



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:18 AM UTC

PDB ID : 3X00 / pdb_00003x00
Title : Crystal structure of the core streptavidin mutant V212 (Y22S/N23D/S27D/S45N/Y83S/R84K/E101D/R103K/E116N) complexed with bis iminobiotin long tail (Bis-IMNtail) at 1.3 Å resolution
Authors : Kawato, T.; Mizohata, E.; Shimizu, Y.; Meshizuka, T.; Yamamoto, T.; Takasu, N.; Matsuoka, M.; Matsumura, H.; Kodama, T.; Kanai, M.; Doi, H.; Inoue, T.; Sugiyama, A.
Deposited on : 2014-10-09
Resolution : 1.30 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)

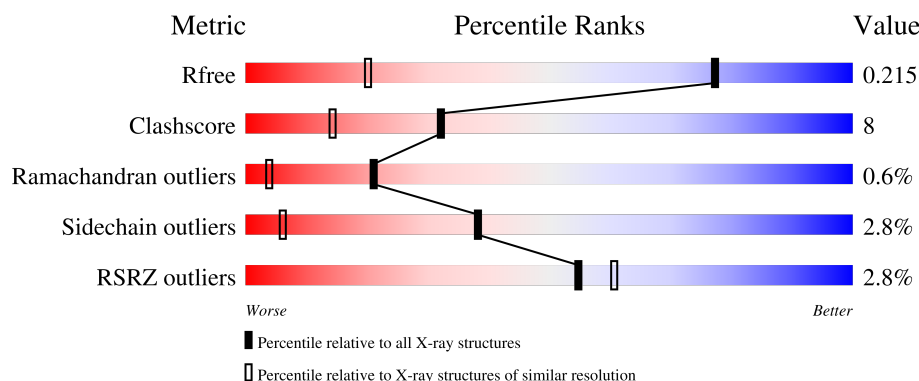
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1553 (1.30-1.30)
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)

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	147	% 70% 13% • 16%
1	B	147	2% 70% 13% •• 16%
1	C	147	3% 73% 12% 16%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	D	147	3% 71% 12% •• 16%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4405 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 Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	124	Total	C	N	O	0	12	0
			968	612	159	197			
1	B	124	Total	C	N	O	0	14	0
			975	617	159	199			
1	C	124	Total	C	N	O	0	10	0
			959	603	159	197			
1	D	124	Total	C	N	O	0	10	0
			961	605	160	196			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P22629
A	0	ALA	-	expression tag	UNP P22629
A	1	SER	-	expression tag	UNP P22629
A	2	MET	-	expression tag	UNP P22629
A	3	THR	-	expression tag	UNP P22629
A	4	GLY	-	expression tag	UNP P22629
A	5	GLY	-	expression tag	UNP P22629
A	6	GLN	-	expression tag	UNP P22629
A	7	GLN	-	expression tag	UNP P22629
A	8	MET	-	expression tag	UNP P22629
A	9	GLY	-	expression tag	UNP P22629
A	10	ARG	-	expression tag	UNP P22629
A	11	GLY	-	expression tag	UNP P22629
A	12	SER	-	expression tag	UNP P22629
A	22	SER	TYR	engineered mutation	UNP P22629
A	23	ASP	ASN	engineered mutation	UNP P22629
A	27	ASP	SER	engineered mutation	UNP P22629
A	45	ASN	SER	engineered mutation	UNP P22629
A	83	SER	TYR	engineered mutation	UNP P22629
A	84	LYS	ARG	engineered mutation	UNP P22629
A	101	ASP	GLU	engineered mutation	UNP P22629

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Chain	Residue	Modelled	Actual	Comment	Reference
A	103	LYS	ARG	engineered mutation	UNP P22629
A	116	ASN	GLU	engineered mutation	UNP P22629
A	140	HIS	-	expression tag	UNP P22629
A	141	HIS	-	expression tag	UNP P22629
A	142	HIS	-	expression tag	UNP P22629
A	143	HIS	-	expression tag	UNP P22629
A	144	HIS	-	expression tag	UNP P22629
A	145	HIS	-	expression tag	UNP P22629
B	-1	MET	-	expression tag	UNP P22629
B	0	ALA	-	expression tag	UNP P22629
B	1	SER	-	expression tag	UNP P22629
B	2	MET	-	expression tag	UNP P22629
B	3	THR	-	expression tag	UNP P22629
B	4	GLY	-	expression tag	UNP P22629
B	5	GLY	-	expression tag	UNP P22629
B	6	GLN	-	expression tag	UNP P22629
B	7	GLN	-	expression tag	UNP P22629
B	8	MET	-	expression tag	UNP P22629
B	9	GLY	-	expression tag	UNP P22629
B	10	ARG	-	expression tag	UNP P22629
B	11	GLY	-	expression tag	UNP P22629
B	12	SER	-	expression tag	UNP P22629
B	22	SER	TYR	engineered mutation	UNP P22629
B	23	ASP	ASN	engineered mutation	UNP P22629
B	27	ASP	SER	engineered mutation	UNP P22629
B	45	ASN	SER	engineered mutation	UNP P22629
B	83	SER	TYR	engineered mutation	UNP P22629
B	84	LYS	ARG	engineered mutation	UNP P22629
B	101	ASP	GLU	engineered mutation	UNP P22629
B	103	LYS	ARG	engineered mutation	UNP P22629
B	116	ASN	GLU	engineered mutation	UNP P22629
B	140	HIS	-	expression tag	UNP P22629
B	141	HIS	-	expression tag	UNP P22629
B	142	HIS	-	expression tag	UNP P22629
B	143	HIS	-	expression tag	UNP P22629
B	144	HIS	-	expression tag	UNP P22629
B	145	HIS	-	expression tag	UNP P22629
C	-1	MET	-	expression tag	UNP P22629
C	0	ALA	-	expression tag	UNP P22629
C	1	SER	-	expression tag	UNP P22629
C	2	MET	-	expression tag	UNP P22629
C	3	THR	-	expression tag	UNP P22629

