



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:57 PM UTC

PDB ID : 6TZ8 / pdb_00006tz8
Title : Crystal structure of Cryptococcus neoformans Calcineurin A, Calcineurin B, and FKBP12 with FK-506
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2019-08-10
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

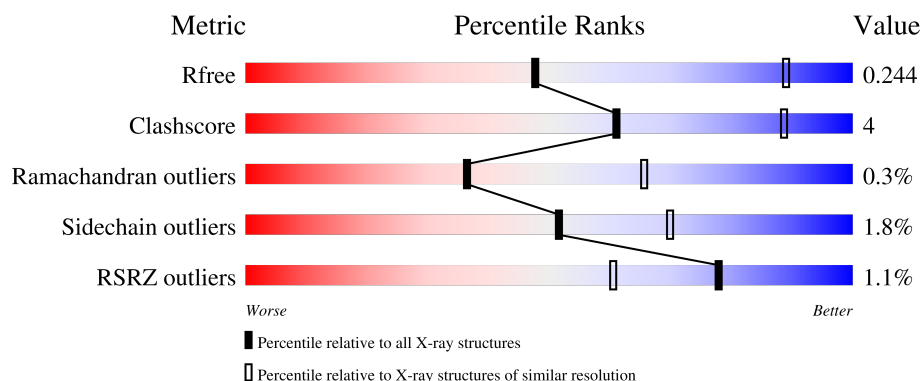
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	390	0% 83% 12% 5%
1	D	390	2% 84% 12% .
2	B	175	90% 9% .
2	E	175	2% 82% 17% .
3	C	122	2% 78% 11% . 9%

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Mol	Chain	Length	Quality of chain
3	F	122	% 84% 6% • 9%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 10282 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 Serine/threonine-protein phosphatase 2B catalytic subunit A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	372	Total	C	N	O	S	0	1	0
			3004	1941	493	548	22			
1	D	373	Total	C	N	O	S	0	1	0
			3024	1952	496	554	22			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	MET	-	expression tag	UNP O42773
A	14	GLY	-	expression tag	UNP O42773
A	15	SER	-	expression tag	UNP O42773
A	16	SER	-	expression tag	UNP O42773
A	17	HIS	-	expression tag	UNP O42773
A	18	HIS	-	expression tag	UNP O42773
A	19	HIS	-	expression tag	UNP O42773
A	20	HIS	-	expression tag	UNP O42773
A	21	HIS	-	expression tag	UNP O42773
A	22	HIS	-	expression tag	UNP O42773
A	23	SER	-	expression tag	UNP O42773
A	24	SER	-	expression tag	UNP O42773
A	25	GLY	-	expression tag	UNP O42773
A	26	GLU	-	expression tag	UNP O42773
A	27	ASN	-	expression tag	UNP O42773
A	28	LEU	-	expression tag	UNP O42773
A	29	TYR	-	expression tag	UNP O42773
A	30	PHE	-	expression tag	UNP O42773
A	31	GLN	-	expression tag	UNP O42773
A	32	GLY	-	expression tag	UNP O42773
A	33	SER	-	expression tag	UNP O42773
D	13	MET	-	expression tag	UNP O42773
D	14	GLY	-	expression tag	UNP O42773
D	15	SER	-	expression tag	UNP O42773

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Chain	Residue	Modelled	Actual	Comment	Reference
D	16	SER	-	expression tag	UNP O42773
D	17	HIS	-	expression tag	UNP O42773
D	18	HIS	-	expression tag	UNP O42773
D	19	HIS	-	expression tag	UNP O42773
D	20	HIS	-	expression tag	UNP O42773
D	21	HIS	-	expression tag	UNP O42773
D	22	HIS	-	expression tag	UNP O42773
D	23	SER	-	expression tag	UNP O42773
D	24	SER	-	expression tag	UNP O42773
D	25	GLY	-	expression tag	UNP O42773
D	26	GLU	-	expression tag	UNP O42773
D	27	ASN	-	expression tag	UNP O42773
D	28	LEU	-	expression tag	UNP O42773
D	29	TYR	-	expression tag	UNP O42773
D	30	PHE	-	expression tag	UNP O42773
D	31	GLN	-	expression tag	UNP O42773
D	32	GLY	-	expression tag	UNP O42773
D	33	SER	-	expression tag	UNP O42773

- Molecule 2 is a protein called Calcineurin subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	174	Total	C	N	O	S	0	1	0
			1256	790	211	249	6			
2	E	174	Total	C	N	O	S	0	1	0
			1254	790	210	248	6			

- Molecule 3 is a protein called FK506-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	111	Total	C	N	O	S	0	0	0
			794	498	134	160	2			
3	F	111	Total	C	N	O	S	0	0	0
			800	502	138	158	2			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	MET	-	expression tag	UNP O94746
C	-8	TRP	-	expression tag	UNP O94746
C	-7	SER	-	expression tag	UNP O94746
C	-6	HIS	-	expression tag	UNP O94746

