



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 4, 2025 – 07:55 pm BST

PDB ID : 9I2U / pdb\_00009i2u  
Title : Alpha-Methylacyl-CoA racemase from Mycobacterium tuberculosis in complex with ibuprofenoyl-CoA  
Authors : Mojanaga, O.O.; Acharya, K.R.; Lloyd, M.D.  
Deposited on : 2025-01-22  
Resolution : 2.17 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](mailto: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>.

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

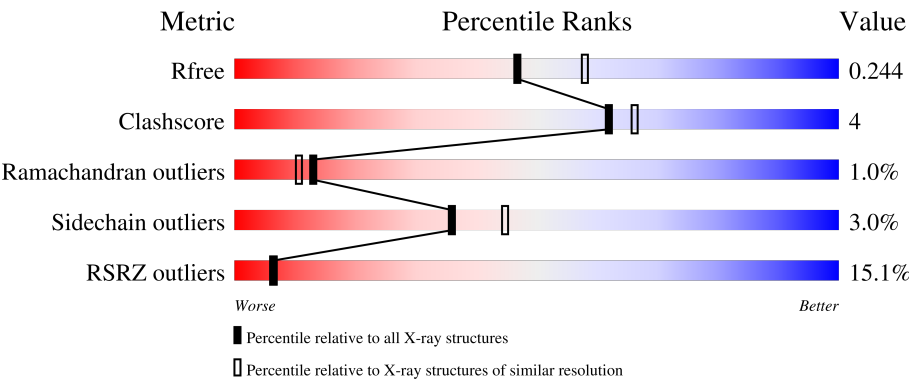
MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

# 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 2.17 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))
$R_{free}$	164625	8336 (2.20-2.16)
Clashscore	180529	9404 (2.20-2.16)
Ramachandran outliers	177936	9297 (2.20-2.16)
Sidechain outliers	177891	9297 (2.20-2.16)
RSRZ outliers	164620	8337 (2.20-2.16)

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  $\geq 3$ , 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	364	
1	B	364	
1	C	364	
1	D	364	
1	E	364	

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Mol	Chain	Length	Quality of chain
1	F	364	<div><div></div><div>16%</div><div>80%</div><div>15%</div><div></div><div></div></div>
1	G	364	<div><div></div><div>25%</div><div>81%</div><div>14%</div><div></div><div></div></div>
1	H	364	<div><div></div><div>21%</div><div>85%</div><div>11%</div><div></div><div></div></div>
1	I	364	<div><div></div><div>11%</div><div>85%</div><div>12%</div><div></div><div></div></div>
1	J	364	<div><div></div><div>8%</div><div>86%</div><div>11%</div><div></div><div></div></div>
1	K	364	<div><div></div><div>10%</div><div>85%</div><div>10%</div><div></div><div></div></div>
1	L	364	<div><div></div><div>17%</div><div>85%</div><div>13%</div><div></div><div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34453 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 Alpha-methylacyl-CoA racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	2	0
			2706	1698	484	508	16			
1	B	354	Total	C	N	O	S	0	3	0
			2692	1689	482	505	16			
1	C	357	Total	C	N	O	S	0	2	0
			2703	1695	484	508	16			
1	D	358	Total	C	N	O	S	0	2	0
			2715	1703	485	511	16			
1	E	355	Total	C	N	O	S	0	2	0
			2693	1690	482	505	16			
1	F	357	Total	C	N	O	S	0	1	0
			2703	1695	484	508	16			
1	G	357	Total	C	N	O	S	0	2	0
			2703	1695	484	508	16			
1	H	356	Total	C	N	O	S	0	2	0
			2698	1693	483	506	16			
1	I	358	Total	C	N	O	S	0	1	0
			2711	1701	485	509	16			
1	J	357	Total	C	N	O	S	0	2	0
			2709	1699	486	508	16			
1	K	355	Total	C	N	O	S	0	3	0
			2697	1691	483	507	16			
1	L	358	Total	C	N	O	S	0	2	0
			2715	1703	485	511	16			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	361	GLY	-	expression tag	UNP O06543
A	362	SER	-	expression tag	UNP O06543
A	363	GLY	-	expression tag	UNP O06543
A	364	CYS	-	expression tag	UNP O06543
B	361	GLY	-	expression tag	UNP O06543