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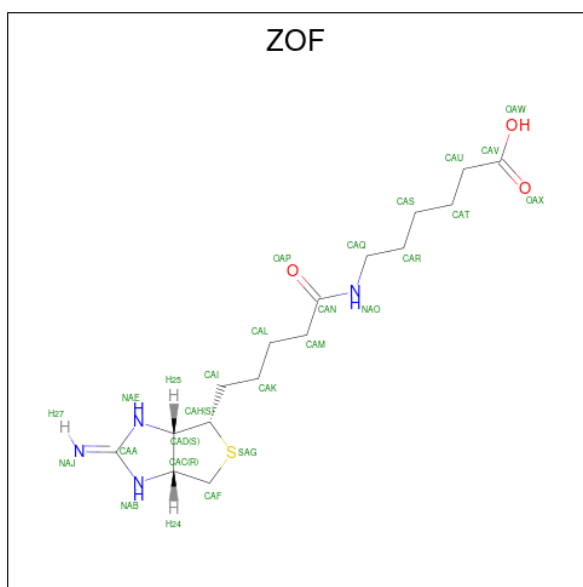
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C	4	GLY	-	expression tag	UNP P22629
C	5	GLY	-	expression tag	UNP P22629
C	6	GLN	-	expression tag	UNP P22629
C	7	GLN	-	expression tag	UNP P22629
C	8	MET	-	expression tag	UNP P22629
C	9	GLY	-	expression tag	UNP P22629
C	10	ARG	-	expression tag	UNP P22629
C	11	GLY	-	expression tag	UNP P22629
C	12	SER	-	expression tag	UNP P22629
C	22	SER	TYR	engineered mutation	UNP P22629
C	23	ASP	ASN	engineered mutation	UNP P22629
C	27	ASP	SER	engineered mutation	UNP P22629
C	45	ASN	SER	engineered mutation	UNP P22629
C	83	SER	TYR	engineered mutation	UNP P22629
C	84	LYS	ARG	engineered mutation	UNP P22629
C	101	ASP	GLU	engineered mutation	UNP P22629
C	103	LYS	ARG	engineered mutation	UNP P22629
C	116	ASN	GLU	engineered mutation	UNP P22629
C	140	HIS	-	expression tag	UNP P22629
C	141	HIS	-	expression tag	UNP P22629
C	142	HIS	-	expression tag	UNP P22629
C	143	HIS	-	expression tag	UNP P22629
C	144	HIS	-	expression tag	UNP P22629
C	145	HIS	-	expression tag	UNP P22629
D	-1	MET	-	expression tag	UNP P22629
D	0	ALA	-	expression tag	UNP P22629
D	1	SER	-	expression tag	UNP P22629
D	2	MET	-	expression tag	UNP P22629
D	3	THR	-	expression tag	UNP P22629
D	4	GLY	-	expression tag	UNP P22629
D	5	GLY	-	expression tag	UNP P22629
D	6	GLN	-	expression tag	UNP P22629
D	7	GLN	-	expression tag	UNP P22629
D	8	MET	-	expression tag	UNP P22629
D	9	GLY	-	expression tag	UNP P22629
D	10	ARG	-	expression tag	UNP P22629
D	11	GLY	-	expression tag	UNP P22629
D	12	SER	-	expression tag	UNP P22629
D	22	SER	TYR	engineered mutation	UNP P22629
D	23	ASP	ASN	engineered mutation	UNP P22629
D	27	ASP	SER	engineered mutation	UNP P22629
D	45	ASN	SER	engineered mutation	UNP P22629

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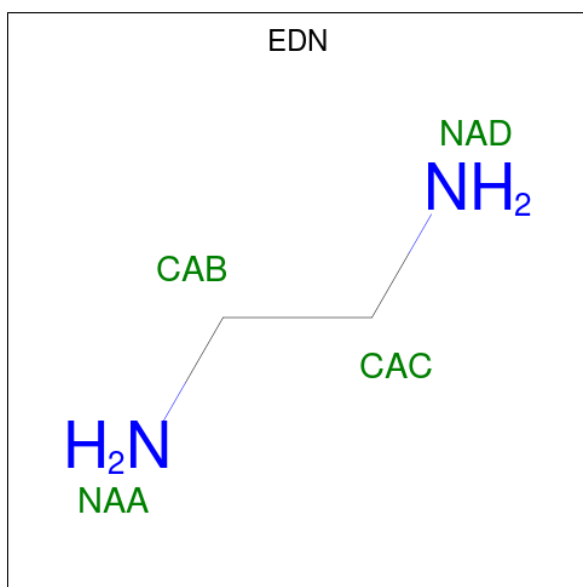
Chain	Residue	Modelled	Actual	Comment	Reference
D	83	SER	TYR	engineered mutation	UNP P22629
D	84	LYS	ARG	engineered mutation	UNP P22629
D	101	ASP	GLU	engineered mutation	UNP P22629
D	103	LYS	ARG	engineered mutation	UNP P22629
D	116	ASN	GLU	engineered mutation	UNP P22629
D	140	HIS	-	expression tag	UNP P22629
D	141	HIS	-	expression tag	UNP P22629
D	142	HIS	-	expression tag	UNP P22629
D	143	HIS	-	expression tag	UNP P22629
D	144	HIS	-	expression tag	UNP P22629
D	145	HIS	-	expression tag	UNP P22629

- Molecule 2 is 6-({5-[(2E,3aS,4S,6aR)-2-iminohexahydro-1H-thieno[3,4-d]imidazol-4-yl]penta noyl}amino)hexanoic acid (CCD ID: ZOF) (formula: C₁₆H₂₈N₄O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			23	16	4	2	1		
2	B	1	Total	C	N	O	S	0	0
			23	16	4	2	1		
2	C	1	Total	C	N	O	S	0	0
			23	16	4	2	1		
2	D	1	Total	C	N	O	S	0	0
			23	16	4	2	1		