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	PRO	-	expression tag	UNP 094746
C	-4	GLN	-	expression tag	UNP 094746
C	-3	PHE	-	expression tag	UNP 094746
C	-2	GLU	-	expression tag	UNP 094746
C	-1	LYS	-	expression tag	UNP 094746
C	0	GLY	-	expression tag	UNP 094746
C	1	SER	-	expression tag	UNP 094746
C	9	LYS	SER	engineered mutation	UNP 094746
C	10	GLU	ALA	conflict	UNP 094746
C	12	ASN	ASP	conflict	UNP 094746
C	14	VAL	LYS	engineered mutation	UNP 094746
C	15	ASP	THR	conflict	UNP 094746
C	16	LYS	PHE	conflict	UNP 094746
C	18	VAL	GLN	conflict	UNP 094746
C	19	LYS	PRO	conflict	UNP 094746
C	69	LEU	VAL	conflict	UNP 094746
C	71	GLU	GLN	conflict	UNP 094746
C	109	SER	-	expression tag	UNP 094746
C	110	LYS	-	expression tag	UNP 094746
C	111	ARG	-	expression tag	UNP 094746
C	112	ALA	-	expression tag	UNP 094746
F	-9	MET	-	expression tag	UNP 094746
F	-8	TRP	-	expression tag	UNP 094746
F	-7	SER	-	expression tag	UNP 094746
F	-6	HIS	-	expression tag	UNP 094746
F	-5	PRO	-	expression tag	UNP 094746
F	-4	GLN	-	expression tag	UNP 094746
F	-3	PHE	-	expression tag	UNP 094746
F	-2	GLU	-	expression tag	UNP 094746
F	-1	LYS	-	expression tag	UNP 094746
F	0	GLY	-	expression tag	UNP 094746
F	1	SER	-	expression tag	UNP 094746
F	9	LYS	SER	engineered mutation	UNP 094746
F	10	GLU	ALA	conflict	UNP 094746
F	12	ASN	ASP	conflict	UNP 094746
F	14	VAL	LYS	engineered mutation	UNP 094746
F	15	ASP	THR	conflict	UNP 094746
F	16	LYS	PHE	conflict	UNP 094746
F	18	VAL	GLN	conflict	UNP 094746
F	19	LYS	PRO	conflict	UNP 094746
F	69	LEU	VAL	conflict	UNP 094746
F	71	GLU	GLN	conflict	UNP 094746

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Chain	Residue	Modelled	Actual	Comment	Reference
F	109	SER	-	expression tag	UNP O94746
F	110	LYS	-	expression tag	UNP O94746
F	111	ARG	-	expression tag	UNP O94746
F	112	ALA	-	expression tag	UNP O94746

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

- Molecule 5 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Fe 1 1	0	0
5	D	1	Total Fe 1 1	0	0

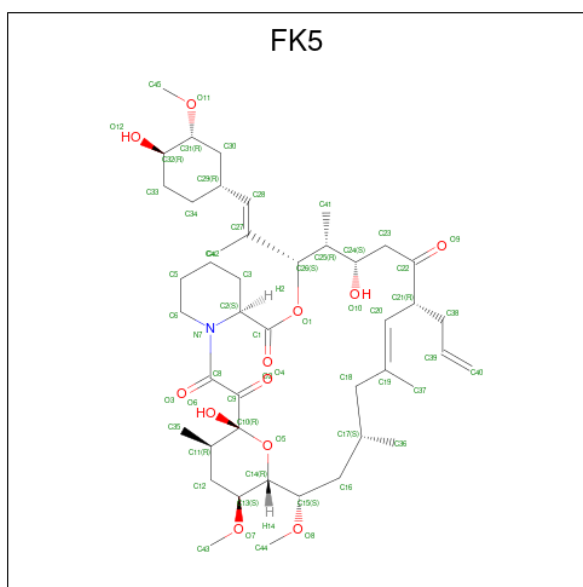
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Zn	0	0
			1	1		
6	D	1	Total	Zn	0	0
			1	1		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	4	Total	Ca	0	0
			4	4		
7	E	4	Total	Ca	0	0
			4	4		

- Molecule 8 is 8-DEETHYL-8-[BUT-3-ENYL]-ASCOMYCIN (CCD ID: FK5) (formula: C₄₄H₆₉NO₁₂) (labeled as "Ligand of Interest" by depositor).



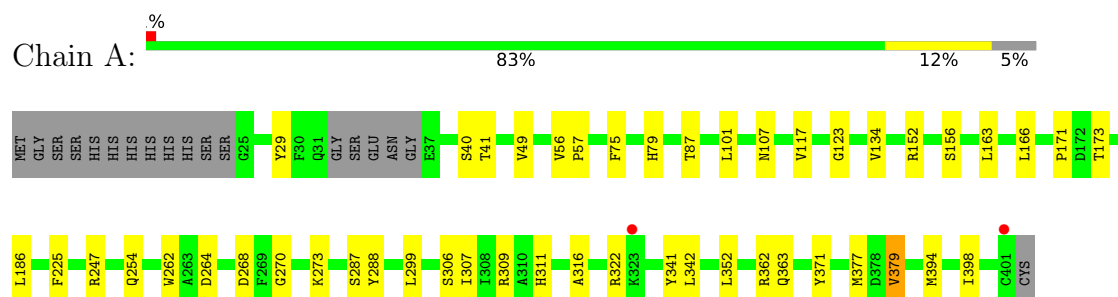
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	2	Total	O	0	0
			2	2		
9	D	2	Total	O	0	0
			2	2		
9	E	2	Total	O	0	0
			2	2		

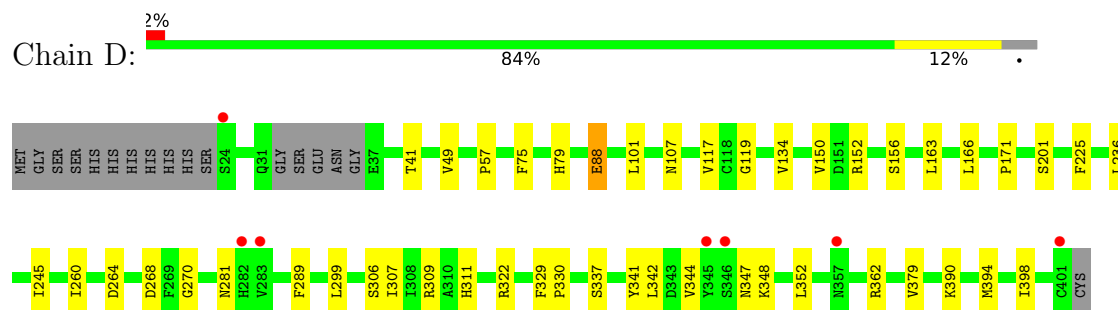
3 Residue-property plots [i](#)

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.