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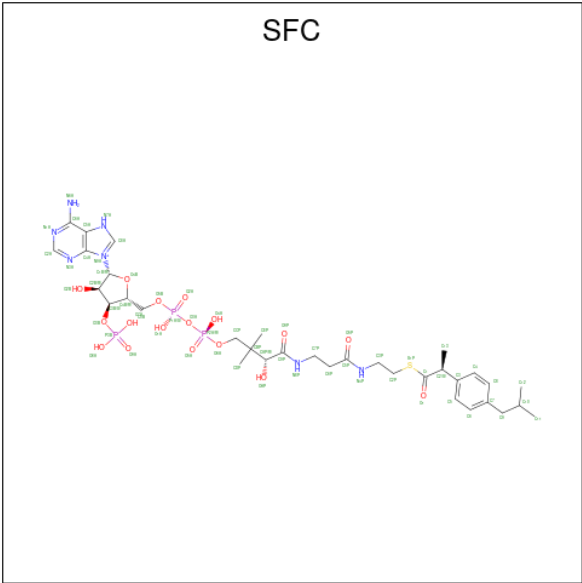
Chain	Residue	Modelled	Actual	Comment	Reference
B	362	SER	-	expression tag	UNP O06543
B	363	GLY	-	expression tag	UNP O06543
B	364	CYS	-	expression tag	UNP O06543
C	361	GLY	-	expression tag	UNP O06543
C	362	SER	-	expression tag	UNP O06543
C	363	GLY	-	expression tag	UNP O06543
C	364	CYS	-	expression tag	UNP O06543
D	361	GLY	-	expression tag	UNP O06543
D	362	SER	-	expression tag	UNP O06543
D	363	GLY	-	expression tag	UNP O06543
D	364	CYS	-	expression tag	UNP O06543
E	361	GLY	-	expression tag	UNP O06543
E	362	SER	-	expression tag	UNP O06543
E	363	GLY	-	expression tag	UNP O06543
E	364	CYS	-	expression tag	UNP O06543
F	361	GLY	-	expression tag	UNP O06543
F	362	SER	-	expression tag	UNP O06543
F	363	GLY	-	expression tag	UNP O06543
F	364	CYS	-	expression tag	UNP O06543
G	361	GLY	-	expression tag	UNP O06543
G	362	SER	-	expression tag	UNP O06543
G	363	GLY	-	expression tag	UNP O06543
G	364	CYS	-	expression tag	UNP O06543
H	361	GLY	-	expression tag	UNP O06543
H	362	SER	-	expression tag	UNP O06543
H	363	GLY	-	expression tag	UNP O06543
H	364	CYS	-	expression tag	UNP O06543
I	361	GLY	-	expression tag	UNP O06543
I	362	SER	-	expression tag	UNP O06543
I	363	GLY	-	expression tag	UNP O06543
I	364	CYS	-	expression tag	UNP O06543
J	361	GLY	-	expression tag	UNP O06543
J	362	SER	-	expression tag	UNP O06543
J	363	GLY	-	expression tag	UNP O06543
J	364	CYS	-	expression tag	UNP O06543
K	361	GLY	-	expression tag	UNP O06543
K	362	SER	-	expression tag	UNP O06543
K	363	GLY	-	expression tag	UNP O06543
K	364	CYS	-	expression tag	UNP O06543
L	361	GLY	-	expression tag	UNP O06543
L	362	SER	-	expression tag	UNP O06543
L	363	GLY	-	expression tag	UNP O06543

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Chain	Residue	Modelled	Actual	Comment	Reference
L	364	CYS	-	expression tag	UNP O06543

- Molecule 2 is (S)-IBUPROFENOYL-COENZYME A (CCD ID: SFC) (formula: C<sub>34</sub>H<sub>53</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	B	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	C	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	D	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	E	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	F	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	G	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	H	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	I	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			
2	J	1	Total	C	N	O	P	S		0	0
			62	34	7	17	3	1			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	K	1	Total	C	N	O	P	S	0	0
			62	34	7	17	3	1		
2	L	1	Total	C	N	O	P	S	0	0
			62	34	7	17	3	1		