- Molecule 3 is ETHANE-1,2-DIAMINE (CCD ID: EDN) (formula: C₂H₈N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	N	0	0
			4	2	2		
3	D	1	Total	C	N	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total	O	0	0
			128	128		
4	B	122	Total	O	0	0
			122	122		
4	C	100	Total	O	0	0
			100	100		
4	D	92	Total	O	0	0
			92	92		

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	77.35Å 77.38Å 174.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.30 50.00 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-1.30) 99.5 (50.00-1.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.48 (at 1.30Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.146 , 0.188 0.180 , 0.215	Depositor DCC
R_{free} test set	6384 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.6	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.477 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	4405	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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: ZOF, EDN

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	1.33	1/1026 (0.1%)	1.13	2/1402 (0.1%)
1	B	1.41	6/1039 (0.6%)	1.14	2/1420 (0.1%)
1	C	1.23	4/1011 (0.4%)	1.11	2/1383 (0.1%)
1	D	1.21	2/1013 (0.2%)	1.09	2/1383 (0.1%)
All	All	1.29	13/4089 (0.3%)	1.12	8/5588 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	50	ALA	C-O	12.07	1.39	1.24
1	B	13	ALA	CA-CB	8.49	1.66	1.53
1	A	13	ALA	CA-CB	7.96	1.65	1.53
1	B	50	ALA	N-CA	7.91	1.56	1.46
1	C	30	ILE	N-CA	-7.10	1.37	1.46
1	B	66	THR	CA-CB	6.12	1.61	1.53
1	C	76	THR	N-CA	-5.36	1.39	1.46
1	C	39	LEU	C-O	5.30	1.30	1.24
1	B	30	ILE	N-CA	-5.26	1.39	1.46
1	B	13	ALA	N-CA	5.24	1.52	1.46
1	C	101	ASP	CA-C	5.22	1.58	1.53
1	D	114	THR	C-O	-5.11	1.17	1.23
1	D	39	LEU	C-O	5.07	1.30	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	107	GLN	CA-CB-CG	-5.87	102.36	114.10
1	C	40	THR	OG1-CB-CG2	-5.68	97.95	109.30
1	A	107	GLN	CA-CB-CG	-5.65	102.80	114.10
1	D	107	GLN	CA-CB-CG	-5.65	102.80	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	49	ASN	N-CA-C	5.33	122.15	110.80
1	B	107	GLN	CA-CB-CG	-5.30	103.50	114.10
1	A	49	ASN	N-CA-C	5.17	117.81	110.10
1	D	49	ASN	N-CA-C	5.09	121.64	110.80

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	968	0	944	22	0
1	B	975	0	956	19	0
1	C	959	0	920	10	0
1	D	961	0	930	14	0
2	A	23	0	27	0	0
2	B	23	0	27	0	0
2	C	23	0	27	0	0
2	D	23	0	27	0	0
3	B	4	0	5	0	0
3	D	4	0	5	0	0
4	A	128	0	0	2	0
4	B	122	0	0	4	0
4	C	100	0	0	0	0
4	D	92	0	0	2	0
All	All	4405	0	3868	63	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 (63) 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:A:43[B]:TYR:CE2	1:A:45[B]:ASN:OD1	1.73	1.39
1:A:43[B]:TYR:CZ	1:A:45[B]:ASN:OD1	1.91	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43[B]:TYR:OH	1:C:45[B]:ASN:OD1	1.53	1.22
1:D:43[B]:TYR:OH	1:D:45[B]:ASN:OD1	1.70	1.09
1:A:43[B]:TYR:OH	1:A:45[B]:ASN:OD1	1.86	0.94
1:B:13:ALA:HA	4:B:393:HOH:O	1.70	0.90
1:A:43[B]:TYR:HE2	1:A:45[B]:ASN:OD1	1.40	0.89
1:C:43[B]:TYR:CZ	1:C:45[B]:ASN:OD1	2.26	0.88
1:C:114:THR:H	1:D:95:GLN:HE22	1.18	0.87
1:A:45[B]:ASN:ND2	1:A:52[B]:SER:HB3	2.00	0.76
1:D:45[B]:ASN:OD1	4:D:392:HOH:O	2.09	0.71
1:A:30:ILE:HB	1:A:42[B]:THR:HG22	1.78	0.66
1:C:43[B]:TYR:CE2	1:C:45[B]:ASN:OD1	2.51	0.64
1:A:49:ASN:HB3	1:A:52[A]:SER:HB3	1.81	0.61
1:B:29[B]:PHE:CZ	1:B:43[B]:TYR:HD1	2.19	0.60
1:D:29[A]:PHE:CE1	1:D:56:LEU:HD21	2.38	0.59
1:B:45[B]:ASN:ND2	1:B:52[B]:SER:HB3	2.18	0.58
1:B:49:ASN:HD21	1:B:51:GLU:HB2	1.67	0.58
1:D:43[B]:TYR:CZ	1:D:45[B]:ASN:OD1	2.58	0.56
1:B:49:ASN:HB3	1:B:52[A]:SER:HB3	1.89	0.54
1:C:29[A]:PHE:CE1	1:C:56:LEU:HD21	2.42	0.54
1:A:29[B]:PHE:CD2	1:A:130:PHE:HE2	2.25	0.53
1:A:103[A]:LYS:NZ	1:A:131:THR:HG22	2.24	0.52
1:C:29[A]:PHE:CD1	1:C:56:LEU:HD21	2.45	0.51
1:B:29[B]:PHE:CD2	1:B:130:PHE:HE2	2.28	0.51
1:C:29[B]:PHE:CD2	1:C:130:PHE:HE2	2.29	0.50
1:D:29[B]:PHE:CD2	1:D:130:PHE:HE2	2.28	0.50
1:A:45[B]:ASN:ND2	4:A:425:HOH:O	2.44	0.50
1:A:44[B]:GLU:OE1	1:A:48:GLY:HA2	2.15	0.47
1:D:29[A]:PHE:CD1	1:D:56:LEU:HD21	2.50	0.47
1:B:49:ASN:ND2	1:B:51:GLU:HB2	2.30	0.47
1:A:103[A]:LYS:CE	1:A:131:THR:HG22	2.44	0.47
1:B:42[B]:THR:HG22	4:B:415:HOH:O	2.15	0.47
1:A:57[B]:THR:HG21	4:B:320:HOH:O	2.15	0.45
1:B:28:THR:HB	1:B:44[B]:GLU:HG3	1.99	0.44
1:A:43[B]:TYR:OH	1:A:45[B]:ASN:CG	2.58	0.44
1:A:51:GLU:HG2	1:A:83:SER:OG	2.17	0.44
1:D:105:ASN:OD1	1:D:129[A]:THR:HG23	2.18	0.44
1:B:103[B]:LYS:CE	1:B:105:ASN:OD1	2.65	0.44
1:C:57[B]:THR:HG21	4:D:322:HOH:O	2.18	0.43
1:D:49:ASN:OD1	1:D:51:GLU:HG2	2.18	0.43
1:B:13:ALA:HB3	4:B:406:HOH:O	2.18	0.43
1:A:23:ASP:HB3	1:A:130:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45[B]:ASN:HD22	1:A:52[B]:SER:HB3	1.76	0.43
1:B:105:ASN:OD1	1:B:129[B]:THR:HG22	2.19	0.43
1:B:45[B]:ASN:HD22	1:B:52[B]:SER:HB3	1.83	0.42
1:A:13:ALA:HB3	4:A:380:HOH:O	2.19	0.42
1:B:103[B]:LYS:HE2	1:B:105:ASN:OD1	2.19	0.42
1:D:29[A]:PHE:HE1	1:D:56:LEU:HD21	1.82	0.42
1:D:70:GLY:HA3	1:D:95:GLN:HE21	1.84	0.42
1:B:44[A]:GLU:OE1	1:B:48:GLY:HA2	2.20	0.41
1:D:29[A]:PHE:CE1	1:D:56:LEU:CD2	3.03	0.41
1:C:91:THR:HB	1:D:91:THR:HB	2.03	0.40
1:A:29[B]:PHE:CZ	1:A:43[B]:TYR:HD1	2.39	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	134/147 (91%)	130 (97%)	4 (3%)	0	100	100
1	B	136/147 (92%)	132 (97%)	3 (2%)	1 (1%)	18	2
1	C	132/147 (90%)	130 (98%)	1 (1%)	1 (1%)	16	2
1	D	132/147 (90%)	129 (98%)	2 (2%)	1 (1%)	16	2
All	All	534/588 (91%)	521 (98%)	10 (2%)	3 (1%)	21	4