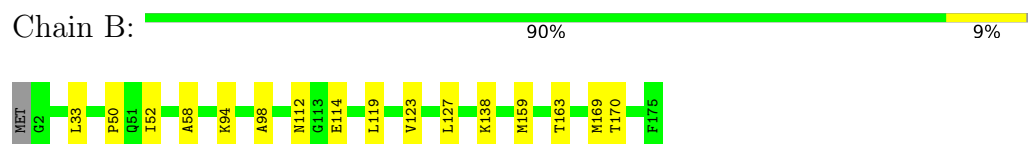
- Molecule 1: Serine/threonine-protein phosphatase 2B catalytic subunit A1



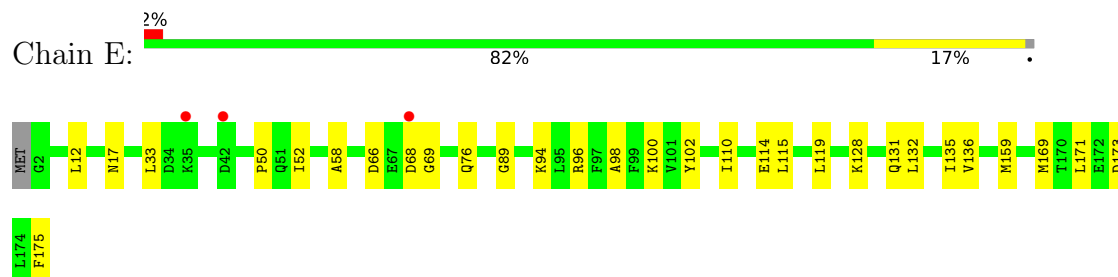
- Molecule 1: Serine/threonine-protein phosphatase 2B catalytic subunit A1



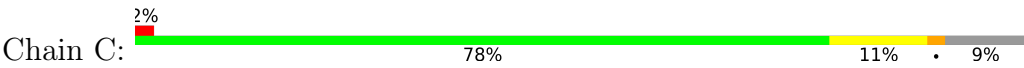
- Molecule 2: Calcineurin subunit B



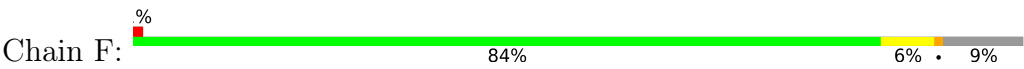
- Molecule 2: Calcineurin subunit B



● Molecule 3: FK506-binding protein 1



● Molecule 3: FK506-binding protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.72Å 120.70Å 134.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.57 – 3.30 44.57 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.57-3.30) 99.8 (44.57-3.30)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 3.33Å)	Xtriage
Refinement program	PHENIX (DEV_2919: ???)	Depositor
R, R_{free}	0.199 , 0.243 0.200 , 0.244	Depositor DCC
R_{free} test set	1484 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	45.2	Xtriage
Anisotropy	0.812	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10282	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.23 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.6859e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CA, FK5, FE, SO4, ZN

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	0.18	0/3092	0.38	0/4204
1	D	0.17	0/3112	0.36	0/4228
2	B	0.18	0/1278	0.30	0/1726
2	E	0.17	0/1276	0.33	0/1723
3	C	0.17	0/811	0.40	0/1109
3	F	0.17	0/817	0.37	0/1115
All	All	0.17	0/10386	0.36	0/14105

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3004	0	2853	27	0
1	D	3024	0	2884	29	0
2	B	1256	0	1096	10	0
2	E	1254	0	1099	18	0
3	C	794	0	721	8	0
3	F	800	0	739	4	0
4	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	5	0	0	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	B	4	0	0	0	0
7	E	4	0	0	0	0
8	C	57	0	69	1	0
8	F	57	0	69	1	0
9	A	3	0	0	0	0
9	B	2	0	0	0	0
9	D	2	0	0	0	0
9	E	2	0	0	0	0
All	All	10282	0	9530	84	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 4.