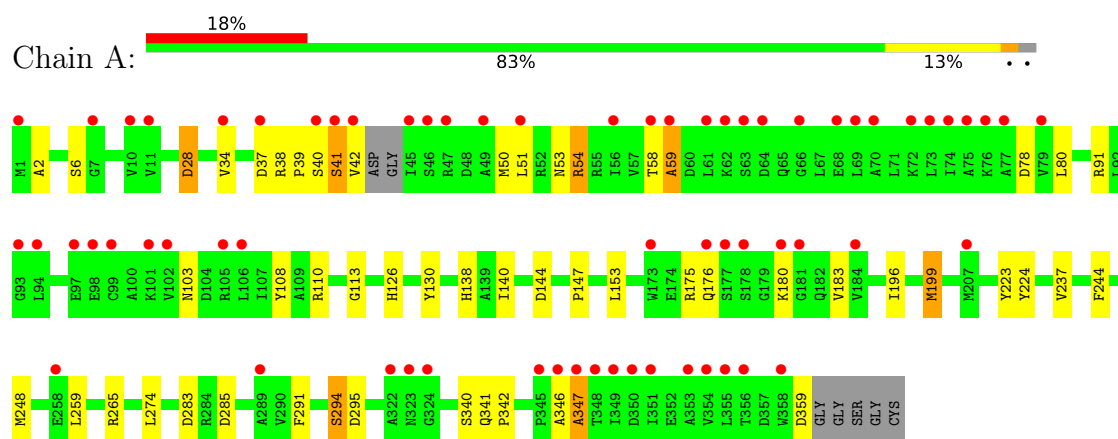
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	99	Total	O	0	0
			99	99		
3	B	103	Total	O	0	0
			103	103		
3	C	105	Total	O	0	0
			105	105		
3	D	106	Total	O	0	0
			106	106		
3	E	108	Total	O	0	0
			108	108		
3	F	104	Total	O	0	0
			104	104		
3	G	92	Total	O	0	0
			92	92		
3	H	101	Total	O	0	0
			101	101		
3	I	110	Total	O	0	0
			110	110		
3	J	121	Total	O	0	0
			121	121		
3	K	114	Total	O	0	0
			114	114		
3	L	101	Total	O	0	0
			101	101		

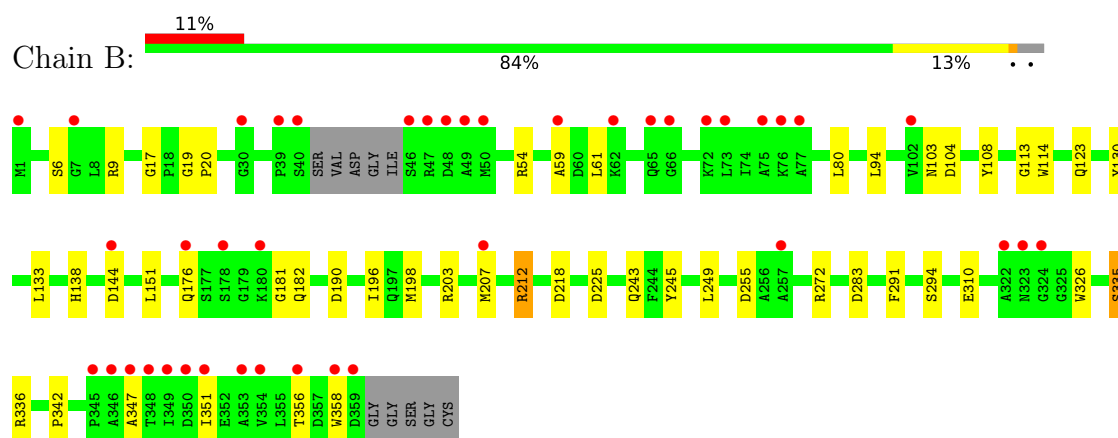
### 3 Residue-property plots [i](#)

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.

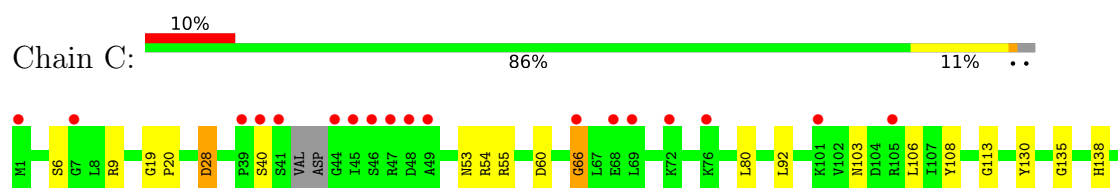
#### • Molecule 1: Alpha-methylacyl-CoA racemase



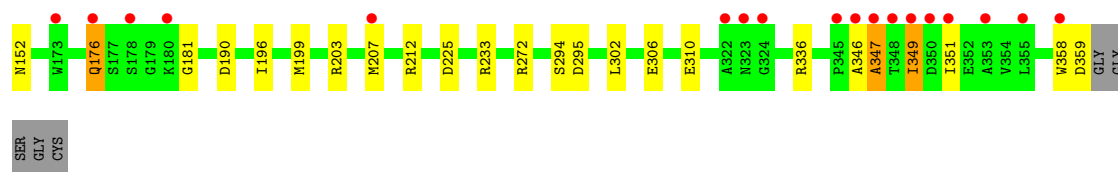
#### • Molecule 1: Alpha-methylacyl-CoA racemase