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	49	ASN
1	D	49	ASN
1	B	49	ASN

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	102/107 (95%)	100 (98%)	2 (2%)	48	12
1	B	104/107 (97%)	103 (99%)	1 (1%)	68	37
1	C	100/107 (94%)	98 (98%)	2 (2%)	48	12
1	D	100/107 (94%)	94 (94%)	6 (6%)	17	1
All	All	406/428 (95%)	395 (97%)	11 (3%)	38	7

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	VAL
1	A	133	VAL
1	B	12	SER
1	C	12	SER
1	C	134	LYS
1	D	12	SER
1	D	40[A]	THR
1	D	40[B]	THR
1	D	56	LEU
1	D	73	LEU
1	D	134	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	B	49	ASN
1	D	95	GLN
1	D	127	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EDN	B	202	2	3,3,3	0.24	0	2,2,2	0.40	0
3	EDN	D	202	2	3,3,3	0.32	0	2,2,2	0.41	0
2	ZOF	B	201	3	22,24,25	1.29	2 (9%)	25,30,32	2.32	8 (32%)
2	ZOF	C	201	3	22,24,25	2.13	5 (22%)	25,30,32	2.84	13 (52%)
2	ZOF	A	201	3	22,24,25	1.25	2 (9%)	25,30,32	2.26	8 (32%)
2	ZOF	D	201	3	22,24,25	2.26	5 (22%)	25,30,32	2.67	9 (36%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDN	B	202	2	-	0/1/1/1	-
3	EDN	D	202	2	-	0/1/1/1	-
2	ZOF	B	201	3	-	1/15/36/37	0/2/2/2
2	ZOF	C	201	3	-	1/15/36/37	0/2/2/2
2	ZOF	A	201	3	-	1/15/36/37	0/2/2/2
2	ZOF	D	201	3	-	1/15/36/37	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	ZOF	CAD-NAE	-6.24	1.34	1.45
2	D	201	ZOF	CAA-NAE	5.55	1.43	1.35
2	C	201	ZOF	CAA-NAE	5.36	1.43	1.35
2	C	201	ZOF	CAD-NAE	-4.50	1.37	1.45
2	C	201	ZOF	CAA-NAB	4.35	1.41	1.35
2	A	201	ZOF	CAA-NAE	3.40	1.40	1.35
2	B	201	ZOF	CAA-NAE	3.34	1.40	1.35
2	D	201	ZOF	CAA-NAB	3.21	1.40	1.35
2	D	201	ZOF	CAQ-NAO	-3.15	1.39	1.46
2	A	201	ZOF	CAD-NAE	-2.56	1.41	1.45
2	C	201	ZOF	CAQ-NAO	-2.47	1.40	1.46
2	D	201	ZOF	CAC-CAD	-2.42	1.48	1.55
2	C	201	ZOF	CAC-CAD	-2.32	1.48	1.55
2	B	201	ZOF	OAP-CAN	2.22	1.27	1.23