All (84) 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:D:394:MET:HE3	2:E:52:ILE:HG23	1.61	0.82
1:A:270:GLY:O	1:A:322:ARG:NH1	2.28	0.67
2:E:94:LYS:NZ	2:E:169:MET:O	2.27	0.66
1:D:398:ILE:HG23	2:E:33:LEU:HD11	1.78	0.66
1:A:398:ILE:HG23	2:B:33:LEU:HD11	1.79	0.65
2:E:17:ASN:HD22	2:E:89:GLY:HA2	1.61	0.65
1:D:41:THR:HB	2:E:114:GLU:HG3	1.82	0.61
1:A:107:ASN:OD1	1:A:247:ARG:NH1	2.29	0.61
2:E:98:ALA:HB2	2:E:169:MET:HE3	1.85	0.58
1:A:152:ARG:NH1	1:A:341:TYR:OH	2.34	0.57
1:D:152:ARG:NH1	1:D:341:TYR:OH	2.36	0.57
2:E:128:LYS:HB2	2:E:131:GLN:HG3	1.86	0.56
1:A:41:THR:HB	2:B:114:GLU:HG3	1.87	0.56
1:D:117:VAL:HB	1:D:352:LEU:HB3	1.88	0.55
1:D:225:PHE:HD1	1:D:306:SER:HB3	1.71	0.54
1:D:134:VAL:O	1:D:362:ARG:NH1	2.40	0.54
3:C:24:THR:HB	3:C:106:LYS:HB2	1.90	0.54
2:E:171:LEU:O	2:E:173:ASP:N	2.41	0.54
1:A:379:VAL:HG11	2:B:119:LEU:HD11	1.89	0.53
1:A:225:PHE:HD2	1:A:306:SER:HB3	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:98:ALA:HB2	2:B:169:MET:HE3	1.92	0.52
2:B:94:LYS:NZ	2:B:170:THR:OG1	2.43	0.51
1:D:344:VAL:HG12	3:F:41:ARG:HB2	1.92	0.51
1:A:56:VAL:HG11	1:A:87:THR:HG22	1.92	0.51
3:C:22:ASN:O	3:C:108:ASN:N	2.43	0.51
1:A:101:LEU:HD13	1:A:171:PRO:HB3	1.92	0.51
1:A:394:MET:HE1	2:B:58:ALA:HA	1.93	0.51
1:D:107:ASN:ND2	1:D:245:ILE:O	2.44	0.51
1:A:264:ASP:OD1	1:A:311:HIS:HD2	1.94	0.50
1:D:88:GLU:OE2	1:D:201:SER:OG	2.17	0.49
1:D:150:VAL:HA	1:D:156:SER:HB3	1.94	0.49
1:D:57:PRO:HB3	1:D:75:PHE:CE2	2.48	0.49
2:E:66:ASP:HB3	2:E:69:GLY:HA2	1.95	0.49
1:A:134:VAL:O	1:A:362:ARG:NH1	2.46	0.48
1:D:101:LEU:HD13	1:D:171:PRO:HB3	1.94	0.48
1:D:57:PRO:HD3	1:D:79:HIS:CE1	2.49	0.48
1:D:379:VAL:HG11	2:E:119:LEU:HD11	1.96	0.48
1:A:57:PRO:HB3	1:A:75:PHE:CE2	2.49	0.48
2:E:115:LEU:HD23	2:E:136:VAL:HG13	1.96	0.48
1:D:394:MET:HE1	2:E:58:ALA:HA	1.96	0.47
2:B:123:VAL:HG11	2:B:127:LEU:HB2	1.94	0.47
1:D:119:GLY:H	1:D:337:SER:HG	1.61	0.47
1:D:236:LEU:HD22	1:D:260:ILE:HD11	1.96	0.47
2:E:12:LEU:HD21	2:E:76:GLN:HG3	1.96	0.46
1:A:316:ALA:O	1:A:363:GLN:NE2	2.48	0.46
3:F:5:VAL:HG22	3:F:75:LEU:HD23	1.98	0.46
1:A:123:GLY:HA2	1:A:156:SER:HA	1.97	0.46
1:A:377:MET:SD	3:C:90:PRO:HG2	2.56	0.46
3:F:41:ARG:NH2	3:F:103:GLU:OE1	2.48	0.46
1:A:287:SER:OG	1:A:288:TYR:N	2.48	0.46
3:C:88:PHE:H	3:C:92:ILE:HB	1.80	0.46
1:D:270:GLY:O	1:D:322:ARG:NH1	2.45	0.46
1:D:299:LEU:HD21	1:D:307:ILE:HG13	1.98	0.46
1:A:29:TYR:CD1	1:A:40:SER:HB3	2.51	0.45
1:A:394:MET:HE3	2:B:52:ILE:HG23	1.98	0.45
1:D:268:ASP:OD1	1:D:268:ASP:N	2.35	0.45
2:E:17:ASN:ND2	2:E:89:GLY:HA2	2.30	0.45
1:A:342:LEU:O	3:C:36:LYS:NZ	2.48	0.45
1:D:347:ASN:ND2	1:D:348:LYS:O	2.49	0.45
1:D:329:PHE:CD2	1:D:330:PRO:HD2	2.51	0.45
1:A:371:TYR:O	2:B:138:LYS:NZ	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:LEU:HD11	1:A:262:TRP:HZ2	1.83	0.43
3:F:89:PRO:HB2	3:F:90:PRO:HD3	2.02	0.42
2:B:94:LYS:NZ	2:B:169:MET:O	2.50	0.42
8:F:200:FK5:H371	8:F:200:FK5:H21	1.79	0.42
1:D:390:LYS:HD3	1:D:390:LYS:HA	1.86	0.42
1:A:268:ASP:OD1	1:A:268:ASP:N	2.41	0.42
1:D:152:ARG:HD3	1:D:342:LEU:HD21	2.02	0.42
1:D:225:PHE:CD1	1:D:306:SER:HB3	2.52	0.42
2:E:132:LEU:HD12	2:E:135:ILE:HD11	2.02	0.42
1:A:117:VAL:HB	1:A:352:LEU:HB3	2.02	0.41
1:D:281:ASN:HA	1:D:289:PHE:CE2	2.54	0.41
2:E:96:ARG:O	2:E:100:LYS:HG3	2.20	0.41
1:A:163:LEU:HA	1:A:166:LEU:HD12	2.02	0.41
1:D:163:LEU:HD23	1:D:166:LEU:HD12	2.01	0.41
2:E:102:TYR:HB2	2:E:110:ILE:HD13	2.03	0.41
2:E:68:ASP:OD1	2:E:69:GLY:N	2.53	0.41
8:C:200:FK5:H29	8:C:200:FK5:H421	1.81	0.40
3:C:6:GLU:HB3	3:C:74:ASN:HB2	2.03	0.40
1:D:264:ASP:OD1	1:D:311:HIS:HD2	2.04	0.40
1:A:57:PRO:HD3	1:A:79:HIS:NE2	2.36	0.40
1:A:299:LEU:HD21	1:A:307:ILE:HG13	2.04	0.40
3:C:27:TYR:CE1	3:C:40:SER:HB3	2.56	0.40
3:C:59:GLY:HA3	3:C:77:CYS:SG	2.62	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	369/390 (95%)	352 (95%)	17 (5%)	0	100	100
1	D	370/390 (95%)	349 (94%)	21 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	173/175 (99%)	165 (95%)	7 (4%)	1 (1%)	21	52
2	E	173/175 (99%)	164 (95%)	8 (5%)	1 (1%)	21	52
3	C	109/122 (89%)	102 (94%)	6 (6%)	1 (1%)	14	43
3	F	109/122 (89%)	104 (95%)	4 (4%)	1 (1%)	14	43
All	All	1303/1374 (95%)	1236 (95%)	63 (5%)	4 (0%)	36	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	50	PRO
2	E	50	PRO
3	C	90	PRO
3	F	90	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	321/349 (92%)	315 (98%)	6 (2%)	50	68
1	D	326/349 (93%)	323 (99%)	3 (1%)	70	78
2	B	113/151 (75%)	110 (97%)	3 (3%)	39	63
2	E	113/151 (75%)	111 (98%)	2 (2%)	51	70
3	C	80/103 (78%)	77 (96%)	3 (4%)	29	57
3	F	81/103 (79%)	79 (98%)	2 (2%)	42	64
All	All	1034/1206 (86%)	1015 (98%)	19 (2%)	51	70