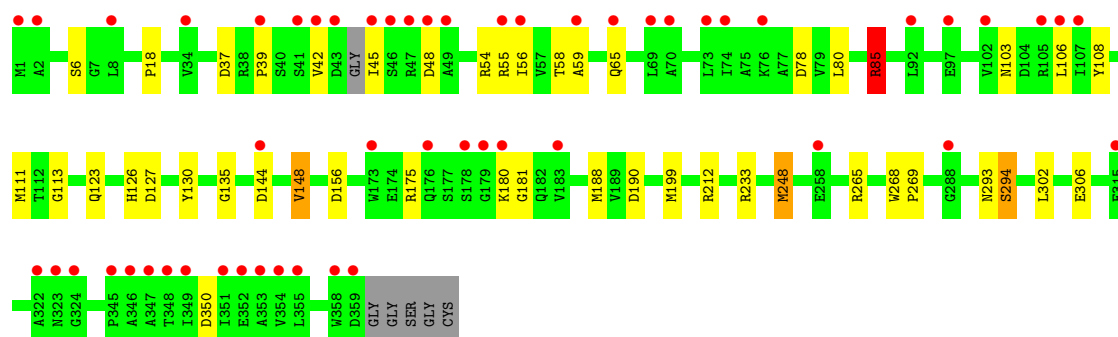
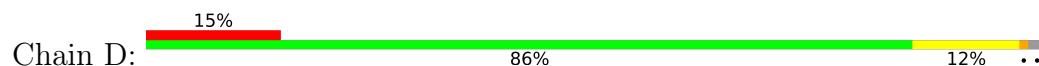
#### • Molecule 1: Alpha-methylacyl-CoA racemase



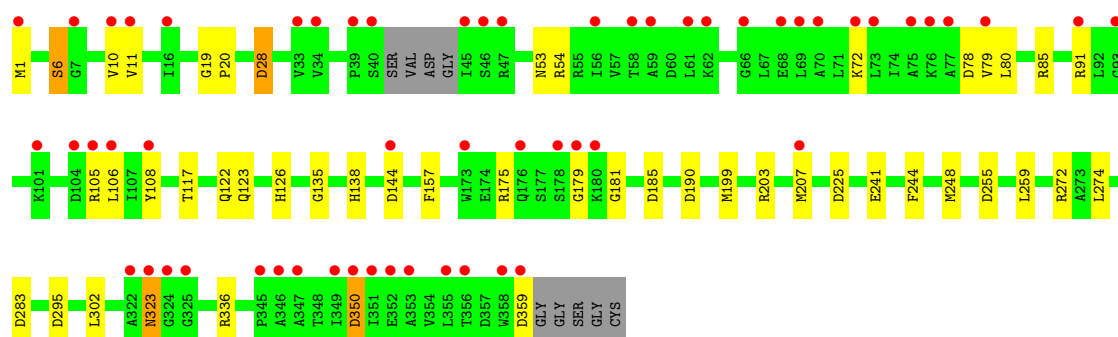
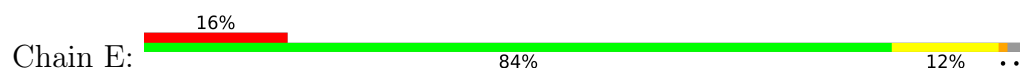




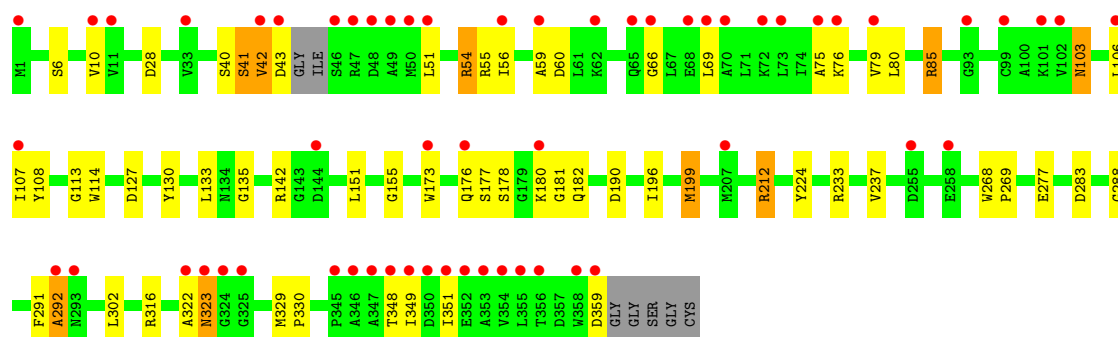
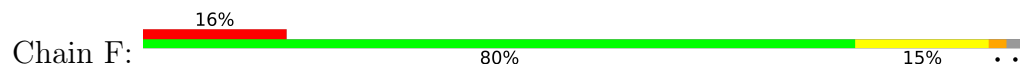
• Molecule 1: Alpha-methylacyl-CoA racemase