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	201	ZOF	NAE-CAA-NAB	-8.22	100.85	109.21
2	D	201	ZOF	NAE-CAA-NAB	-7.54	101.55	109.21
2	B	201	ZOF	CAF-CAC-NAB	-6.43	104.90	113.18
2	D	201	ZOF	CAC-CAD-NAE	5.80	109.22	102.68
2	A	201	ZOF	CAF-CAC-NAB	-5.71	105.83	113.18
2	B	201	ZOF	CAC-CAF-SAG	5.40	113.50	106.06
2	C	201	ZOF	CAH-CAD-CAC	5.22	115.28	108.89
2	A	201	ZOF	CAC-CAF-SAG	5.04	113.00	106.06
2	C	201	ZOF	OAP-CAN-CAM	-4.12	114.55	122.02
2	C	201	ZOF	CAF-CAC-NAB	-3.86	108.21	113.18
2	B	201	ZOF	NAE-CAA-NAB	-3.76	105.39	109.21
2	D	201	ZOF	CAF-CAC-NAB	-3.73	108.38	113.18
2	D	201	ZOF	CAR-CAQ-NAO	-3.59	102.12	112.20
2	A	201	ZOF	CAH-CAD-NAE	-3.48	109.65	113.34
2	A	201	ZOF	CAC-CAD-NAE	3.46	106.58	102.68
2	D	201	ZOF	CAH-CAD-CAC	3.36	113.01	108.89
2	C	201	ZOF	CAS-CAT-CAU	-3.35	97.76	113.86
2	C	201	ZOF	OAP-CAN-NAO	3.30	129.50	123.03
2	C	201	ZOF	CAC-CAD-NAE	3.23	106.32	102.68
2	D	201	ZOF	OAP-CAN-CAM	-3.16	116.30	122.02
2	D	201	ZOF	CAS-CAT-CAU	-3.16	98.69	113.86
2	C	201	ZOF	CAF-CAC-CAD	-2.90	104.47	109.06
2	B	201	ZOF	CAD-CAC-NAB	-2.89	99.22	102.43
2	B	201	ZOF	OAP-CAN-CAM	-2.85	116.86	122.02
2	C	201	ZOF	CAD-CAH-SAG	-2.84	101.80	105.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	201	ZOF	CAC-CAD-NAE	2.79	105.83	102.68
2	A	201	ZOF	CAQ-NAO-CAN	2.79	128.02	122.82
2	A	201	ZOF	NAE-CAA-NAB	-2.79	106.37	109.21
2	B	201	ZOF	CAH-CAD-NAE	-2.66	110.53	113.34
2	C	201	ZOF	CAR-CAQ-NAO	-2.61	104.88	112.20
2	B	201	ZOF	CAF-CAC-CAD	-2.55	105.02	109.06
2	A	201	ZOF	OAP-CAN-CAM	-2.52	117.46	122.02
2	A	201	ZOF	CAD-CAC-NAB	-2.45	99.71	102.43
2	D	201	ZOF	CAS-CAR-CAQ	-2.35	102.72	113.56
2	D	201	ZOF	CAD-CAC-NAB	-2.20	99.98	102.43
2	C	201	ZOF	CAC-CAF-SAG	2.17	109.06	106.06
2	C	201	ZOF	CAS-CAR-CAQ	-2.06	104.05	113.56
2	C	201	ZOF	CAR-CAS-CAT	-2.05	104.02	114.37

There are no chirality outliers.

