



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:41 PM UTC

PDB ID : 7VJU / pdb_00007vju
Title : Crystal Structure of terephthalate dioxygenase from Comamonas testosteroni KF1
Authors : Mahto, J.K.; Kumar, P.
Deposited on : 2021-09-28
Resolution : 2.27 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:

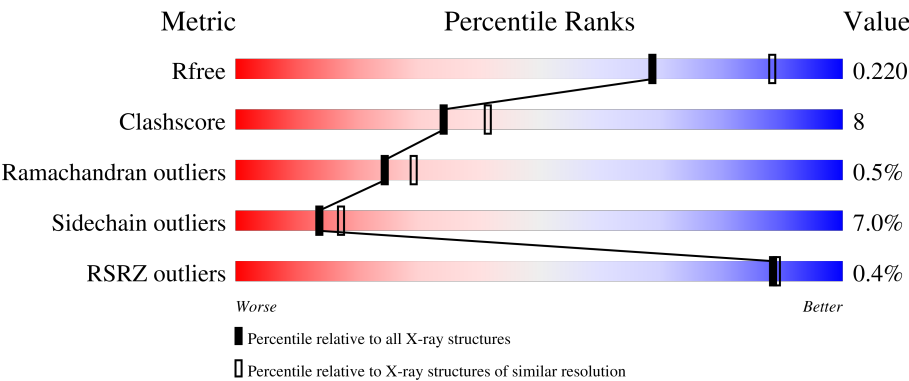
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

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

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	413	75%14%8%
1	C	413	75%17%5%
1	E	413	% 71%18%8%
2	B	154	74%21%. .
2	D	154	73%25%. .

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Mol	Chain	Length	Quality of chain
2	F	154	% 70% 24% 5% ..

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PEG	E	504	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 13744 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 Rieske (2Fe-2S) domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	378	Total	C	N	O	S	0	0	0
			2973	1880	517	563	13			
1	C	393	Total	C	N	O	S	0	1	0
			3106	1959	543	590	14			
1	E	378	Total	C	N	O	S	0	1	0
			2979	1882	520	564	13			

- Molecule 2 is a protein called Aromatic-ring-hydroxylating dioxygenase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1206	756	210	234	6			
2	D	154	Total	C	N	O	S	0	0	0
			1214	761	211	235	7			
2	F	153	Total	C	N	O	S	0	0	0
			1206	756	210	234	6			

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Fe	0	0
			1	1		
4	C	1	Total	Fe	0	0
			1	1		
4	E	1	Total	Fe	0	0
			1	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



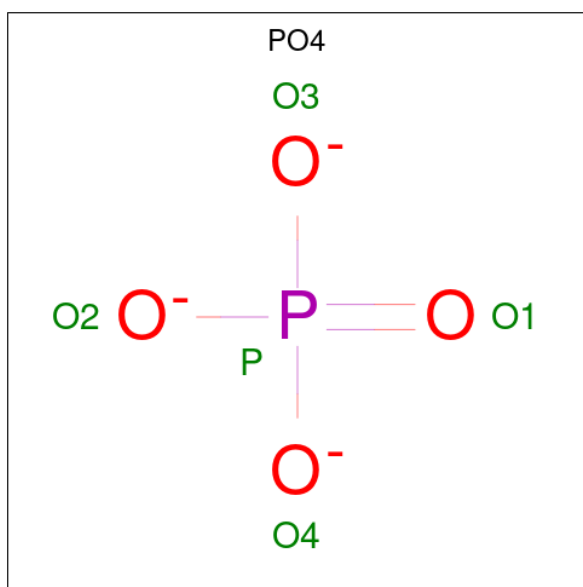
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



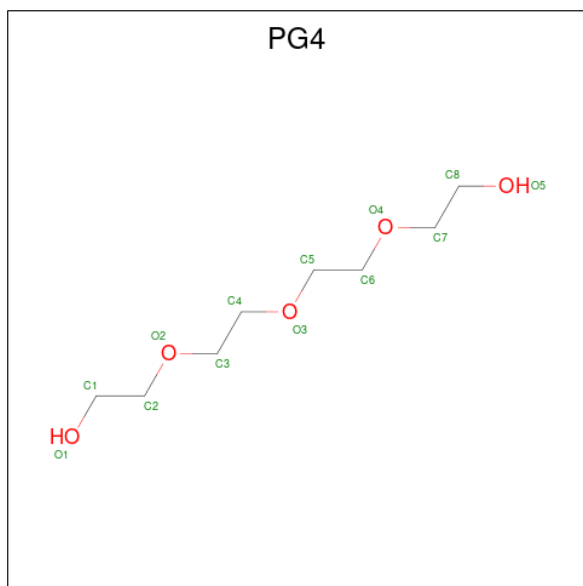
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	P	0	0
			5	4	1		
7	C	1	Total	O	P	0	0
			5	4	1		
7	C	1	Total	O	P	0	0
			5	4	1		
7	C	1	Total	O	P	0	0
			5	4	1		
7	D	1	Total	O	P	0	0
			5	4	1		
7	D	1	Total	O	P	0	0
			5	4	1		
7	E	1	Total	O	P	0	0
			5	4	1		
7	E	1	Total	O	P	0	0
			5	4	1		
7	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			13	8	5		

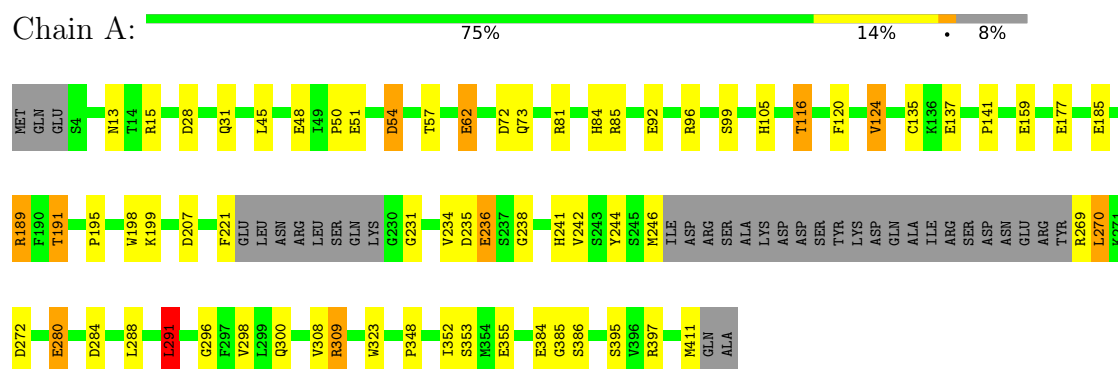
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	218	Total 218	O 218	0	0
9	B	79	Total 79	O 79	0	0
9	C	252	Total 252	O 252	0	0
9	D	84	Total 84	O 84	0	0
9	E	214	Total 214	O 214	0	0
9	F	68	Total 68	O 68	0	0

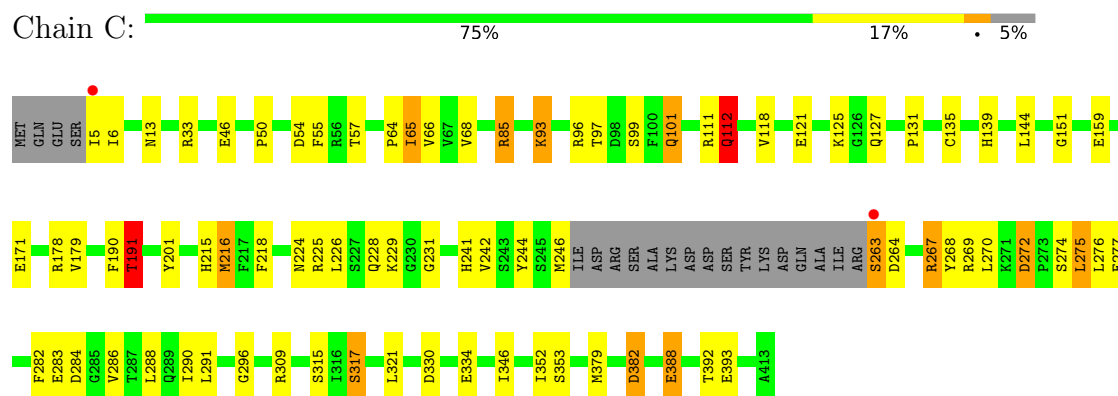
3 Residue-property plots [i](#)

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.

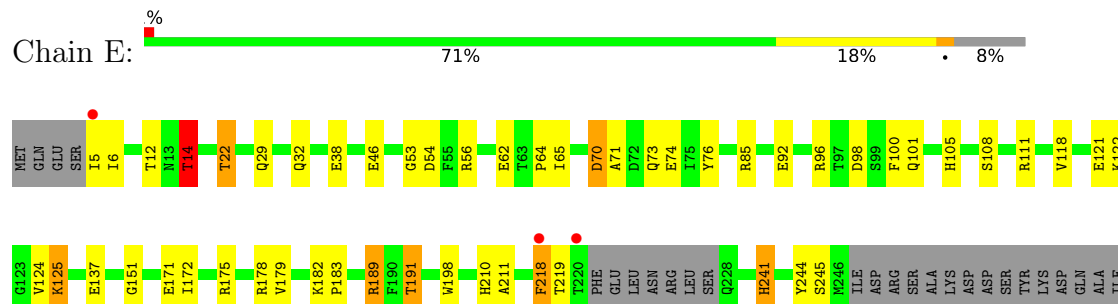
• Molecule 1: Rieske (2Fe-2S) domain protein



• Molecule 1: Rieske (2Fe-2S) domain protein



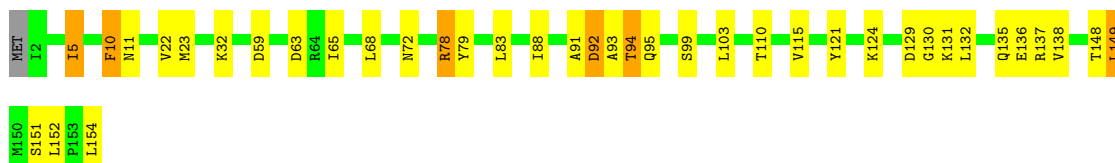
• Molecule 1: Rieske (2Fe-2S) domain protein





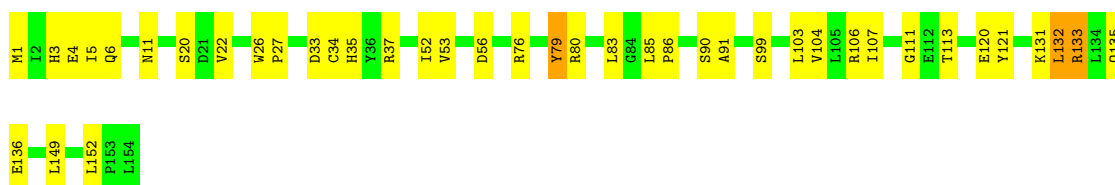
- Molecule 2: Aromatic-ring-hydroxylating dioxygenase beta subunit

Chain B: 74% 21% ..