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	VAL
1	A	173	THR
1	A	254	GLN

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Mol	Chain	Res	Type
1	A	273	LYS
1	A	309	ARG
1	A	379	VAL
2	B	112	ASN
2	B	159	MET
2	B	163	THR
3	C	26	HIS
3	C	28	VAL
3	C	74	ASN
1	D	49	VAL
1	D	88	GLU
1	D	309	ARG
2	E	159	MET
2	E	175	PHE
3	F	26	HIS
3	F	28	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	GLN
1	A	224	GLN
1	A	237	HIS
1	A	280	HIS
1	A	311	HIS
2	B	112	ASN
2	B	133	GLN
1	D	78	ASN
1	D	224	GLN
2	E	15	ASN
2	E	112	ASN
2	E	133	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 12 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	FK5	F	200	-	54,60,60	3.62	11 (20%)	64,86,86	1.79	15 (23%)
4	SO4	A	504	-	4,4,4	0.25	0	6,6,6	0.14	0
8	FK5	C	200	-	54,60,60	3.65	11 (20%)	64,86,86	1.81	10 (15%)
4	SO4	A	501	5,6	4,4,4	0.24	0	6,6,6	0.10	0
4	SO4	D	500	5,6	4,4,4	0.25	0	6,6,6	0.18	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
8	FK5	F	200	-	-	7/68/114/114	0/3/4/4
8	FK5	C	200	-	-	6/68/114/114	0/3/4/4

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	F	200	FK5	O9-C22	11.96	1.41	1.21
8	C	200	FK5	O9-C22	11.93	1.41	1.21
8	F	200	FK5	O4-C9	11.07	1.41	1.22
8	C	200	FK5	C8-C9	-11.04	1.39	1.53
8	C	200	FK5	O4-C9	10.95	1.41	1.22
8	F	200	FK5	C8-C9	-10.36	1.40	1.53
8	F	200	FK5	C20-C19	10.00	1.47	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	200	FK5	C20-C19	9.98	1.47	1.33
8	C	200	FK5	O3-C8	8.99	1.41	1.23
8	F	200	FK5	O3-C8	8.91	1.41	1.23
8	C	200	FK5	O2-C1	8.11	1.41	1.21
8	F	200	FK5	O2-C1	8.00	1.41	1.21
8	F	200	FK5	C28-C27	6.37	1.47	1.33
8	C	200	FK5	C28-C27	6.12	1.47	1.33
8	F	200	FK5	O1-C1	-3.69	1.25	1.34
8	C	200	FK5	O6-C10	3.52	1.45	1.39
8	F	200	FK5	O6-C10	3.50	1.45	1.39
8	C	200	FK5	O1-C1	-3.47	1.26	1.34
8	C	200	FK5	C40-C39	2.84	1.47	1.29
8	F	200	FK5	C40-C39	2.80	1.47	1.29
8	F	200	FK5	O5-C14	-2.46	1.40	1.44
8	C	200	FK5	O5-C14	-2.19	1.40	1.44