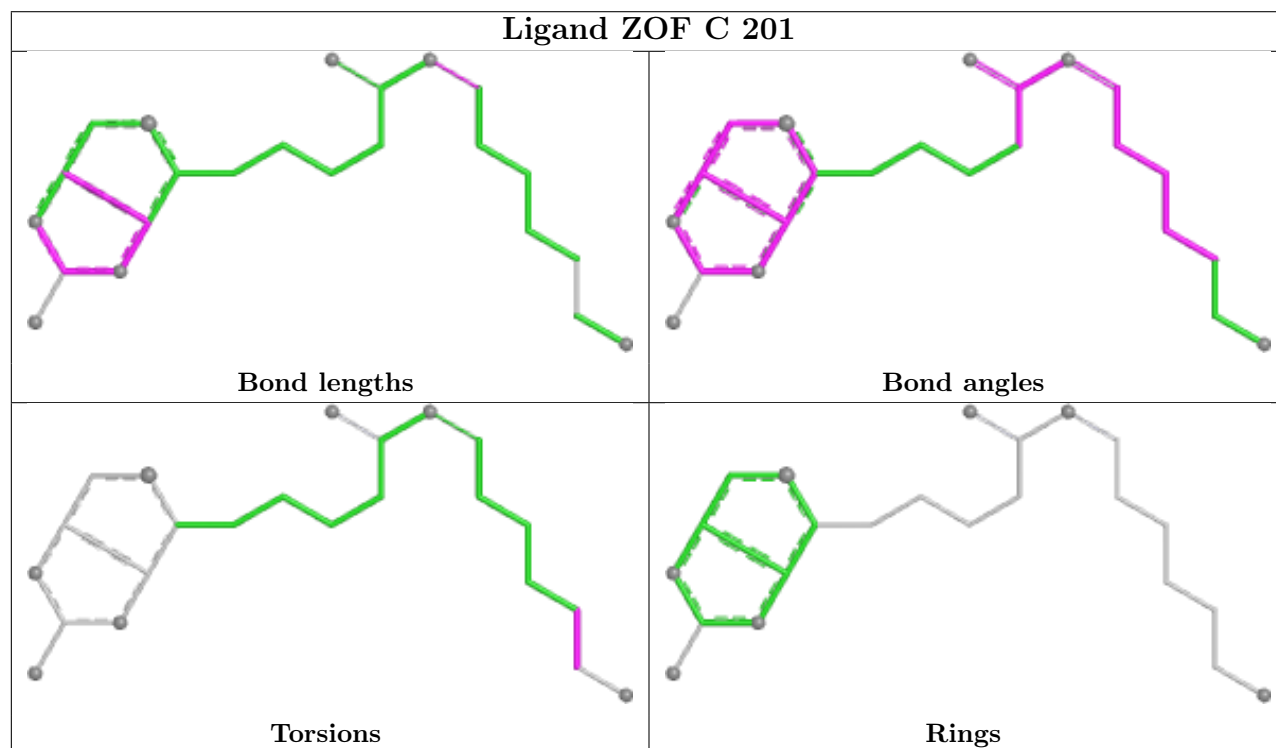
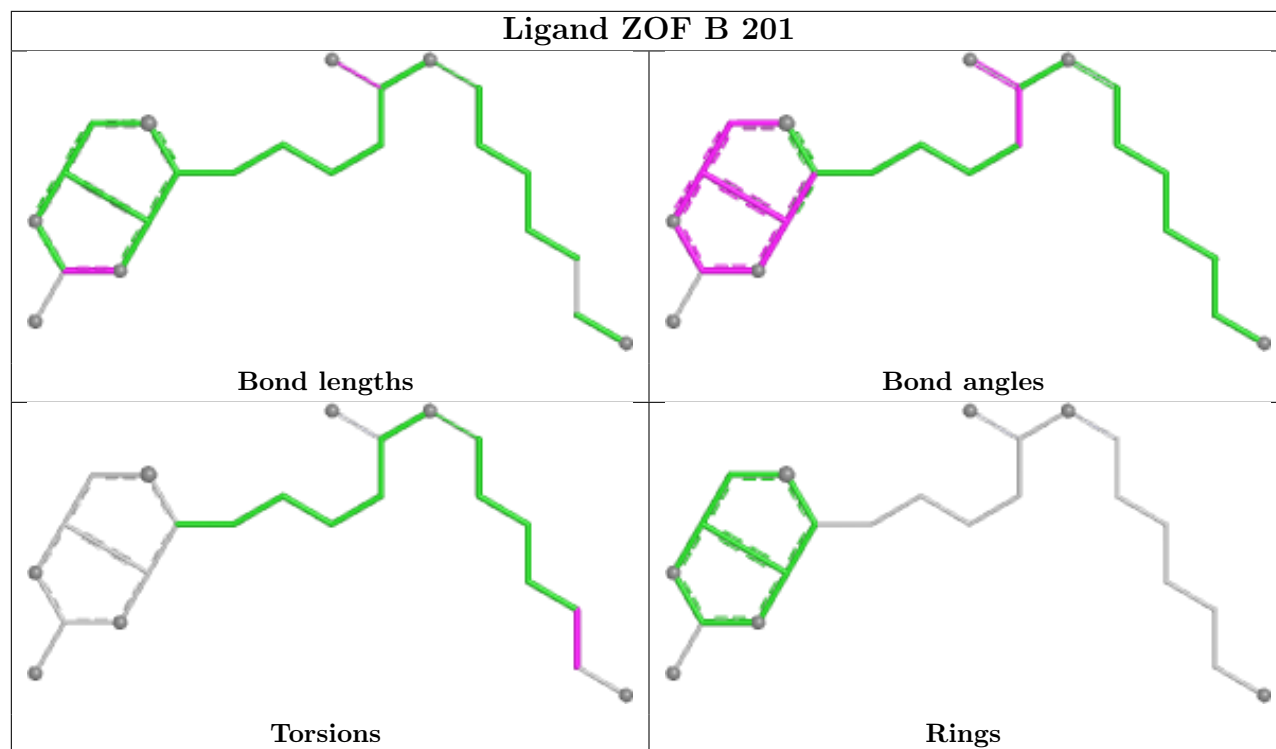
All (4) torsion outliers are listed below:

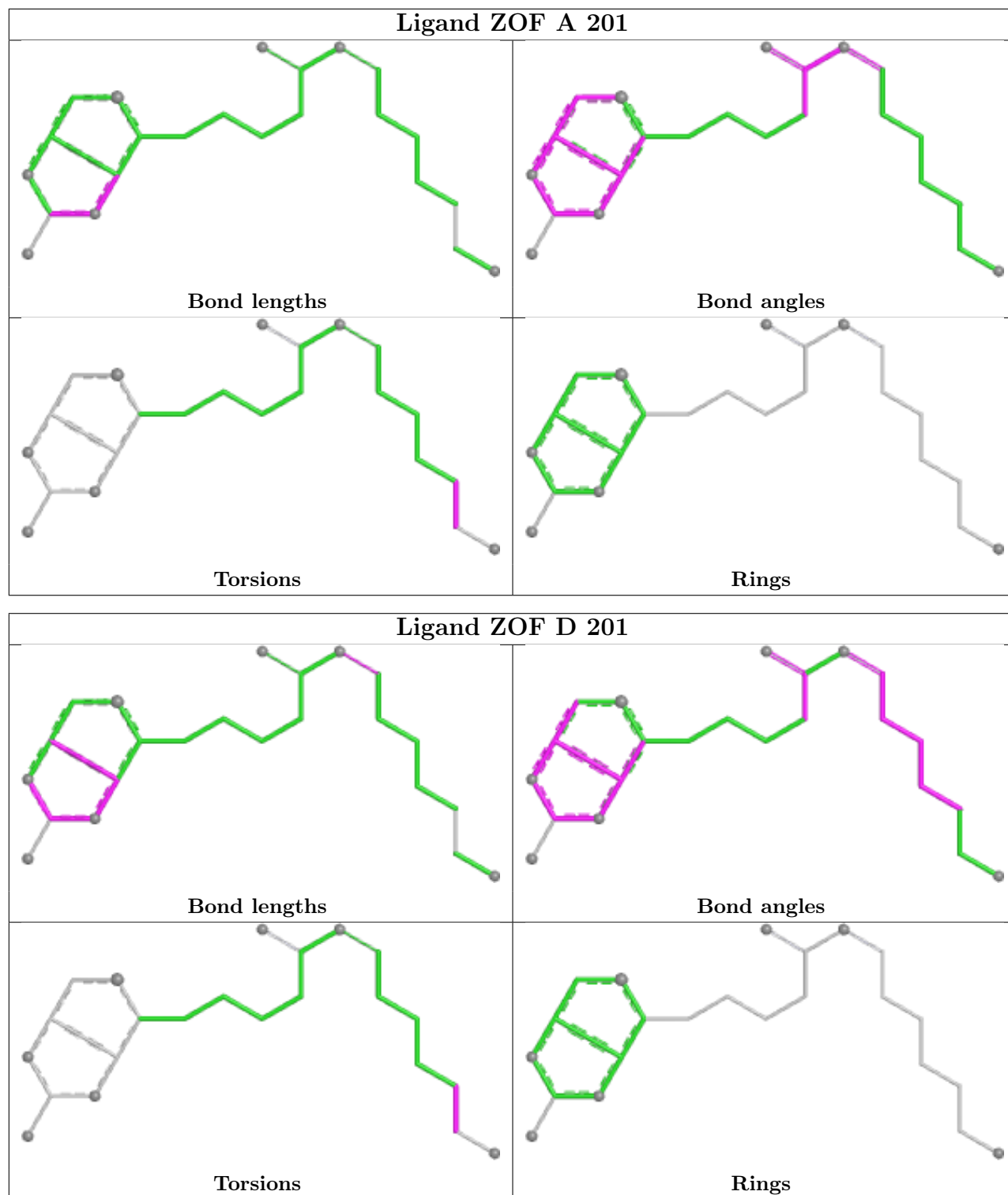
Mol	Chain	Res	Type	Atoms
2	A	201	ZOF	CAT-CAU-CAV-OAX
2	B	201	ZOF	CAT-CAU-CAV-OAX
2	C	201	ZOF	CAT-CAU-CAV-OAX
2	D	201	ZOF	CAT-CAU-CAV-OAX