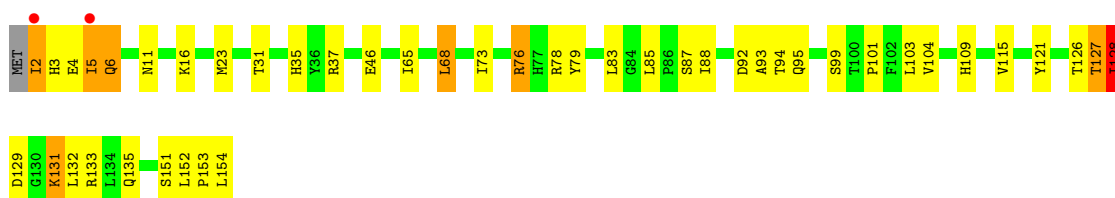
- Molecule 2: Aromatic-ring-hydroxylating dioxygenase beta subunit

Chain D: 73% 25% .



- Molecule 2: Aromatic-ring-hydroxylating dioxygenase beta subunit

Chain F: 70% 24% 5% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.56Å 134.21Å 145.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.15 – 2.27 67.15 – 2.27	Depositor EDS
% Data completeness (in resolution range)	96.5 (67.15-2.27) 96.5 (67.15-2.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.157 , 0.221 0.157 , 0.220	Depositor DCC
R_{free} test set	3959 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13744	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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: PG4, FES, FE2, PO4, PEG, GOL

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	0.78	1/3041 (0.0%)	1.36	22/4106 (0.5%)
1	C	0.81	1/3179 (0.0%)	1.34	19/4292 (0.4%)
1	E	0.76	1/3049 (0.0%)	1.35	21/4116 (0.5%)
2	B	0.77	1/1231 (0.1%)	1.33	8/1674 (0.5%)
2	D	0.78	0/1239	1.36	7/1684 (0.4%)
2	F	0.74	0/1231	1.36	11/1674 (0.7%)
All	All	0.78	4/12970 (0.0%)	1.35	88/17546 (0.5%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	84	HIS	CE1-NE2	6.52	1.39	1.32
1	C	215	HIS	CE1-NE2	5.54	1.38	1.32
2	B	151	SER	CA-CB	-5.35	1.45	1.53
1	E	62	GLU	CD-OE2	5.18	1.35	1.25

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	309	ARG	CB-CG-CD	11.01	136.62	111.30
2	D	133	ARG	CG-CD-NE	-9.11	91.96	112.00
1	A	116	THR	CA-CB-OG1	-8.94	96.19	109.60
2	F	126	THR	CA-CB-OG1	-8.46	96.90	109.60
1	E	111	ARG	CB-CG-CD	8.27	130.32	111.30
2	F	76	ARG	CB-CG-CD	8.23	130.22	111.30
1	A	236	GLU	CA-C-N	7.86	130.81	120.28
1	A	236	GLU	C-N-CA	7.86	130.81	120.28
1	A	189	ARG	CD-NE-CZ	7.73	135.22	124.40
2	F	101	PRO	CB-CA-C	-7.45	101.30	111.21
1	C	382	ASP	CA-CB-CG	7.12	119.72	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	153	PRO	CB-CA-C	-6.76	102.12	110.98
1	C	13	ASN	CA-CB-CG	-6.74	105.86	112.60
1	C	191	THR	CA-CB-OG1	6.63	119.55	109.60
1	E	98	ASP	CB-CA-C	-6.56	99.77	110.79
2	D	80	ARG	CG-CD-NE	-6.53	97.64	112.00
2	F	127	THR	CB-CA-C	6.50	120.39	109.48
1	A	54	ASP	CB-CA-C	-6.45	99.56	109.89
1	E	388	GLU	CB-CG-CD	6.40	123.47	112.60
1	C	112	GLN	CB-CA-C	-6.27	99.62	110.09
2	F	95	GLN	CB-CG-CD	6.24	123.21	112.60
1	A	284	ASP	CA-CB-CG	6.16	118.76	112.60
1	A	348	PRO	CB-CA-C	-6.15	103.11	111.85
1	A	189	ARG	CG-CD-NE	-6.09	98.61	112.00
1	E	22	THR	CB-CA-C	6.08	117.00	109.16
1	C	330	ASP	CA-CB-CG	6.04	118.64	112.60
1	E	191	THR	OG1-CB-CG2	5.96	121.22	109.30
1	C	131	PRO	CB-CA-C	-5.95	103.16	110.95
1	A	309	ARG	CB-CG-CD	5.94	124.96	111.30
2	F	135	GLN	N-CA-C	-5.90	104.25	112.45
2	D	79	TYR	CB-CA-C	-5.79	99.71	109.50
1	C	57	THR	CA-CB-OG1	-5.76	100.97	109.60
1	A	92	GLU	CB-CG-CD	5.75	122.38	112.60
2	B	129	ASP	CB-CA-C	-5.74	109.94	116.54
2	B	110	THR	CA-C-N	-5.74	116.65	123.08
2	B	110	THR	C-N-CA	-5.74	116.65	123.08
1	E	22	THR	OG1-CB-CG2	5.74	120.78	109.30
2	B	137	ARG	CA-C-N	-5.72	115.68	123.12
2	B	137	ARG	C-N-CA	-5.72	115.68	123.12
1	E	125	LYS	CB-CA-C	-5.71	102.54	111.39
1	C	85	ARG	NE-CZ-NH1	-5.70	115.80	121.50
2	F	95	GLN	CB-CA-C	5.68	120.22	109.37
1	C	111	ARG	CB-CG-CD	5.63	124.24	111.30
1	C	229	LYS	CA-C-N	5.60	126.42	122.33
1	C	229	LYS	C-N-CA	5.60	126.42	122.33
1	A	189	ARG	NE-CZ-NH2	-5.58	114.18	119.20
1	A	15	ARG	CA-C-N	-5.56	118.49	123.33
1	A	15	ARG	C-N-CA	-5.56	118.49	123.33
2	D	106	ARG	CG-CD-NE	-5.56	99.77	112.00
1	E	175	ARG	CG-CD-NE	5.56	124.23	112.00
1	C	33	ARG	N-CA-C	-5.49	106.94	113.97
1	A	284	ASP	CB-CA-C	5.49	117.58	109.29
1	C	6	ILE	CA-C-N	5.48	129.13	121.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	6	ILE	C-N-CA	5.48	129.13	121.24
2	B	63	ASP	CB-CA-C	-5.48	101.54	110.85
1	E	29	GLN	CB-CG-CD	-5.45	103.34	112.60
1	E	172	ILE	N-CA-C	-5.43	105.23	110.72
1	C	315	SER	N-CA-C	-5.37	101.29	108.86
1	A	385	GLY	CA-C-N	5.36	128.69	120.82
1	A	385	GLY	C-N-CA	5.36	128.69	120.82
1	A	28	ASP	CB-CA-C	-5.34	101.92	110.79
1	E	189	ARG	CB-CG-CD	5.33	123.56	111.30
1	E	365	ARG	CG-CD-NE	-5.32	100.30	112.00
2	B	92	ASP	CB-CA-C	-5.31	99.85	110.42
1	E	218	PHE	CA-C-N	5.30	131.66	121.54
1	E	218	PHE	C-N-CA	5.30	131.66	121.54
1	E	287	THR	CB-CA-C	-5.29	101.26	110.09
1	E	14	THR	CB-CA-C	5.28	121.35	110.31
1	C	272	ASP	CB-CA-C	5.27	119.29	110.97
1	E	38	GLU	CB-CA-C	5.27	119.31	111.88
2	D	33	ASP	CA-CB-CG	5.26	117.86	112.60
2	D	56	ASP	CA-CB-CG	5.26	117.86	112.60
2	B	154	LEU	CA-C-O	-5.24	111.90	120.80
1	A	207	ASP	CA-CB-CG	5.22	117.82	112.60
2	D	111	GLY	N-CA-C	5.22	119.17	113.58
1	E	137	GLU	CB-CG-CD	5.19	121.43	112.60
1	A	62	GLU	CB-CG-CD	5.19	121.42	112.60
1	C	317	SER	N-CA-CB	-5.16	103.11	110.80
1	C	85	ARG	CG-CD-NE	-5.16	100.65	112.00
1	A	189	ARG	CB-CG-CD	5.15	123.14	111.30
1	A	189	ARG	NE-CZ-NH1	5.13	126.63	121.50
1	E	70	ASP	CB-CA-C	5.10	120.57	110.42
1	C	392	THR	CA-CB-OG1	-5.09	101.96	109.60
2	F	87	SER	CB-CA-C	5.07	118.52	109.65
1	E	92	GLU	CB-CG-CD	5.06	121.20	112.60
2	F	128	ILE	O-C-N	5.06	127.36	122.30
1	A	291	LEU	N-CA-CB	-5.04	102.35	110.81
2	F	154	LEU	CA-C-O	-5.01	112.29	120.80