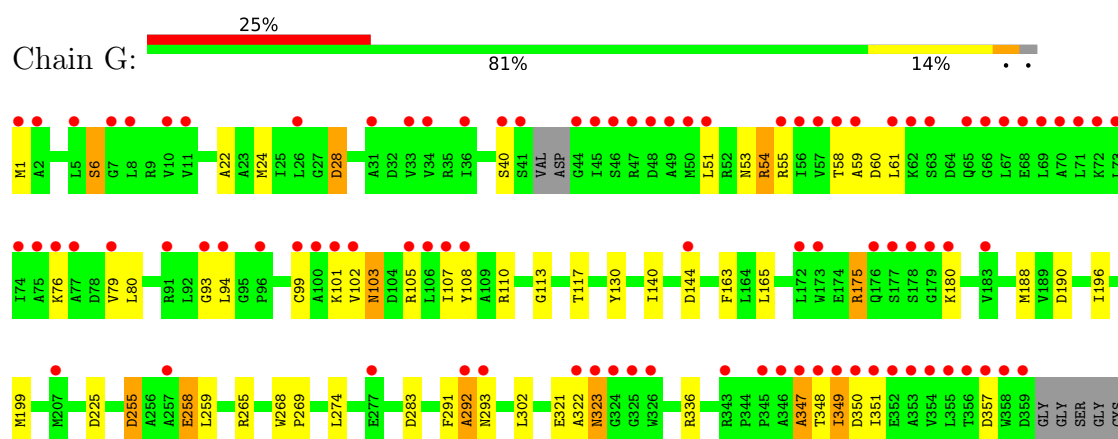
• Molecule 1: Alpha-methylacyl-CoA racemase



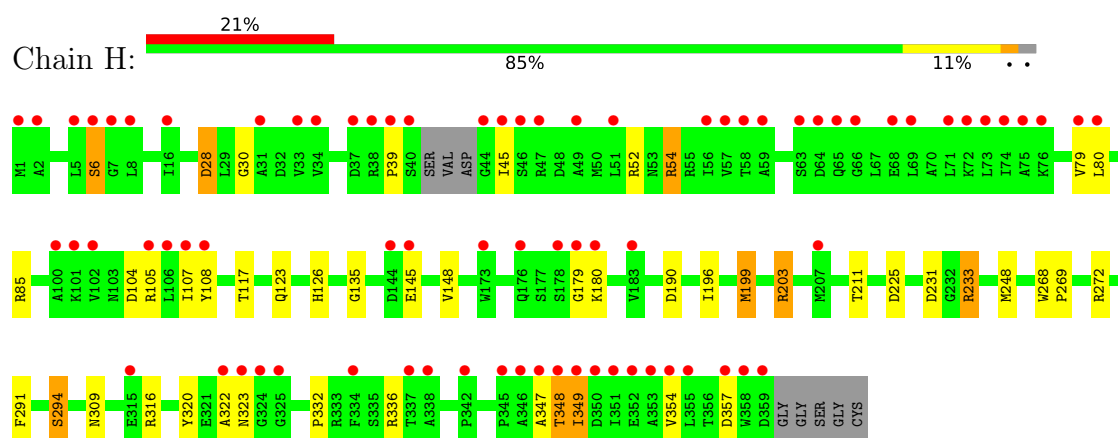
• Molecule 1: Alpha-methylacyl-CoA racemase



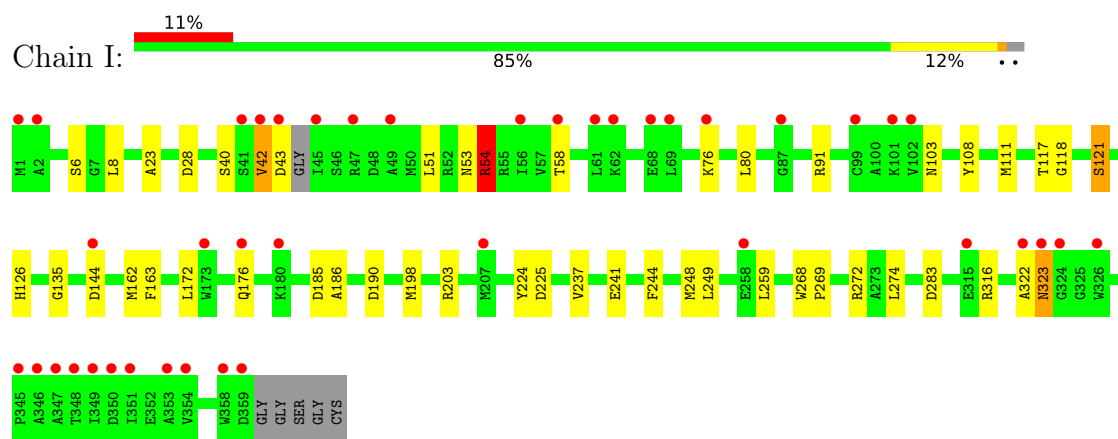
• Molecule 1: Alpha-methylacyl-CoA racemase