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	200	FK5	C21-C20-C19	-7.59	120.39	127.63
8	C	200	FK5	C21-C20-C19	-7.55	120.43	127.63
8	C	200	FK5	O1-C1-C2	5.38	121.97	110.80
8	F	200	FK5	O1-C1-C2	5.28	121.78	110.80
8	C	200	FK5	O1-C26-C25	4.88	111.50	105.91
8	F	200	FK5	C9-C8-N7	3.05	122.74	119.25
8	F	200	FK5	O1-C26-C25	2.93	109.27	105.91
8	C	200	FK5	O2-C1-C2	-2.91	118.04	124.46
8	F	200	FK5	O2-C1-C2	-2.73	118.44	124.46
8	F	200	FK5	C6-N7-C2	2.67	121.34	115.81
8	C	200	FK5	C34-C29-C28	-2.67	107.58	111.14
8	C	200	FK5	C37-C19-C20	-2.64	118.87	123.85
8	C	200	FK5	C6-N7-C2	2.56	121.11	115.81
8	F	200	FK5	C34-C29-C28	-2.45	107.87	111.14
8	C	200	FK5	O3-C8-C9	2.43	120.27	116.28
8	F	200	FK5	O5-C14-C13	-2.41	105.99	109.36
8	C	200	FK5	C37-C19-C18	2.40	120.61	115.28
8	F	200	FK5	C37-C19-C20	-2.34	119.44	123.85
8	F	200	FK5	O1-C1-O2	-2.31	119.78	123.95
8	F	200	FK5	O3-C8-N7	-2.21	117.85	122.17
8	C	200	FK5	O1-C1-O2	-2.20	119.99	123.95
8	F	200	FK5	C37-C19-C18	2.15	120.05	115.28
8	F	200	FK5	C34-C33-C32	-2.12	108.65	111.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	200	FK5	C17-C16-C15	-2.12	112.66	115.93
8	F	200	FK5	C24-C23-C22	-2.02	109.77	114.27

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	200	FK5	C15-C16-C17-C36
8	C	200	FK5	C22-C21-C38-C39
8	F	200	FK5	C15-C16-C17-C36
8	C	200	FK5	C15-C16-C17-C18
8	F	200	FK5	C15-C16-C17-C18
8	C	200	FK5	C36-C17-C18-C19
8	F	200	FK5	C36-C17-C18-C19
8	F	200	FK5	C16-C17-C18-C19
8	C	200	FK5	C19-C20-C21-C22
8	F	200	FK5	C19-C20-C21-C22
8	F	200	FK5	C22-C21-C38-C39
8	C	200	FK5	C20-C21-C38-C39
8	F	200	FK5	C20-C21-C38-C39

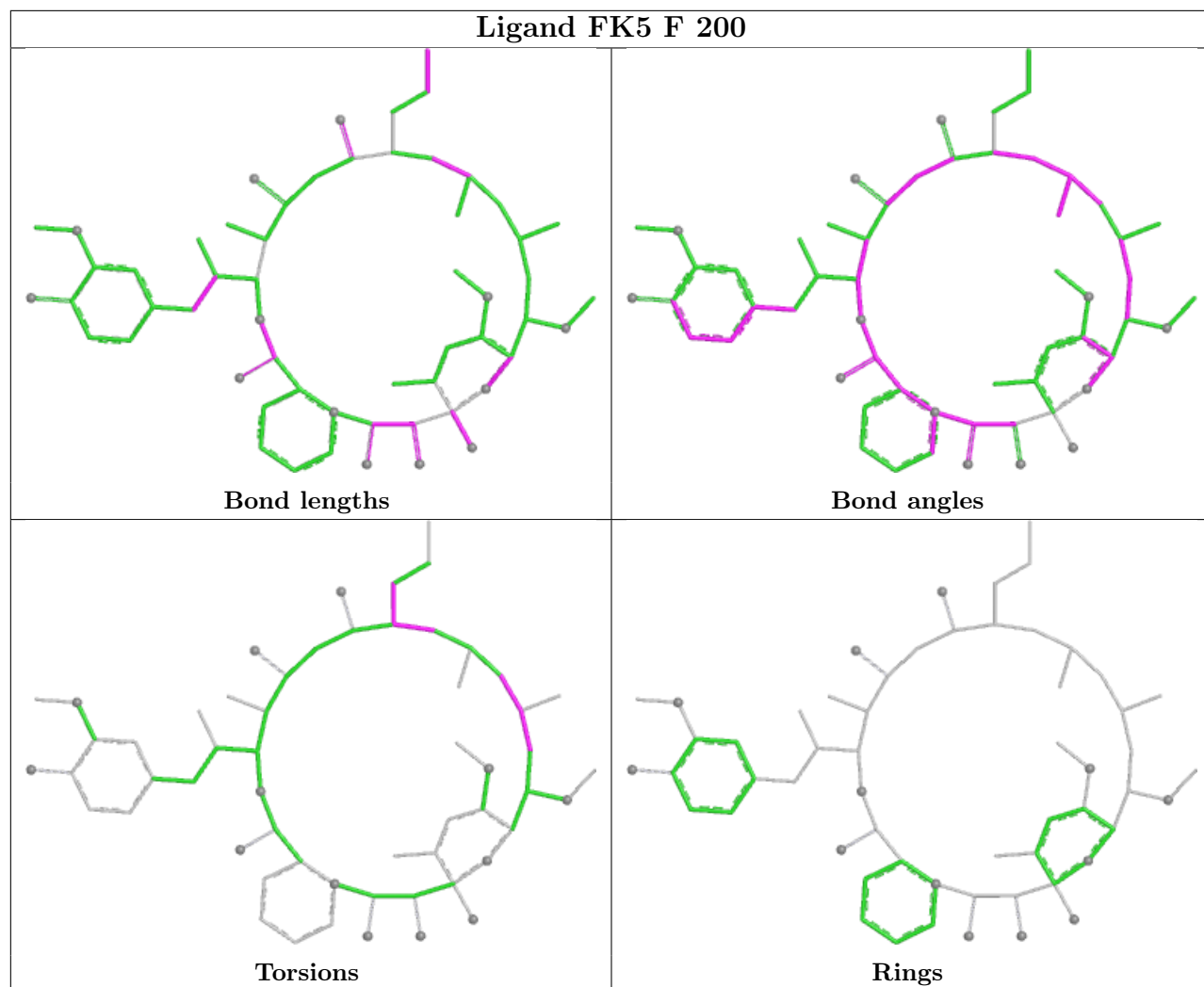
There are no ring outliers.