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	2973	0	2855	34	0
1	C	3106	0	2985	46	0
1	E	2979	0	2868	38	0
2	B	1206	0	1163	20	0
2	D	1214	0	1175	27	0
2	F	1206	0	1163	31	0
3	A	4	0	0	1	0
3	C	4	0	0	0	0
3	E	4	0	0	1	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
5	A	14	0	20	1	0
5	C	14	0	20	0	0
5	E	14	0	20	7	0
5	F	7	0	10	1	0
6	A	6	0	8	0	0
6	D	6	0	8	0	0
6	E	6	0	8	1	0
7	A	5	0	0	0	0
7	B	5	0	0	0	0
7	C	15	0	0	0	0
7	D	10	0	0	1	0
7	E	10	0	0	1	0
7	F	5	0	0	0	0
8	A	13	0	18	0	0
9	A	218	0	0	4	0
9	B	79	0	0	1	0
9	C	252	0	0	5	0
9	D	84	0	0	0	0
9	E	214	0	0	3	0
9	F	68	0	0	1	0
All	All	13744	0	12321	191	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (191) 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)
2:D:131:LYS:HG2	2:D:132:LEU:H	1.19	1.03
1:E:101:GLN:H	5:E:504:PEG:H21	1.30	0.96
1:C:139:HIS:HD2	9:C:666:HOH:O	1.54	0.89
1:C:216:MET:HA	1:C:216:MET:HE2	1.55	0.87
1:C:216:MET:HA	1:C:216:MET:CE	2.05	0.86
2:F:68:LEU:HD11	2:F:151:SER:HB2	1.57	0.84
1:A:189:ARG:HD3	9:A:629:HOH:O	1.76	0.84
2:F:131:LYS:HG2	5:F:201:PEG:H22	1.59	0.83
1:A:231:GLY:HA3	1:A:244:TYR:CE2	2.14	0.82
1:E:5:ILE:HG21	9:E:796:HOH:O	1.82	0.80
2:B:5:ILE:HD13	2:F:5:ILE:HD11	1.63	0.79
1:C:93:LYS:HE3	2:F:109:HIS:O	1.82	0.78
2:D:131:LYS:HG2	2:D:132:LEU:N	1.96	0.78
2:B:124:LYS:HG2	2:B:136:GLU:HB2	1.68	0.76
2:D:3:HIS:CE1	2:D:6:GLN:HG3	2.22	0.75
1:E:105:HIS:HB2	3:E:501:FES:S1	2.27	0.74
2:F:2:ILE:O	2:F:2:ILE:HG13	1.90	0.71
2:F:99:SER:HA	2:F:121:TYR:O	1.91	0.70
1:A:298:VAL:HB	1:A:309:ARG:HB2	1.72	0.70
2:F:92:ASP:OD1	2:F:93:ALA:N	2.24	0.69
2:F:2:ILE:HA	2:F:6:GLN:HE22	1.58	0.68
1:C:228:GLN:HG2	1:C:246:MET:C	2.19	0.68
1:E:53:GLY:O	1:E:96:ARG:HA	1.94	0.67
1:E:56:ARG:HE	6:E:505:GOL:H12	1.61	0.66
5:E:504:PEG:H31	5:E:504:PEG:O1	1.93	0.65
1:E:12:THR:OG1	1:E:14:THR:HB	1.95	0.65
1:C:191:THR:HG22	9:C:783:HOH:O	1.97	0.65
1:C:225:ARG:HD3	1:C:268:TYR:CE1	2.31	0.65
1:A:384:GLU:HA	1:A:384:GLU:OE1	1.96	0.64
1:A:411:MET:C	9:A:705:HOH:O	2.42	0.63
2:D:76:ARG:HD3	7:D:203:PO4:O3	1.98	0.63
1:E:411:MET:C	9:E:721:HOH:O	2.41	0.62
1:C:288:LEU:HD21	1:C:290:ILE:HD12	1.80	0.62
2:D:149:LEU:C	2:D:149:LEU:HD12	2.25	0.62
2:D:35:HIS:HB3	2:D:136:GLU:HG3	1.82	0.62
1:A:57:THR:HB	5:A:503:PEG:C1	2.31	0.61
1:E:101:GLN:N	5:E:504:PEG:H21	2.09	0.61
2:F:92:ASP:OD1	2:F:94:THR:N	2.26	0.59
2:F:127:THR:O	2:F:128:ILE:HD13	2.03	0.58
2:D:20:SER:OG	2:D:22:VAL:HG23	2.03	0.58
1:A:280:GLU:OE2	1:A:280:GLU:HA	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:GLU:HG2	1:E:76:TYR:CZ	2.39	0.58
2:F:79:TYR:CE2	2:F:152:LEU:HB2	2.39	0.57
1:A:309:ARG:HD2	1:A:323:TRP:CZ3	2.39	0.57
2:B:88:ILE:HG21	2:B:91:ALA:HB2	1.85	0.57
1:E:241:HIS:ND1	1:E:292:SER:OG	2.29	0.57
2:D:99:SER:OG	2:F:16:LYS:HE3	2.05	0.57
2:D:103:LEU:HD12	2:D:104:VAL:N	2.19	0.57
2:F:23:MET:HG2	2:F:65:ILE:HD12	1.86	0.57
1:E:244:TYR:HA	1:E:288:LEU:O	2.04	0.56
1:E:300:GLN:O	1:E:300:GLN:HG3	2.04	0.56
2:F:2:ILE:HA	2:F:6:GLN:NE2	2.21	0.55
1:C:288:LEU:HD21	1:C:290:ILE:CD1	2.35	0.55
1:E:74:GLU:HG2	1:E:76:TYR:CE2	2.41	0.55
1:C:268:TYR:C	1:C:270:LEU:H	2.15	0.55
1:A:31:GLN:HG3	1:A:62:GLU:CD	2.32	0.54
1:A:105:HIS:HB2	3:A:501:FES:S1	2.48	0.54
1:A:137:GLU:H	1:A:137:GLU:CD	2.15	0.54
1:E:100:PHE:HA	5:E:504:PEG:H22	1.89	0.54
2:F:11:ASN:HB3	2:F:83:LEU:HD13	1.88	0.54
2:B:92:ASP:HB2	2:B:95:GLN:H	1.73	0.53
1:C:263:SER:O	1:C:264:ASP:HB2	2.07	0.53
2:D:1:MET:HE1	2:D:91:ALA:HB3	1.89	0.53
1:E:377:ILE:HG22	1:E:377:ILE:O	2.08	0.53
2:B:148:THR:HG22	2:B:149:LEU:HD23	1.89	0.53
2:B:92:ASP:HB2	2:B:94:THR:H	1.75	0.52
1:A:85:ARG:HD2	9:C:606:HOH:O	2.09	0.52
2:B:99:SER:HA	2:B:121:TYR:O	2.10	0.51
2:B:23:MET:HG3	2:B:65:ILE:HD12	1.92	0.51
1:E:275:LEU:HD11	1:E:344:ASN:HB2	1.92	0.51
2:F:2:ILE:HB	2:F:6:GLN:OE1	2.11	0.51
1:C:224:ASN:HB2	1:C:267:ARG:HB2	1.93	0.50
1:C:225:ARG:HD3	1:C:268:TYR:HE1	1.75	0.50
1:E:118:VAL:HB	1:E:121:GLU:HB2	1.94	0.50
1:C:275:LEU:HD12	1:C:275:LEU:O	2.12	0.50
1:A:191:THR:HG21	9:B:350:HOH:O	2.11	0.49
1:E:281:GLU:OE1	1:E:339:ARG:NH2	2.26	0.49
1:C:50:PRO:HD2	1:C:54:ASP:OD2	2.12	0.49
1:C:85:ARG:HD2	9:E:625:HOH:O	2.11	0.49
9:A:696:HOH:O	2:D:76:ARG:HG3	2.12	0.49
2:F:11:ASN:HB3	2:F:83:LEU:CD1	2.42	0.49
2:D:11:ASN:HB3	2:D:83:LEU:CD1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:601:HOH:O	1:E:85:ARG:HD2	2.12	0.49
1:A:235:ASP:CG	1:A:236:GLU:N	2.70	0.49
1:E:298:VAL:HB	1:E:309:ARG:HG3	1.94	0.49
1:A:45:LEU:HB2	1:A:48:GLU:HG3	1.93	0.49
2:D:107:ILE:HG13	2:D:113:THR:HG23	1.94	0.49
2:B:92:ASP:CB	2:B:94:THR:H	2.26	0.48
2:D:1:MET:HE1	2:D:91:ALA:CB	2.43	0.48
2:D:26:TRP:N	2:D:27:PRO:CD	2.77	0.48
1:A:234:VAL:CG1	1:A:238:GLY:HA2	2.44	0.48
1:E:182:LYS:HB2	1:E:183:PRO:CD	2.43	0.48
2:B:79:TYR:CE2	2:B:152:LEU:HB2	2.49	0.48
1:A:355:GLU:OE1	2:B:72:ASN:HA	2.14	0.48
1:C:275:LEU:HG	1:C:276:LEU:HG	1.95	0.48
1:C:224:ASN:ND2	1:C:267:ARG:HH21	2.12	0.47
2:F:35:HIS:CE1	2:F:37:ARG:HE	2.32	0.47
1:A:291:LEU:C	1:A:291:LEU:HD23	2.39	0.47
1:C:64:PRO:O	1:C:65:ILE:HD13	2.14	0.47
1:E:54:ASP:OD1	1:E:96:ARG:HD2	2.14	0.47
2:F:31:THR:CG2	2:F:133:ARG:HG2	2.45	0.47
1:A:234:VAL:HG12	1:A:238:GLY:HA2	1.96	0.47
1:E:124:VAL:O	1:E:125:LYS:HB2	2.15	0.47
2:D:79:TYR:CZ	2:D:152:LEU:HB2	2.50	0.47
1:E:189:ARG:NH2	2:F:46:GLU:OE2	2.48	0.47
2:F:103:LEU:HD12	2:F:104:VAL:N	2.30	0.47
1:C:244:TYR:HA	1:C:288:LEU:O	2.14	0.46
1:E:100:PHE:HA	5:E:504:PEG:C2	2.44	0.46
1:E:346:ILE:HA	1:E:353:SER:OG	2.15	0.46
1:C:379:MET:HB2	1:C:393:GLU:HG3	1.97	0.46
2:D:1:MET:CE	2:D:91:ALA:HB1	2.45	0.46
2:D:37:ARG:HA	2:D:53:VAL:O	2.16	0.46
2:F:128:ILE:HG22	2:F:128:ILE:O	2.15	0.46
1:A:50:PRO:HD2	1:A:54:ASP:OD2	2.16	0.46
2:D:35:HIS:O	2:D:136:GLU:HA	2.15	0.46
2:F:35:HIS:HE1	2:F:37:ARG:HH21	1.64	0.46
1:C:201:TYR:CZ	1:C:321:LEU:HD22	2.51	0.46
2:D:1:MET:HE3	2:D:91:ALA:HB1	1.97	0.46
1:C:309:ARG:HB3	1:C:321:LEU:HD11	1.97	0.45
1:E:210:HIS:O	1:E:211:ALA:C	2.58	0.45
1:C:274:SER:O	1:C:275:LEU:C	2.59	0.45
1:C:263:SER:HB3	1:C:264:ASP:H	1.67	0.45
2:F:31:THR:HG23	2:F:133:ARG:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:ARG:O	1:A:141:PRO:HB3	2.17	0.45
1:C:178:ARG:NH2	1:C:286:VAL:HB	2.32	0.45
1:E:182:LYS:HE3	1:E:330:ASP:OD1	2.16	0.45
2:F:78:ARG:HG3	9:F:348:HOH:O	2.17	0.45
1:A:72:ASP:O	1:A:73:GLN:CB	2.65	0.45
2:F:4:GLU:HB3	2:F:85:LEU:HD11	1.99	0.45
1:C:46:GLU:HG2	1:C:151:GLY:HA2	1.99	0.45
1:C:291:LEU:C	1:C:291:LEU:HD23	2.42	0.45
1:A:352:ILE:O	1:A:353:SER:C	2.57	0.44
1:C:277:GLU:O	1:C:277:GLU:HG3	2.16	0.44
2:B:11:ASN:HB3	2:B:83:LEU:CD1	2.47	0.44
2:D:79:TYR:CE2	2:D:152:LEU:HB2	2.52	0.44
1:A:13:ASN:O	1:A:397:ARG:HG2	2.17	0.44
1:A:120:PHE:CD1	1:A:124:VAL:HG12	2.53	0.44
1:C:144:LEU:HD12	1:C:144:LEU:N	2.33	0.44
1:E:32:GLN:HG2	7:E:507:PO4:O3	2.17	0.44
1:A:135:CYS:SG	1:A:137:GLU:OE1	2.68	0.44
1:E:275:LEU:HD12	1:E:341:LYS:O	2.17	0.44
2:B:79:TYR:CZ	2:B:152:LEU:HB2	2.53	0.43
1:A:221:PHE:HB3	1:A:270:LEU:HD13	2.00	0.43
2:D:1:MET:CE	2:D:91:ALA:CB	2.96	0.43
2:D:99:SER:HA	2:D:121:TYR:O	2.18	0.43
1:A:272:ASP:HB2	2:B:59:ASP:HB2	2.01	0.43
2:B:68:LEU:HD21	2:B:152:LEU:HD23	2.00	0.43
1:E:46:GLU:HG3	1:E:151:GLY:HA2	2.00	0.43
1:E:282:PHE:C	1:E:284:ASP:H	2.26	0.43
1:C:190:PHE:CE1	2:D:52:ILE:HG13	2.53	0.43
2:B:10:PHE:CD1	2:B:10:PHE:C	2.96	0.43
2:F:152:LEU:HD23	2:F:152:LEU:N	2.34	0.43
1:C:216:MET:HE2	1:C:216:MET:CA	2.37	0.43
1:C:346:ILE:HA	1:C:353:SER:OG	2.18	0.43
1:E:178:ARG:NH2	1:E:286:VAL:HB	2.34	0.43
2:F:23:MET:CG	2:F:65:ILE:HD12	2.49	0.43
1:C:216:MET:HA	1:C:216:MET:HE3	1.95	0.42
1:C:282:PHE:CB	1:C:284:ASP:HB2	2.48	0.42
1:A:272:ASP:OD1	1:A:272:ASP:C	2.62	0.42
2:F:6:GLN:HG2	2:F:132:LEU:HD11	2.00	0.42
2:D:34:CYS:HA	2:D:135:GLN:O	2.19	0.42
2:D:85:LEU:HD12	2:D:86:PRO:HD2	2.01	0.42
1:E:64:PRO:O	1:E:65:ILE:HD13	2.19	0.42
1:E:182:LYS:HE3	1:E:330:ASP:CG	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:35:HIS:HE1	2:F:37:ARG:HE	1.67	0.42
1:A:244:TYR:HA	1:A:288:LEU:O	2.19	0.42
1:C:101:GLN:HG2	9:C:768:HOH:O	2.18	0.42
1:C:191:THR:CG2	9:C:783:HOH:O	2.62	0.42
1:C:218:PHE:HE1	1:C:352:ILE:HD11	1.83	0.42
1:C:388:GLU:CD	1:C:388:GLU:N	2.77	0.42
5:E:504:PEG:O1	5:E:504:PEG:C3	2.62	0.42
1:C:55:PHE:HB3	1:C:68:VAL:HG23	2.01	0.42
1:A:198:TRP:CE2	1:A:199:LYS:HG3	2.55	0.41
1:C:118:VAL:HB	1:C:121:GLU:HB2	2.02	0.41
1:E:70:ASP:CG	1:E:71:ALA:H	2.28	0.41
2:B:92:ASP:HB3	2:B:93:ALA:H	1.49	0.41
2:B:103:LEU:CD1	2:B:115:VAL:HG13	2.50	0.41
1:C:231:GLY:HA3	1:C:244:TYR:CZ	2.55	0.41
2:B:68:LEU:HD12	2:B:68:LEU:HA	1.93	0.41
1:E:198:TRP:CD1	1:E:313:PRO:HB3	2.56	0.41
2:F:68:LEU:CD1	2:F:151:SER:HB2	2.39	0.41
2:B:78:ARG:HG2	2:B:78:ARG:HH11	1.86	0.41
1:C:272:ASP:OD2	1:C:274:SER:OG	2.39	0.41
2:D:4:GLU:OE1	2:D:4:GLU:N	2.48	0.41
1:A:31:GLN:OE1	1:A:62:GLU:HG2	2.21	0.40
1:C:112:GLN:H	1:C:112:GLN:HG2	1.70	0.40
1:E:101:GLN:H	5:E:504:PEG:C2	2.15	0.40
1:C:201:TYR:CE1	1:C:321:LEU:HD22	2.57	0.40
1:C:242:VAL:HA	1:C:290:ILE:O	2.21	0.40
1:A:244:TYR:C	1:A:244:TYR:CD2	2.99	0.40
1:A:384:GLU:OE1	1:A:384:GLU:CA	2.67	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	372/413 (90%)	351 (94%)	20 (5%)	1 (0%)	36	44
1	C	390/413 (94%)	364 (93%)	23 (6%)	3 (1%)	16	18
1	E	373/413 (90%)	348 (93%)	23 (6%)	2 (0%)	24	29
2	B	151/154 (98%)	146 (97%)	4 (3%)	1 (1%)	18	21
2	D	152/154 (99%)	146 (96%)	6 (4%)	0	100	100
2	F	151/154 (98%)	141 (93%)	9 (6%)	1 (1%)	18	21
All	All	1589/1701 (93%)	1496 (94%)	85 (5%)	8 (0%)	24	29