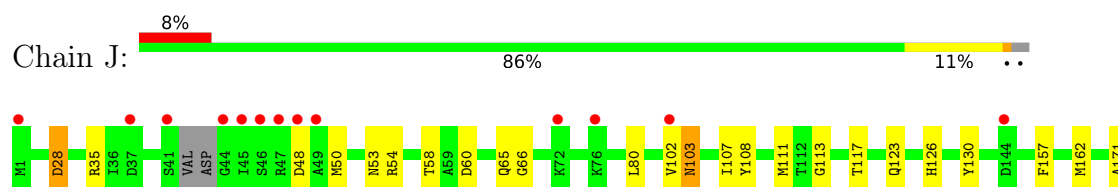
• Molecule 1: Alpha-methylacyl-CoA racemase



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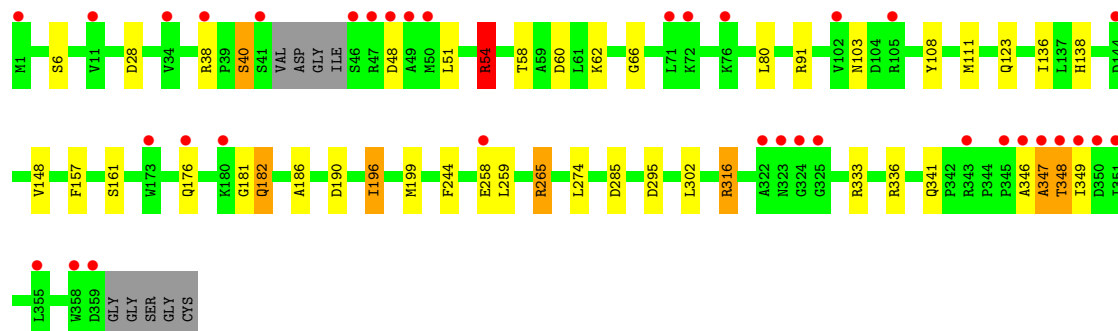
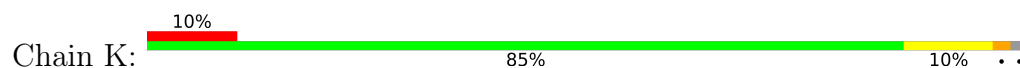


• Molecule 1: Alpha-methylacyl-CoA racemase

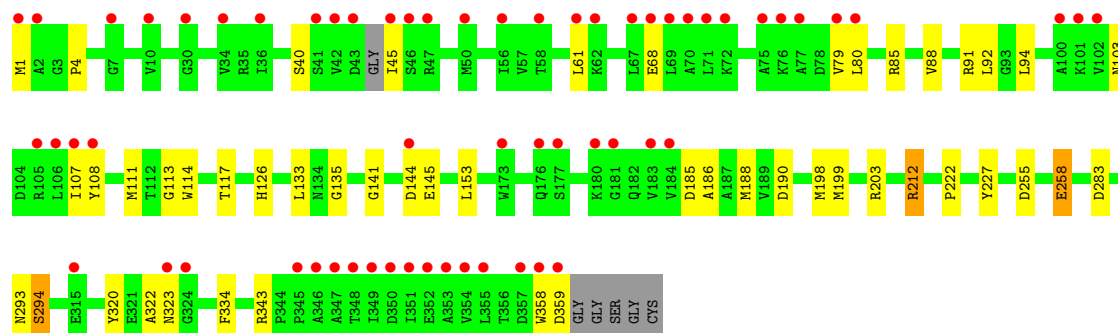
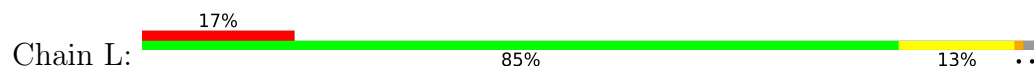