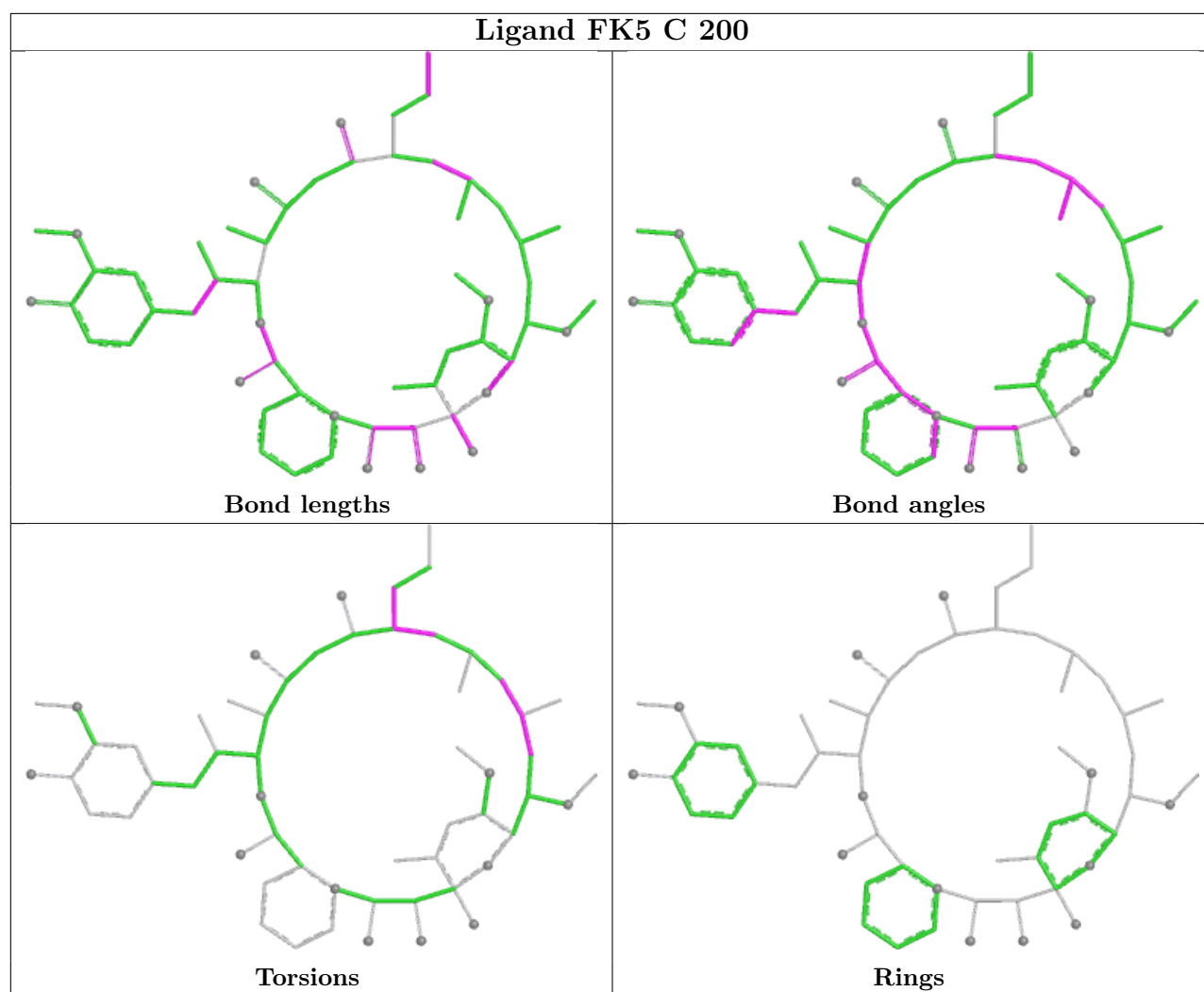
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	F	200	FK5	1	0
8	C	200	FK5	1	0

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

Ligand FK5 F 200





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	372/390 (95%)	-0.14	2 (0%) 87 76	20, 34, 55, 77	1 (0%)
1	D	373/390 (95%)	-0.21	7 (1%) 66 48	19, 34, 54, 80	1 (0%)
2	B	174/175 (99%)	0.02	0 100 100	24, 50, 73, 97	1 (0%)
2	E	174/175 (99%)	0.14	3 (1%) 69 50	22, 48, 79, 94	1 (0%)
3	C	111/122 (90%)	-0.16	2 (1%) 67 49	29, 43, 62, 72	0
3	F	111/122 (90%)	-0.16	1 (0%) 81 65	22, 38, 54, 64	0
All	All	1315/1374 (95%)	-0.11	15 (1%) 78 60	19, 37, 66, 97	4 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	401	CYS	4.1
1	D	282	HIS	2.8
3	F	89	PRO	2.8
1	D	24	SER	2.7
1	A	323[A]	LYS	2.6
1	D	357	ASN	2.6
1	D	345	TYR	2.4
3	C	89	PRO	2.4
2	E	42	ASP	2.4
1	D	401	CYS	2.3
2	E	68	ASP	2.2
1	D	283	VAL	2.2
3	C	42	ASP	2.1
1	D	346	SER	2.0
2	E	35	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