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	219	THR
1	C	269	ARG
1	C	275	LEU
2	F	129	ASP
1	E	391	ALA
1	A	296	GLY
2	B	130	GLY
1	C	296	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	312/344 (91%)	291 (93%)	21 (7%)	15	19
1	C	327/344 (95%)	300 (92%)	27 (8%)	10	12
1	E	313/344 (91%)	293 (94%)	20 (6%)	16	20
2	B	128/131 (98%)	117 (91%)	11 (9%)	10	11
2	D	129/131 (98%)	124 (96%)	5 (4%)	28	41
2	F	128/131 (98%)	117 (91%)	11 (9%)	10	11
All	All	1337/1425 (94%)	1242 (93%)	95 (7%)	14	17

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	GLU
1	A	96	ARG
1	A	99	SER
1	A	116	THR
1	A	124	VAL
1	A	159	GLU
1	A	177	GLU
1	A	185	GLU
1	A	191	THR
1	A	195	PRO
1	A	241	HIS
1	A	242	VAL
1	A	246	MET
1	A	269	ARG
1	A	270	LEU
1	A	280	GLU
1	A	291	LEU
1	A	300	GLN
1	A	308	VAL
1	A	386	SER
1	A	395	SER
2	B	5	ILE
2	B	10	PHE
2	B	22	VAL
2	B	32	LYS
2	B	78	ARG
2	B	94	THR
2	B	131	LYS
2	B	132	LEU
2	B	135	GLN
2	B	138	VAL
2	B	149	LEU
1	C	5	ILE
1	C	65	ILE
1	C	66	VAL
1	C	93	LYS
1	C	96	ARG
1	C	97	THR
1	C	99	SER
1	C	101	GLN
1	C	112	GLN
1	C	125	LYS