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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	124/147 (84%)	-0.41	2 (1%) 70 74	6, 15, 53, 86	12 (9%)
1	B	124/147 (84%)	-0.33	3 (2%) 59 65	6, 14, 53, 85	14 (11%)
1	C	124/147 (84%)	-0.13	5 (4%) 42 48	8, 18, 54, 102	10 (8%)
1	D	124/147 (84%)	-0.28	4 (3%) 50 56	10, 19, 56, 91	10 (8%)
All	All	496/588 (84%)	-0.29	14 (2%) 55 61	6, 17, 59, 102	46 (9%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	47	VAL	4.2
1	B	47	VAL	3.7
1	A	47	VAL	3.6
1	C	46	ALA	3.4
1	D	47	VAL	3.2
1	B	11	GLY	3.1
1	C	35	ALA	3.0
1	C	48	GLY	2.9
1	B	133	VAL	2.7
1	D	45[A]	ASN	2.6
1	D	46	ALA	2.3
1	D	35	ALA	2.2
1	C	11	GLY	2.1
1	A	100	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

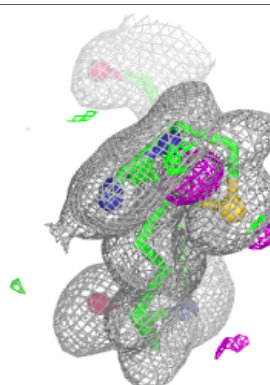
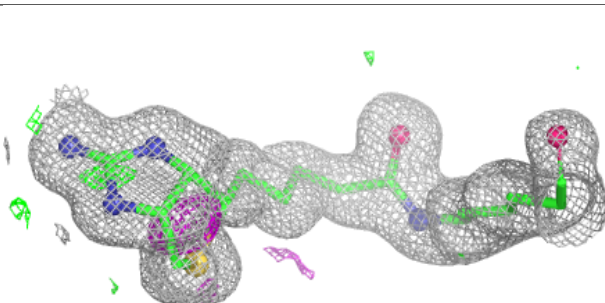
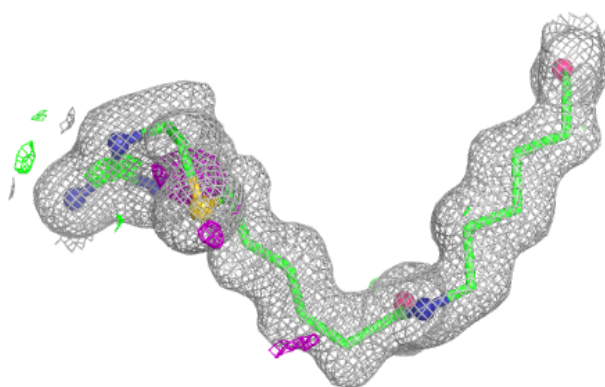
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZOF	A	201	23/24	0.99	0.04	15,19,27,31	0
2	ZOF	B	201	23/24	0.99	0.04	15,19,26,29	0
2	ZOF	C	201	23/24	0.99	0.04	19,24,32,35	0
2	ZOF	D	201	23/24	0.99	0.05	19,24,33,36	0
3	EDN	B	202	4/4	0.99	0.04	23,26,29,30	0
3	EDN	D	202	4/4	0.99	0.04	23,25,28,30	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.

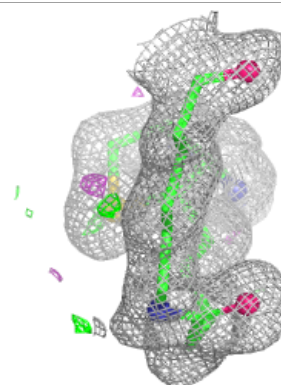
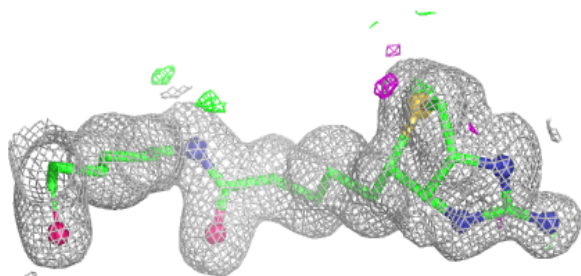
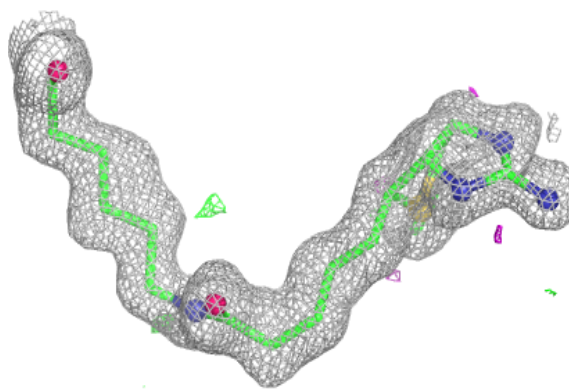
Electron density around ZOF A 201:

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

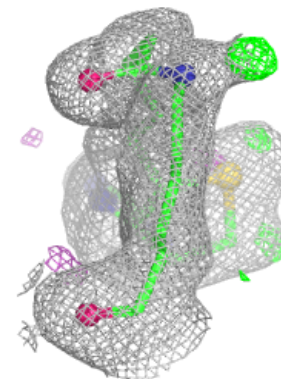
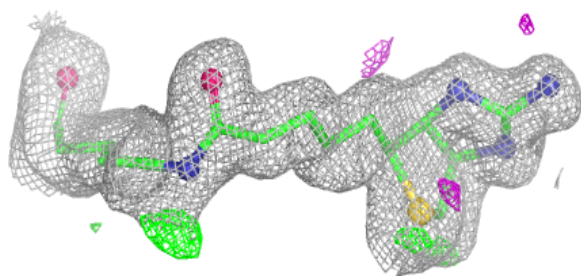
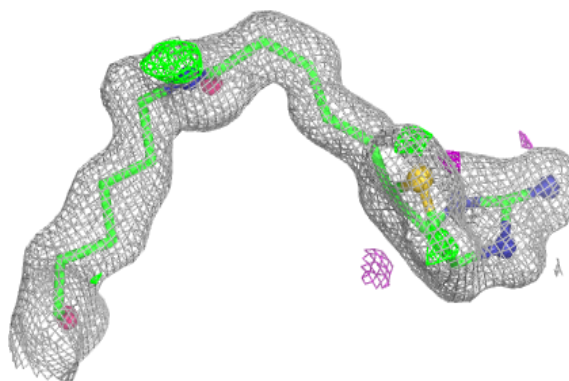


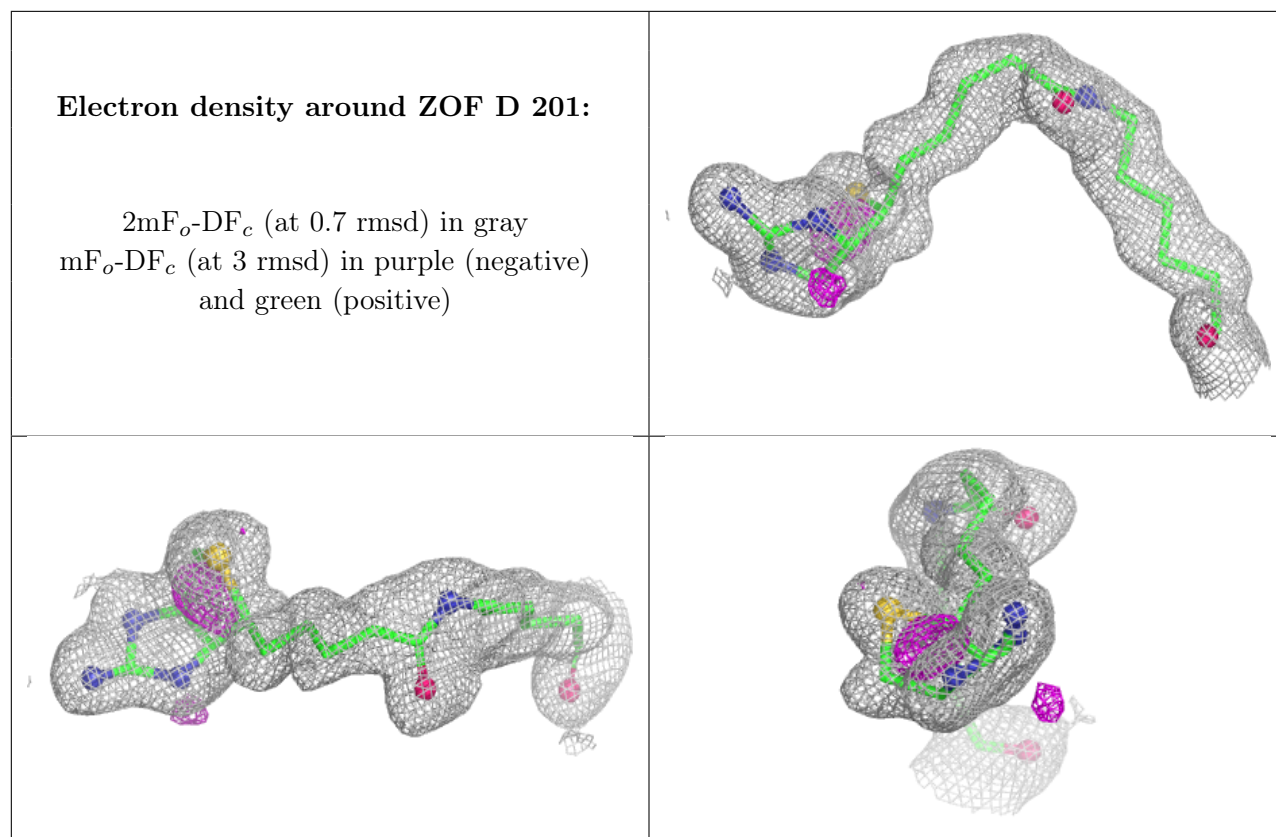
Electron density around ZOF B 201:

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

**Electron density around ZOF C 201:**

$2mF_o-DF_c$ (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.