• Molecule 1: Alpha-methylacyl-CoA racemase



• Molecule 1: Alpha-methylacyl-CoA racemase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	277.03Å 277.03Å 390.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	196.66 – 2.17 196.66 – 2.17	Depositor EDS
% Data completeness (in resolution range)	100.0 (196.66-2.17) 99.9 (196.66-2.17)	Depositor EDS
$R_{merge}$	0.28	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.88)	Depositor
R, $R_{free}$	0.201 , 0.239 0.209 , 0.244	Depositor DCC
$R_{free}$ test set	19763 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.4	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for -1/2*h+1/2*k-1/2*l,1/2*h-1/2*k-1/2*l,-h-k 0.012 for -1/2*h-1/2*k+1/2*l,-1/2*h-1/2*k-1/2*l,h-k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	34453	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SFC

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	0.64	0/2778	1.15	8/3778 (0.2%)
1	B	0.64	0/2765	1.17	18/3760 (0.5%)
1	C	0.64	0/2775	1.14	6/3773 (0.2%)
1	D	0.64	0/2785	1.19	11/3788 (0.3%)
1	E	0.64	0/2765	1.13	10/3760 (0.3%)
1	F	0.64	0/2769	1.15	4/3766 (0.1%)
1	G	0.62	0/2775	1.17	11/3773 (0.3%)
1	H	0.63	0/2768	1.16	10/3764 (0.3%)
1	I	0.63	0/2777	1.10	6/3777 (0.2%)
1	J	0.62	0/2775	1.15	8/3773 (0.2%)
1	K	0.64	0/2772	1.13	8/3769 (0.2%)
1	L	0.64	0/2785	1.16	8/3788 (0.2%)
All	All	0.63	0/33289	1.15	108/45269 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	C	0	2
1	D	0	4
1	E	0	1
1	F	0	2
1	G	0	2
1	H	0	4
1	J	0	2
1	K	0	3
1	L	0	3
All	All	0	26

There are no bond length outliers.