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Mol	Chain	Res	Type
1	C	127	GLN
1	C	135[A]	CYS
1	C	135[B]	CYS
1	C	159	GLU
1	C	171	GLU
1	C	179	VAL
1	C	191	THR
1	C	216	MET
1	C	226	LEU
1	C	241	HIS
1	C	263	SER
1	C	267	ARG
1	C	283	GLU
1	C	317	SER
1	C	334	GLU
1	C	382	ASP
1	C	388	GLU
2	D	5	ILE
2	D	90	SER
2	D	120	GLU
2	D	132	LEU
2	D	133	ARG
1	E	6	ILE
1	E	14	THR
1	E	22	THR
1	E	73	GLN
1	E	108	SER
1	E	122	LYS
1	E	171	GLU
1	E	179	VAL
1	E	191	THR
1	E	218	PHE
1	E	241	HIS
1	E	245	SER
1	E	269	ARG
1	E	303	GLN
1	E	308	VAL
1	E	309	ARG
1	E	312	LEU
1	E	373	LEU
1	E	390	ARG
1	E	405	LYS

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Mol	Chain	Res	Type
2	F	2	ILE
2	F	3	HIS
2	F	5	ILE
2	F	6	GLN
2	F	68	LEU
2	F	73	ILE
2	F	76	ARG
2	F	88	ILE
2	F	115	VAL
2	F	128	ILE
2	F	131	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	112	GLN
1	A	127	GLN
1	A	196	ASN
1	A	204	ASN
1	A	372	ASN
1	A	406	HIS
2	B	58	GLN
2	B	95	GLN
2	B	135	GLN
1	C	139	HIS
1	C	204	ASN
1	C	224	ASN
1	C	303	GLN
2	D	89	GLN
1	E	41	ASN
1	E	196	ASN
1	E	228	GLN
2	F	3	HIS
2	F	6	GLN
2	F	72	ASN
2	F	89	GLN

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](#)

Of 27 ligands modelled in this entry, 3 are monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	GOL	A	505	-	5,5,5	0.27	0	5,5,5	1.25	1 (20%)
3	FES	E	501	1	0,4,4	-	-	-		
7	PO4	C	505	-	4,4,4	0.83	0	6,6,6	0.53	0
3	FES	A	501	1	0,4,4	-	-	-		
7	PO4	C	506	-	4,4,4	0.43	0	6,6,6	0.72	0
5	PEG	A	503	-	6,6,6	0.40	0	5,5,5	0.66	0
7	PO4	C	507	-	4,4,4	0.76	0	6,6,6	0.49	0
5	PEG	F	201	-	6,6,6	0.19	0	5,5,5	0.23	0
5	PEG	C	504	-	6,6,6	0.38	0	5,5,5	0.70	0
6	GOL	E	505	-	5,5,5	0.06	0	5,5,5	0.30	0
5	PEG	E	503	-	6,6,6	0.37	0	5,5,5	0.76	0
7	PO4	F	202	-	4,4,4	0.82	0	6,6,6	0.46	0
7	PO4	D	202	-	4,4,4	0.51	0	6,6,6	0.56	0
7	PO4	E	507	-	4,4,4	0.56	0	6,6,6	0.53	0
6	GOL	D	201	-	5,5,5	0.35	0	5,5,5	0.94	0
8	PG4	A	507	-	12,12,12	0.22	0	11,11,11	0.09	0
7	PO4	D	203	-	4,4,4	0.85	0	6,6,6	0.58	0
5	PEG	E	504	-	6,6,6	0.31	0	5,5,5	0.49	0
3	FES	C	502	1	0,4,4	-	-	-		
7	PO4	E	506	-	4,4,4	0.61	0	6,6,6	0.54	0
5	PEG	A	504	-	6,6,6	0.74	0	5,5,5	0.59	0
7	PO4	A	506	-	4,4,4	0.86	0	6,6,6	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	PO4	B	201	-	4,4,4	0.62	0	6,6,6	0.58	0
5	PEG	C	501	-	6,6,6	0.20	0	5,5,5	0.21	0

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
5	PEG	A	503	-	-	3/4/4/4	-
5	PEG	A	504	-	-	4/4/4/4	-
6	GOL	A	505	-	-	3/4/4/4	-
6	GOL	D	201	-	-	2/4/4/4	-
5	PEG	F	201	-	-	1/4/4/4	-
8	PG4	A	507	-	-	4/10/10/10	-
5	PEG	C	504	-	-	3/4/4/4	-
3	FES	C	502	1	-	-	0/1/1/1
6	GOL	E	505	-	-	2/4/4/4	-
5	PEG	E	503	-	-	2/4/4/4	-
3	FES	E	501	1	-	-	0/1/1/1
5	PEG	C	501	-	-	3/4/4/4	-
5	PEG	E	504	-	-	2/4/4/4	-
3	FES	A	501	1	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	505	GOL	O2-C2-C3	2.10	117.86	109.18

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	505	GOL	C1-C2-C3-O3
6	D	201	GOL	O1-C1-C2-O2
6	D	201	GOL	O1-C1-C2-C3
6	E	505	GOL	O1-C1-C2-C3
5	A	503	PEG	C1-C2-O2-C3

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Mol	Chain	Res	Type	Atoms
5	E	504	PEG	C1-C2-O2-C3
5	C	504	PEG	O2-C3-C4-O4
5	A	504	PEG	O2-C3-C4-O4
5	E	503	PEG	O2-C3-C4-O4
6	A	505	GOL	O2-C2-C3-O3
6	E	505	GOL	O1-C1-C2-O2
6	A	505	GOL	O1-C1-C2-O2
5	A	503	PEG	O1-C1-C2-O2
8	A	507	PG4	C6-C5-O3-C4
5	A	504	PEG	C4-C3-O2-C2
5	A	504	PEG	C1-C2-O2-C3
8	A	507	PG4	O3-C5-C6-O4
5	C	501	PEG	C1-C2-O2-C3
5	E	503	PEG	C4-C3-O2-C2
5	A	504	PEG	O1-C1-C2-O2
5	C	501	PEG	O2-C3-C4-O4
5	C	501	PEG	O1-C1-C2-O2
5	A	503	PEG	C4-C3-O2-C2
8	A	507	PG4	C3-C4-O3-C5
5	E	504	PEG	O1-C1-C2-O2
5	C	504	PEG	C4-C3-O2-C2
5	F	201	PEG	C1-C2-O2-C3
5	C	504	PEG	C1-C2-O2-C3
8	A	507	PG4	C1-C2-O2-C3

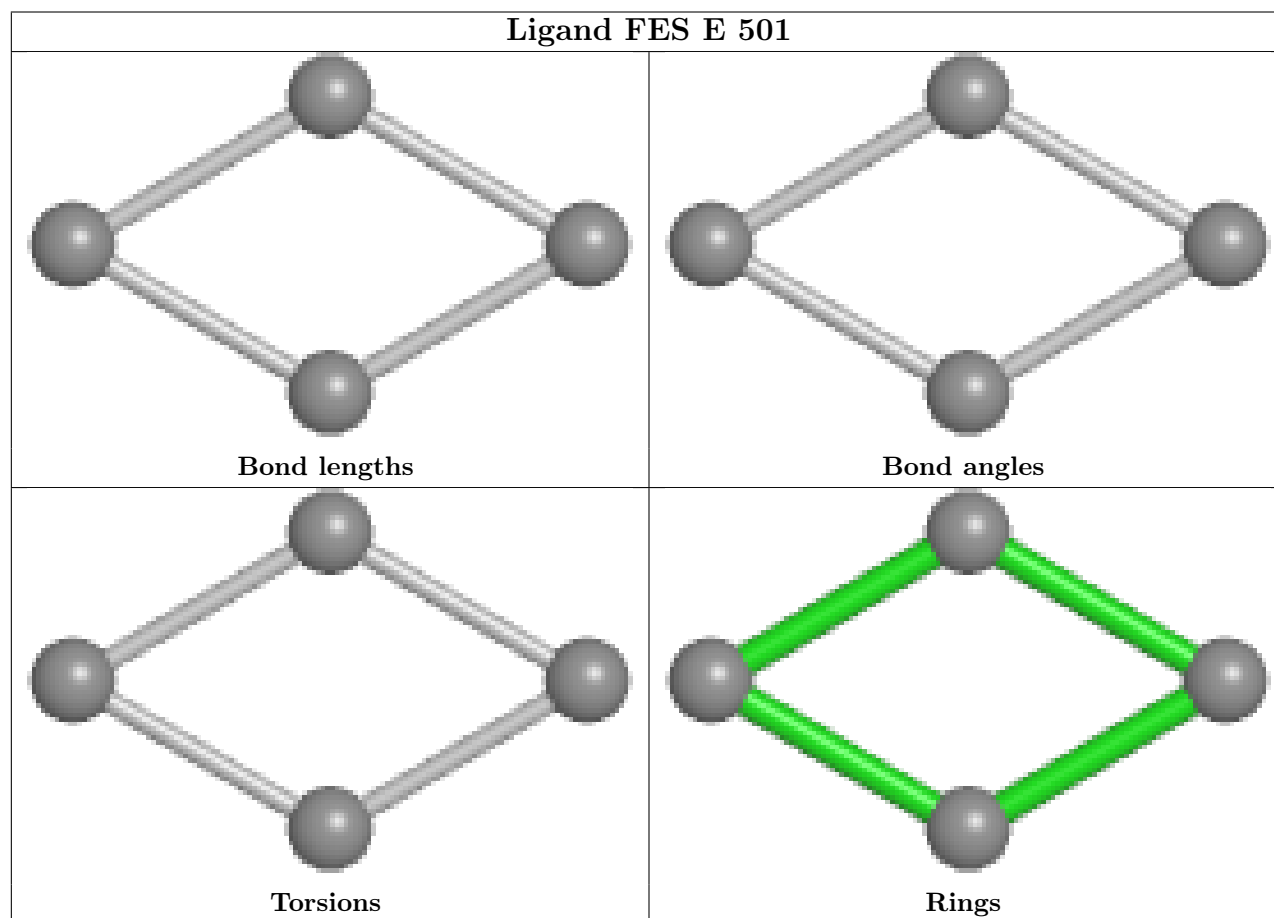
There are no ring outliers.