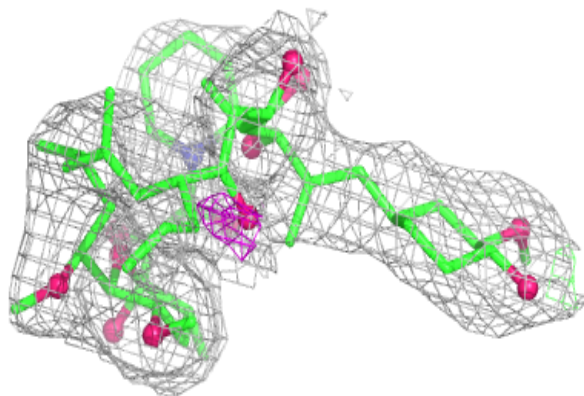
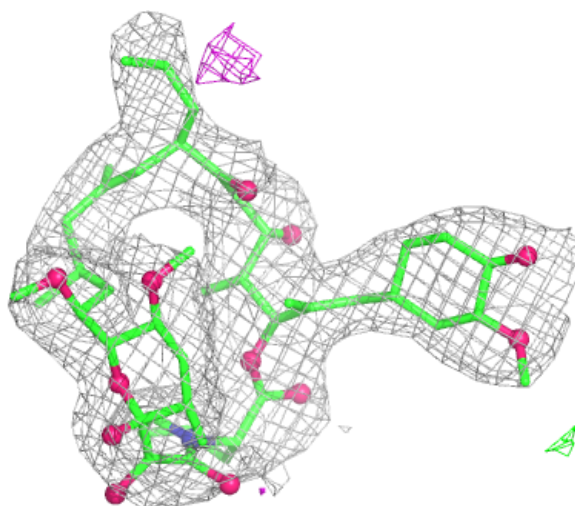
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	A	504	5/5	0.61	0.20	72,84,88,109	0
4	SO4	A	501	5/5	0.96	0.08	35,41,51,59	0
4	SO4	D	500	5/5	0.96	0.13	42,43,54,55	0
8	FK5	F	200	57/57	0.96	0.09	16,25,35,41	0
8	FK5	C	200	57/57	0.97	0.08	18,28,35,37	0
7	CA	B	300	1/1	0.97	0.06	67,67,67,67	0
5	FE	D	501	1/1	0.98	0.06	72,72,72,72	0
7	CA	E	300	1/1	0.98	0.04	81,81,81,81	0
7	CA	B	301	1/1	0.99	0.04	49,49,49,49	0
7	CA	B	302	1/1	0.99	0.04	38,38,38,38	0
7	CA	B	303	1/1	0.99	0.03	40,40,40,40	0
6	ZN	A	503	1/1	0.99	0.03	50,50,50,50	0
7	CA	E	301	1/1	0.99	0.05	54,54,54,54	0
7	CA	E	302	1/1	0.99	0.03	29,29,29,29	0
7	CA	E	303	1/1	0.99	0.02	38,38,38,38	0
6	ZN	D	502	1/1	0.99	0.03	45,45,45,45	0
5	FE	A	502	1/1	0.99	0.03	64,64,64,64	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.

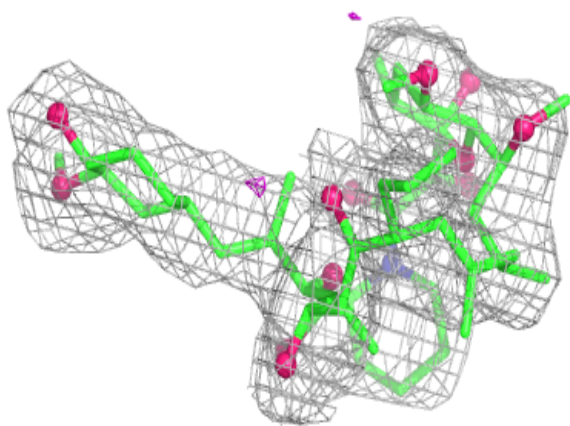
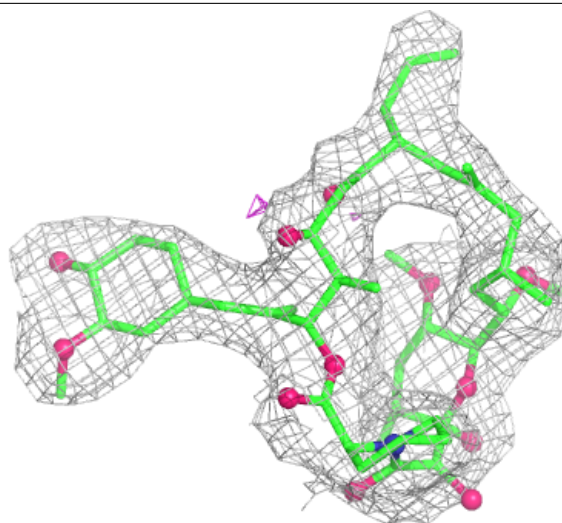
Electron density around FK5 F 200:

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



Electron density around FK5 C 200:

$2mF_o-DF_c$ (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.