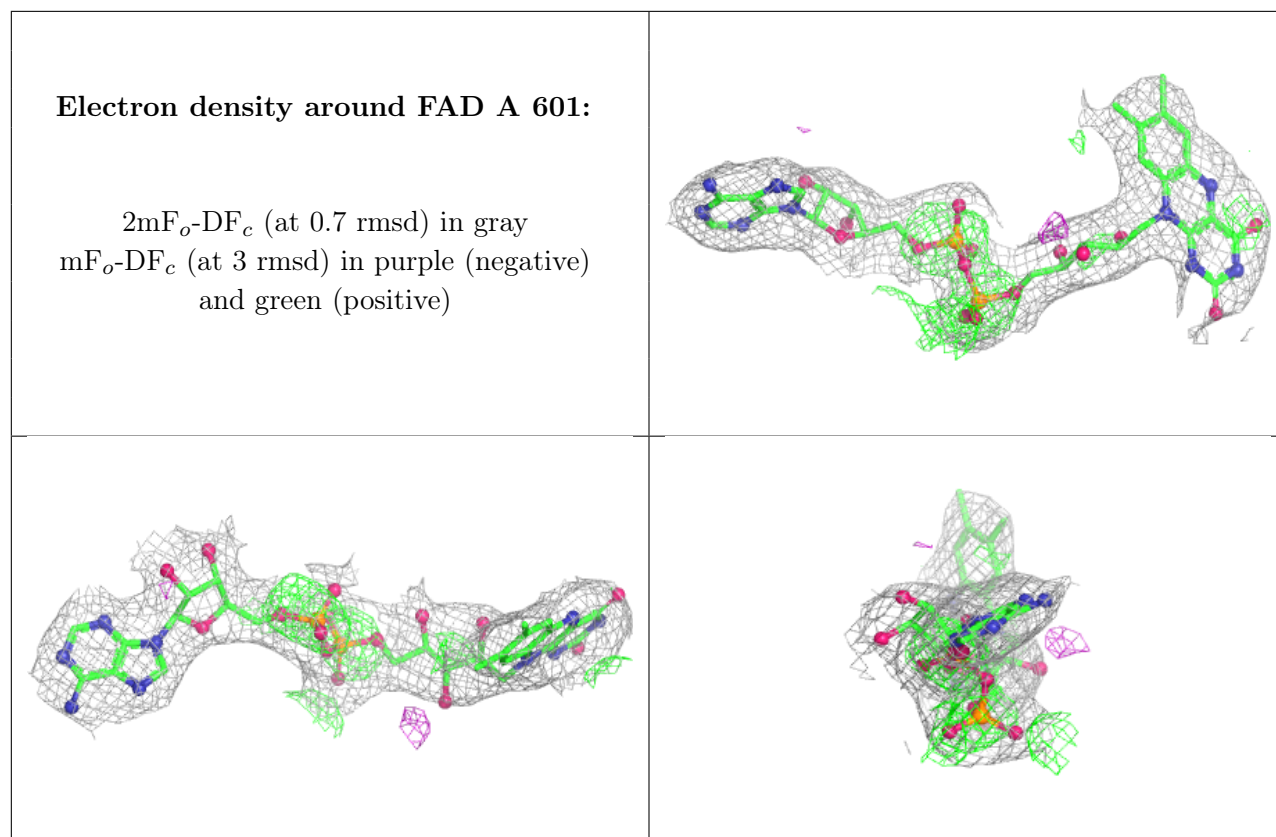
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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(Å ²)	Q<0.9
6	3NP	A	602	6/8	0.69	0.23	74,76,76,77	0
5	FAD	M	601	53/53	0.71	0.17	124,134,143,143	0
8	F3S	N	245	7/7	0.92	0.14	124,124,125,126	0
7	FES	N	244	4/4	0.95	0.09	105,105,105,106	0
9	SF4	N	246	8/8	0.95	0.07	97,97,97,98	0
5	FAD	A	601	53/53	0.96	0.12	60,65,75,76	0
9	SF4	B	246	8/8	0.97	0.10	79,79,80,80	0
8	F3S	B	245	7/7	0.98	0.14	100,101,102,102	0
7	FES	B	244	4/4	0.98	0.09	59,60,61,61	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.