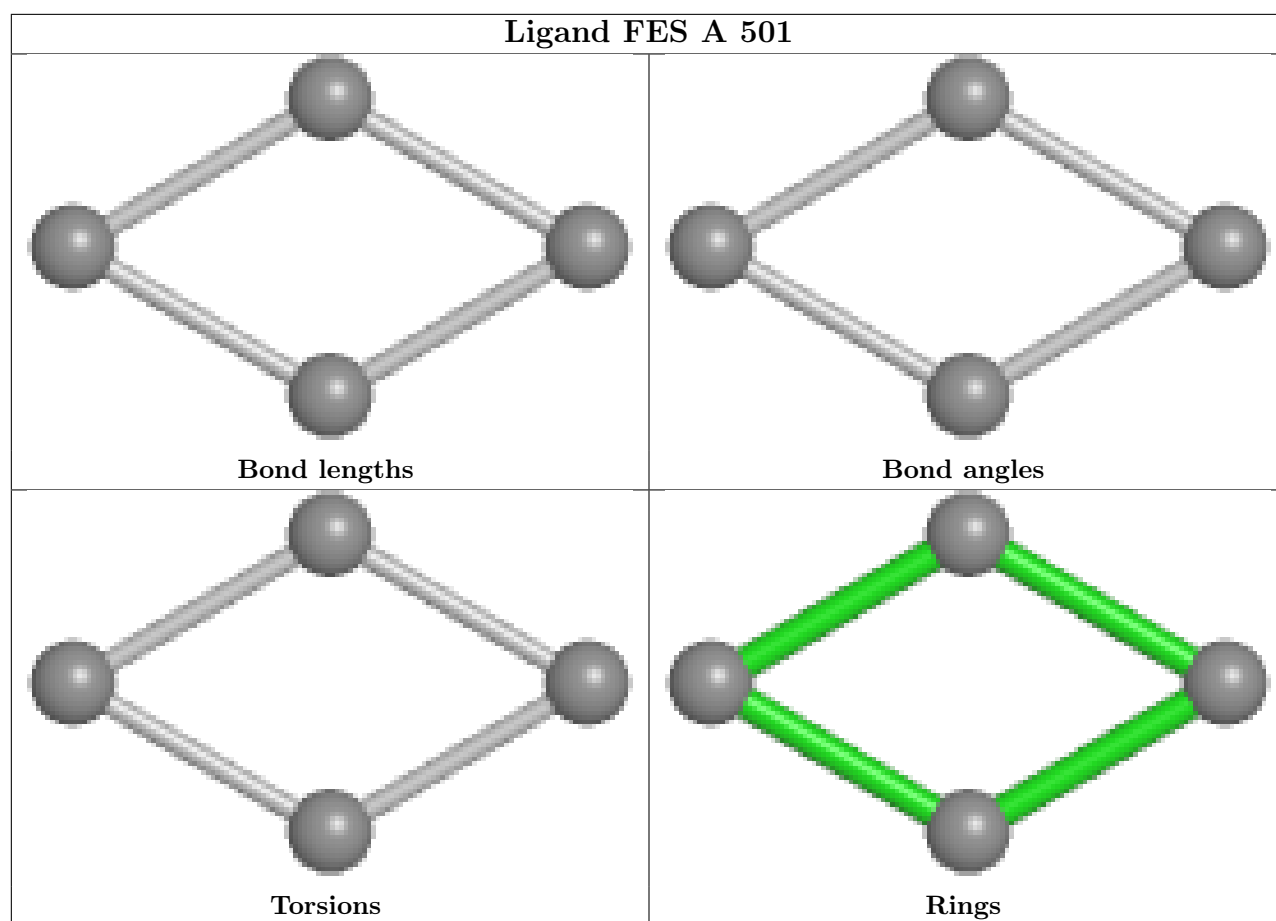
8 monomers are involved in 14 short contacts:

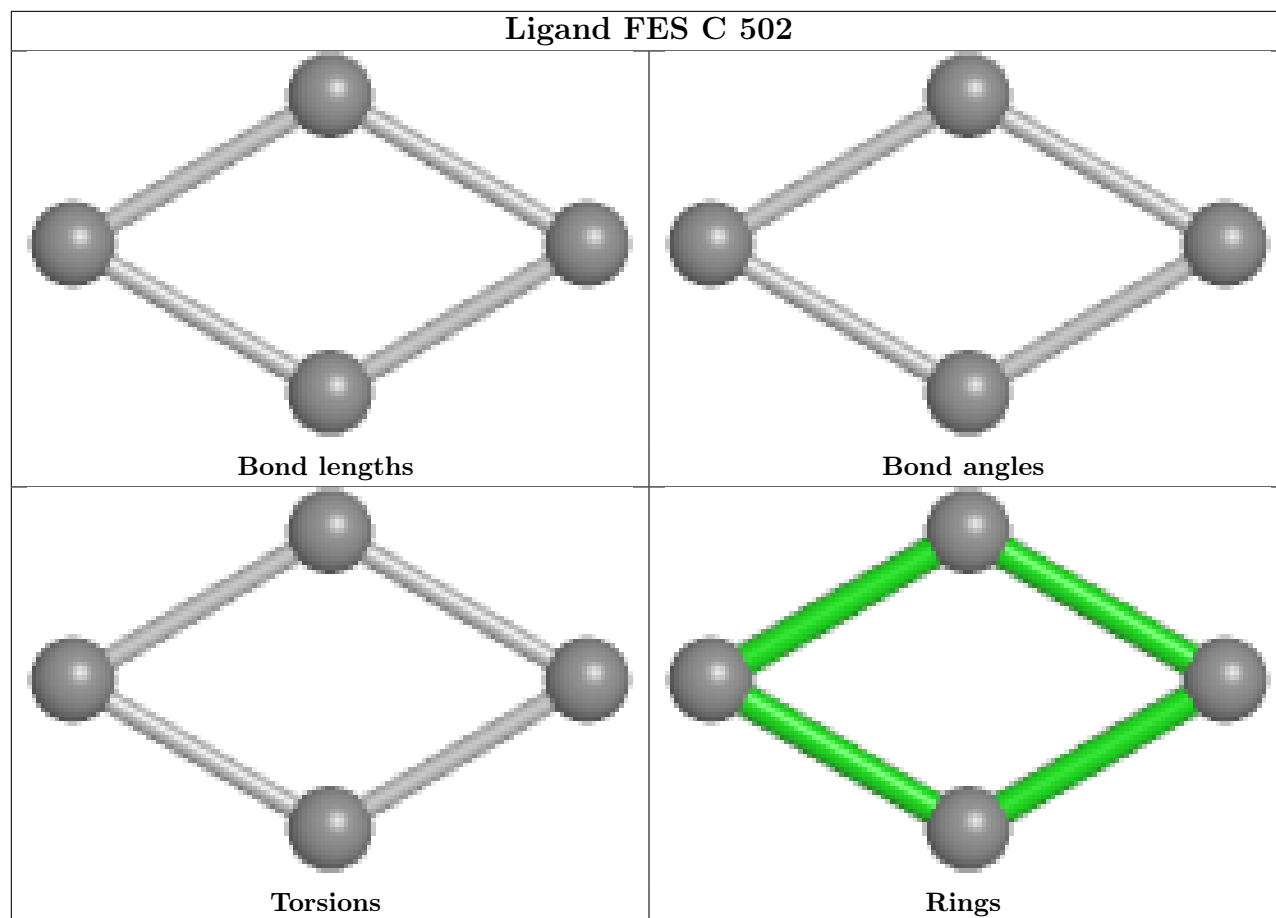
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	501	FES	1	0
3	A	501	FES	1	0
5	A	503	PEG	1	0
5	F	201	PEG	1	0
6	E	505	GOL	1	0
7	E	507	PO4	1	0
7	D	203	PO4	1	0
5	E	504	PEG	7	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	378/413 (91%)	-0.49	0 100 100	28, 45, 75, 105	0
1	C	393/413 (95%)	-0.48	2 (0%) 87 88	26, 43, 87, 125	1 (0%)
1	E	378/413 (91%)	-0.43	3 (0%) 82 84	23, 47, 80, 135	1 (0%)
2	B	153/154 (99%)	-0.41	0 100 100	32, 50, 78, 87	0
2	D	154/154 (100%)	-0.45	0 100 100	33, 48, 85, 96	0
2	F	153/154 (99%)	-0.19	2 (1%) 75 76	34, 56, 90, 116	0
All	All	1609/1701 (94%)	-0.43	7 (0%) 88 89	23, 47, 82, 135	2 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	5	ILE	4.0
1	E	218	PHE	3.7
1	E	5	ILE	3.3
1	C	263	SER	2.7
2	F	2	ILE	2.6
1	E	220	THR	2.3
2	F	5	ILE	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 ⓘ

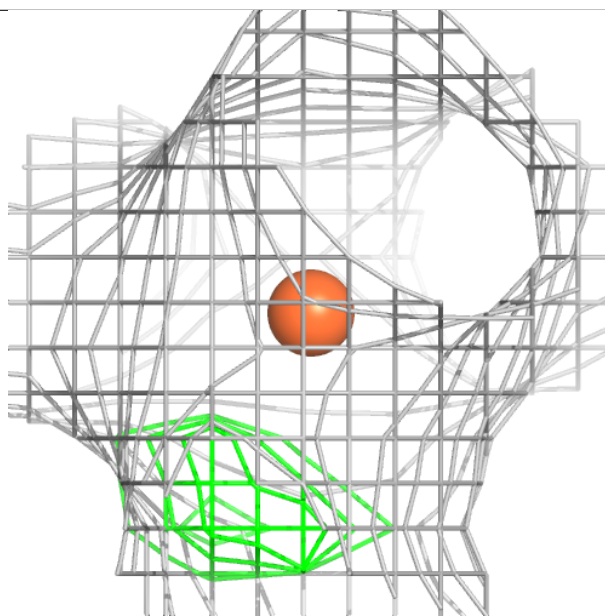
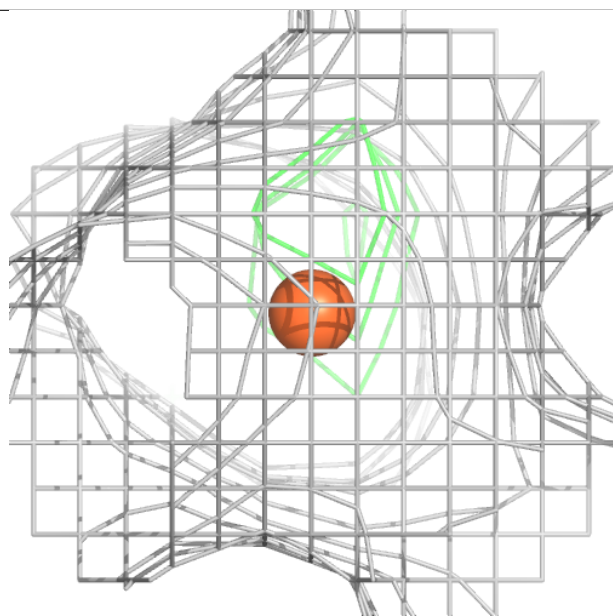
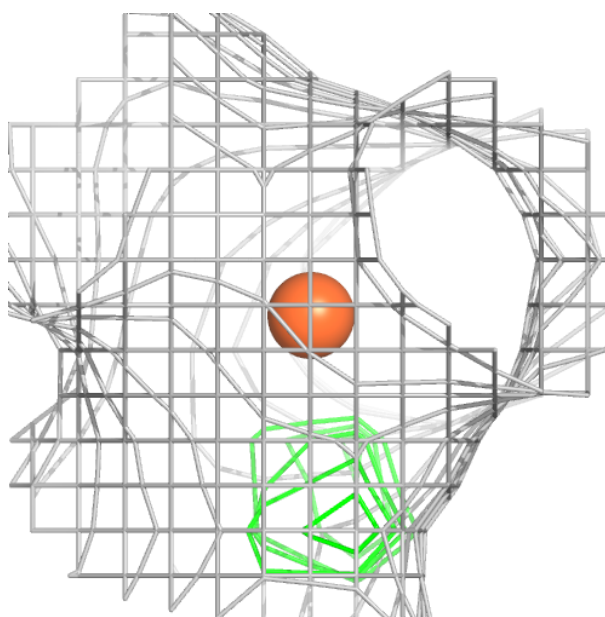
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	PO4	B	201	5/5	0.77	0.09	80,88,98,110	0
6	GOL	D	201	6/6	0.86	0.16	44,63,67,74	0
7	PO4	C	507	5/5	0.86	0.10	91,91,97,98	0
7	PO4	D	202	5/5	0.86	0.07	68,70,79,81	0
7	PO4	F	202	5/5	0.86	0.10	82,102,106,115	0
5	PEG	E	503	7/7	0.87	0.16	37,49,54,55	0
7	PO4	C	505	5/5	0.88	0.10	70,84,91,95	0
5	PEG	C	504	7/7	0.88	0.17	43,48,53,56	0
7	PO4	E	507	5/5	0.89	0.09	76,82,84,87	0
8	PG4	A	507	13/13	0.89	0.14	67,89,105,109	0
7	PO4	A	506	5/5	0.90	0.09	76,82,88,93	0
6	GOL	E	505	6/6	0.90	0.11	47,60,65,69	0
5	PEG	A	504	7/7	0.91	0.12	48,54,62,66	0
6	GOL	A	505	6/6	0.91	0.12	42,46,55,59	0
5	PEG	F	201	7/7	0.92	0.13	77,79,85,87	0
5	PEG	E	504	7/7	0.92	0.12	45,50,62,63	0
5	PEG	A	503	7/7	0.93	0.15	42,49,52,56	0
7	PO4	C	506	5/5	0.94	0.09	55,59,65,66	0
7	PO4	D	203	5/5	0.96	0.07	52,54,57,65	0
7	PO4	E	506	5/5	0.97	0.07	55,59,63,66	0
5	PEG	C	501	7/7	0.97	0.09	62,65,67,68	0
4	FE2	E	502	1/1	0.99	0.03	42,42,42,42	0
3	FES	E	501	4/4	1.00	0.02	36,37,38,39	0
4	FE2	A	502	1/1	1.00	0.03	42,42,42,42	0
4	FE2	C	503	1/1	1.00	0.02	38,38,38,38	0
3	FES	A	501	4/4	1.00	0.02	31,32,32,33	0
3	FES	C	502	4/4	1.00	0.02	33,33,34,34	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.

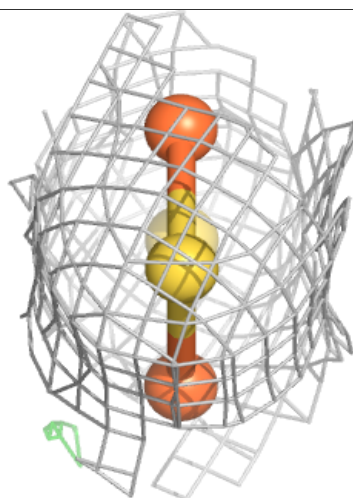
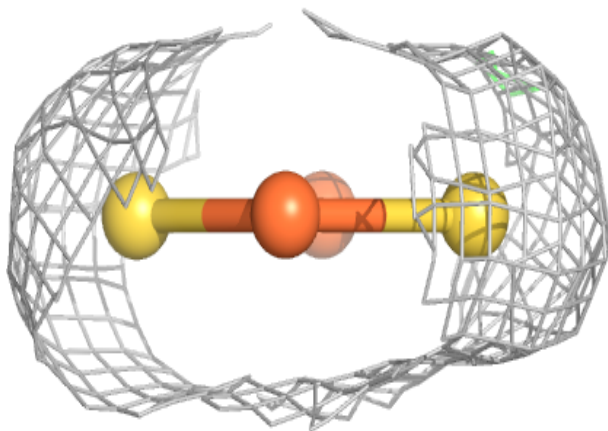
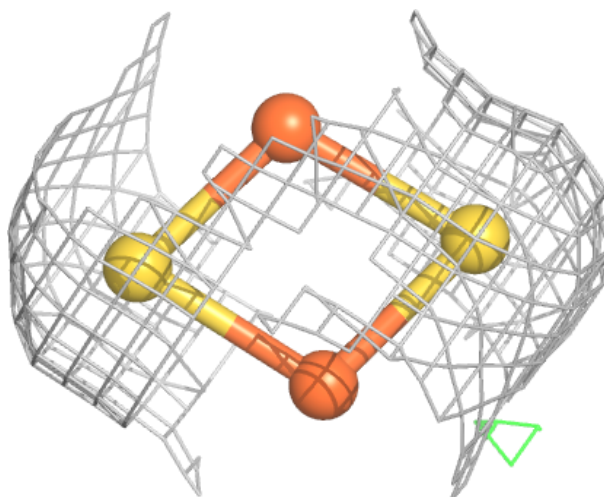
Electron density around FE2 E 502:

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



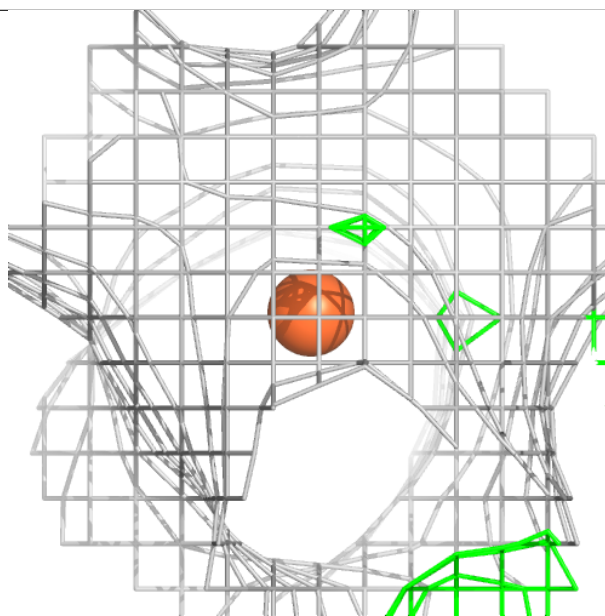
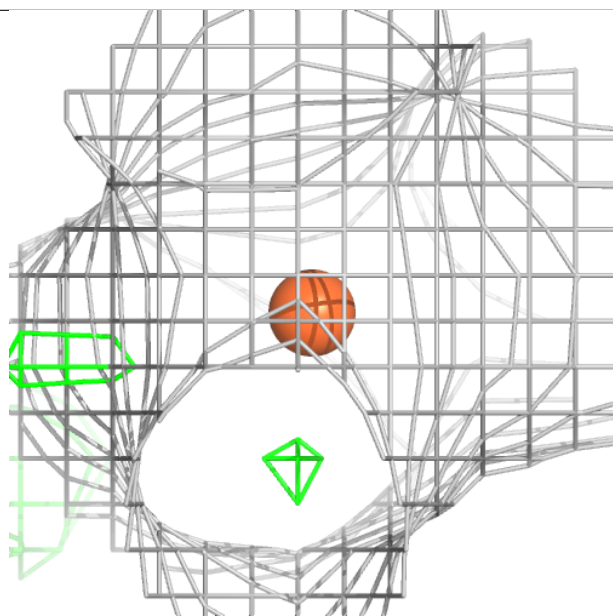
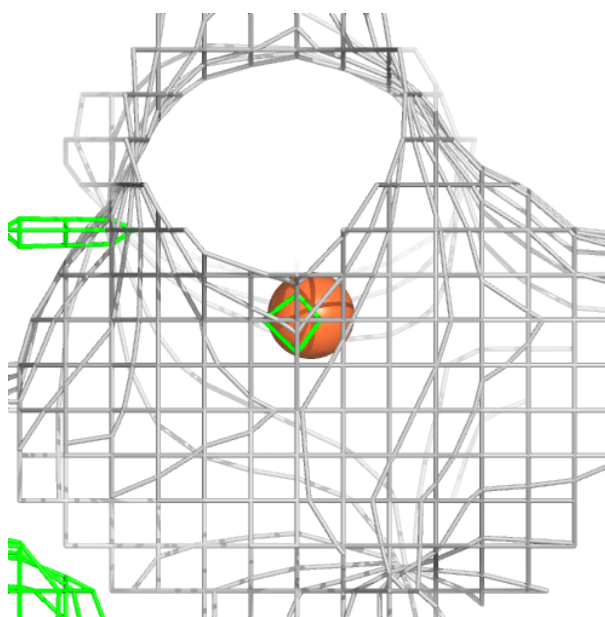
Electron density around FES E 501:

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



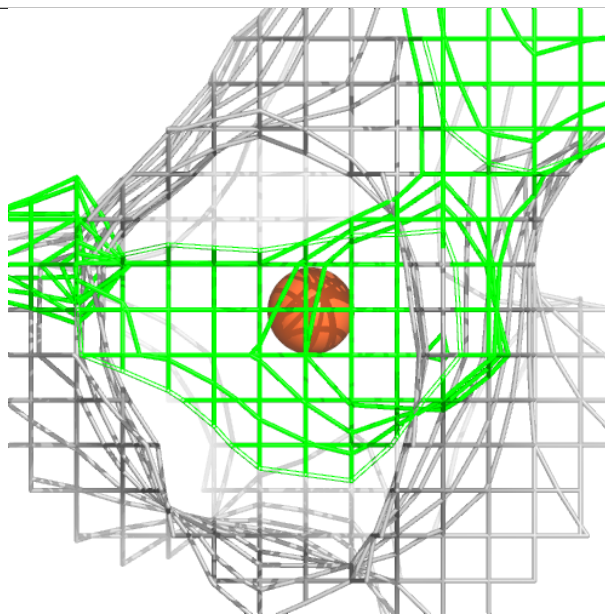
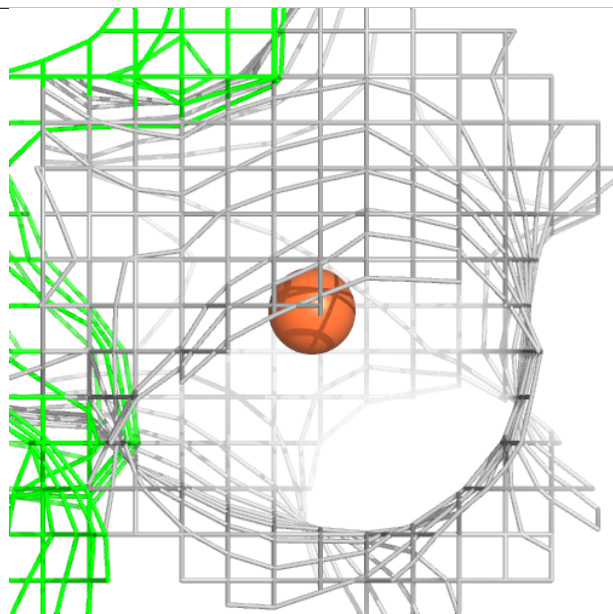
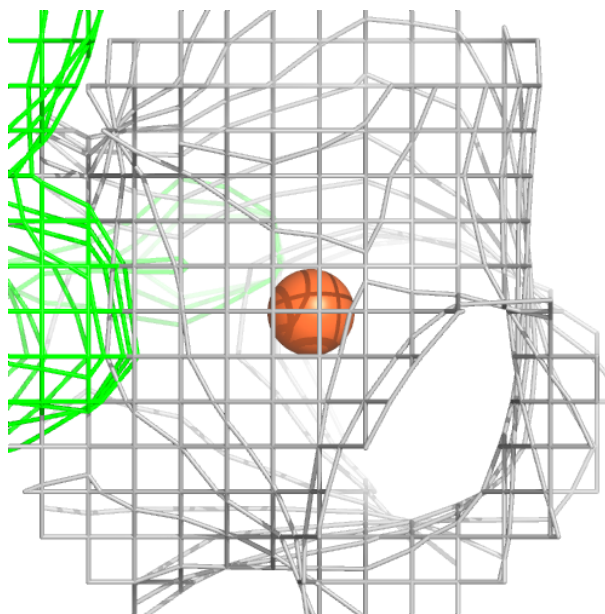
Electron density around FE2 A 502:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



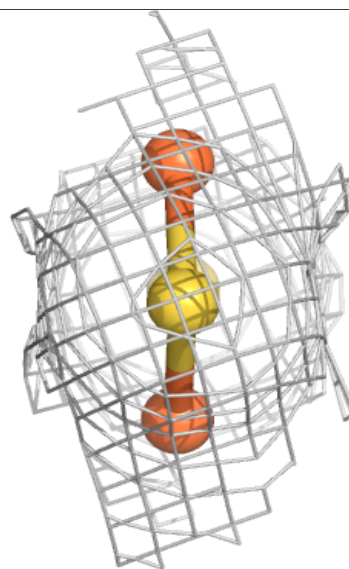
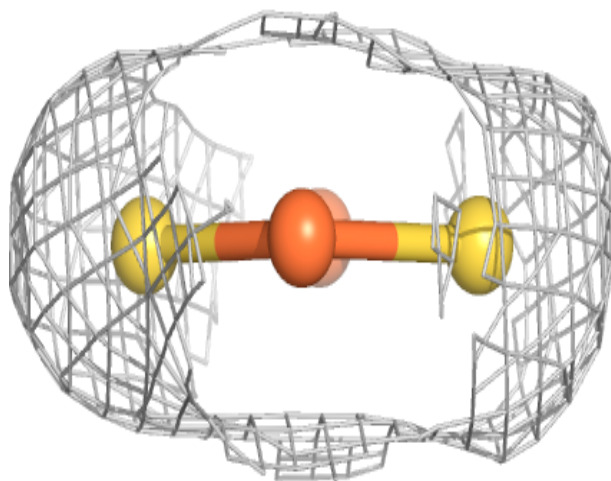
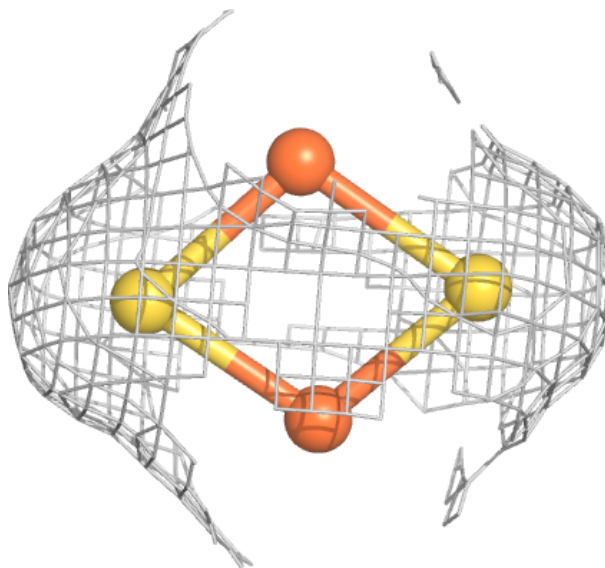
Electron density around FE2 C 503:

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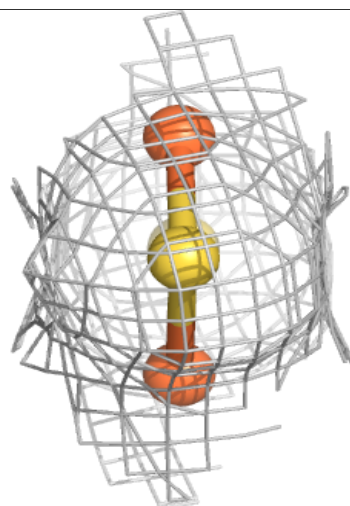
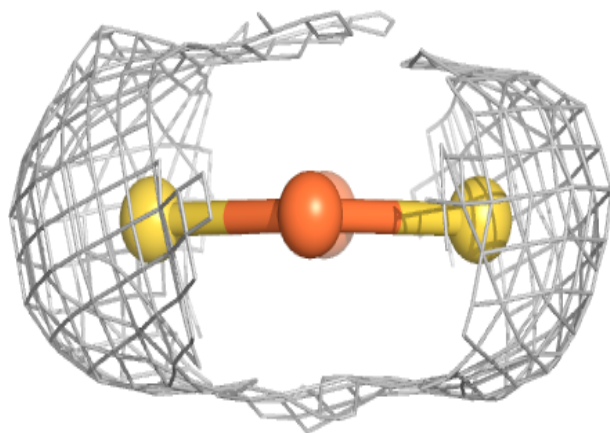
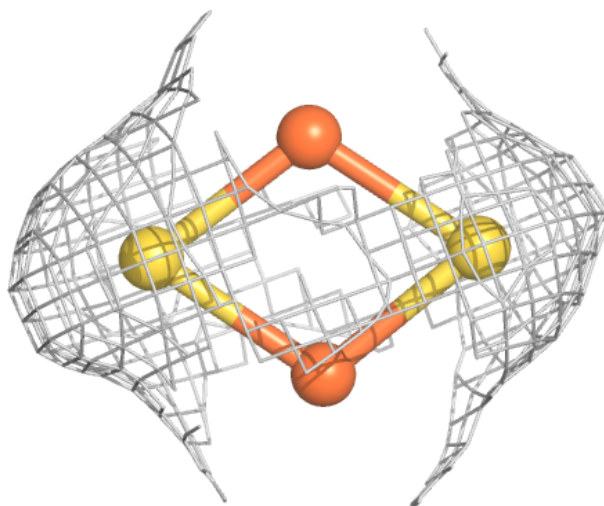
Electron density around FES A 501:

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



Electron density around FES C 502:

$2mF_o - DF_c$ (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.