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	123	GLN	CB-CA-C	10.23	126.52	109.84
1	B	212	ARG	NE-CZ-NH1	-9.24	112.26	121.50
1	B	212	ARG	CD-NE-CZ	-9.15	111.59	124.40
1	D	248	MET	CG-SD-CE	8.69	120.02	100.90
1	B	203	ARG	CB-CA-C	-8.60	94.16	110.67
1	B	203	ARG	N-CA-CB	8.58	123.59	110.28
1	G	190	ASP	CA-CB-CG	7.76	120.36	112.60
1	G	283	ASP	CA-CB-CG	7.76	120.36	112.60
1	C	203	ARG	N-CA-CB	7.67	122.17	110.28
1	G	255	ASP	CB-CA-C	7.64	122.98	110.22
1	E	123	GLN	CB-CA-C	-7.48	97.31	109.72
1	J	54	ARG	CB-CA-C	-7.45	94.08	109.94
1	J	28	ASP	CA-CB-CG	7.39	119.99	112.60
1	J	123	GLN	N-CA-CB	-7.35	98.56	109.95
1	E	28	ASP	CA-CB-CG	7.25	119.84	112.60
1	K	28	ASP	CA-CB-CG	7.19	119.79	112.60
1	E	190	ASP	CA-CB-CG	7.13	119.73	112.60
1	J	190	ASP	CA-CB-CG	7.10	119.70	112.60
1	D	123	GLN	N-CA-CB	-6.99	99.43	109.85
1	D	123	GLN	CB-CA-C	6.97	121.04	109.89
1	E	203	ARG	CB-CA-C	-6.93	99.06	110.85
1	F	190	ASP	CA-CB-CG	6.78	119.38	112.60
1	C	203	ARG	CB-CA-C	-6.75	97.71	110.67
1	D	65	GLN	N-CA-CB	-6.74	100.08	109.91
1	L	190	ASP	CA-CB-CG	6.72	119.32	112.60
1	B	190	ASP	CA-CB-CG	6.71	119.31	112.60
1	H	28	ASP	CA-CB-CG	6.61	119.21	112.60
1	E	283	ASP	CA-CB-CG	6.45	119.05	112.60
1	F	54	ARG	CB-CA-C	-6.44	95.27	109.56
1	J	185	ASP	CA-CB-CG	6.42	119.02	112.60
1	B	255	ASP	CB-CA-C	6.37	120.73	110.29
1	I	203	ARG	CB-CA-C	-6.35	100.25	110.79
1	D	54	ARG	CB-CA-C	-6.27	95.64	109.56
1	G	357	ASP	CA-CB-CG	6.26	118.86	112.60
1	B	144	ASP	CA-CB-CG	6.22	118.82	112.60
1	B	212	ARG	NE-CZ-NH2	6.22	124.79	119.20
1	B	283[A]	ASP	CA-CB-CG	6.21	118.81	112.60
1	B	283[B]	ASP	CA-CB-CG	6.21	118.81	112.60
1	I	190	ASP	CA-CB-CG	6.21	118.81	112.60
1	L	144	ASP	CA-CB-CG	6.15	118.75	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	357	ASP	CA-CB-CG	6.13	118.73	112.60
1	G	350	ASP	CB-CA-C	6.05	120.18	109.72
1	K	341	GLN	CB-CA-C	6.04	118.72	109.60
1	A	285	ASP	CB-CA-C	5.95	122.53	110.38
1	H	145	GLU	N-CA-CB	-5.95	101.37	110.42
1	D	48	ASP	CA-CB-CG	5.93	118.53	112.60
1	I	283	ASP	CA-CB-CG	5.91	118.51	112.60
1	H	148	VAL	CA-C-O	5.88	123.38	119.38
1	I	54	ARG	N-CA-CB	-5.87	100.62	111.53
1	J	357	ASP	CA-CB-CG	5.85	118.45	112.60
1	G	144	ASP	CA-CB-CG	5.84	118.44	112.60
1	C	306	GLU	CB-CA-C	-5.78	99.85	109.55
1	G	258	GLU	CB-CA-C	-5.76	99.65	110.01
1	G	60	ASP	CA-CB-CG	5.74	118.34	112.60
1	K	285	ASP	CB-CA-C	5.74	120.31	110.79
1	E	255	ASP	CB-CA-C	5.71	119.56	110.19
1	C	190	ASP	CA-CB-CG	5.67	118.27	112.60
1	B	54	ARG	CB-CA-C	-5.64	98.23	109.79
1	H	211	THR	CA-CB-OG1	-5.61	101.19	109.60
1	G	28	ASP	CA-CB-CG	5.60	118.20	112.60
1	K	190	ASP	CA-CB-CG	5.58	118.18	112.60
1	D	190	ASP	CA-CB-CG	5.55	118.15	112.60
1	B	123	GLN	N-CA-CB	-5.51	101.41	109.95
1	I	144	ASP	CA-CB-CG	5.51	118.11	112.60
1	K	123	GLN	CB-CA-C	-5.51	101.08	109.89
1	D	148	VAL	N-CA-CB	-5.48	105.75	111.61
1	H	309	ASN	CB-CA-C	-5.42	102.01	110.94
1	F	283	ASP	CA-CB-CG	5.41	118.01	112.60
1	L	185	ASP	CA-CB-CG	5.39	117.99	112.60
1	L	255	ASP	CA-CB-CG	5.38	117.98	112.60
1	D	144	ASP	CA-CB-CG	5.36	117.96	112.60
1	H	190	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	283	ASP	CA-CB-CG	5.35	117.95	112.60
1	C	310	GLU	CB-CG-CD	5.32	121.64	112.60
1	K	123	GLN	N-CA-CB	5.29	117.74	109.85
1	J	65	GLN	CB-CA-C	5.28	120.28	109.67
1	K	258	GLU	CB-CA-C	-5.28	100.51	110.01
1	I	185	ASP	CA-CB-CG	5.27	117.87	112.60
1	C	28	ASP	CA-CB-CG	5.26	117.86	112.60
1	H	123	GLN	CB-CA-C	5.24	118.38	109.53
1	A	144	ASP	CA-CB-CG	5.23	117.83	112.60
1	E	91	ARG	N-CA-CB	5.17	117.72	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	258	GLU	CB-CA-C	-5.17	100.29	110.11
1	F	28	ASP	CA-CB-CG	5.14	117.74	112.60
1	A	28	ASP	CA-CB-CG	5.12	117.72	112.60
1	A	37	ASP	CA-CB-CG	5.12	117.72	112.60
1	H	54	ARG	CB-CA-C	-5.08	99.37	109.79
1	B	104	ASP	CA-CB-CG	5.08	117.68	112.60
1	E	185	ASP	CA-CB-CG	5.08	117.68	112.60
1	G	99	CYS	CB-CA-C	5.06	119.68	110.11
1	B	218	ASP	CA-CB-CG	5.06	117.66	112.60
1	L	198	MET	CG-SD-CE	-5.06	89.77	100.90
1	B	243[A]	GLN	CB-CA-C	-5.06	102.25	110.85
1	B	243[B]	GLN	CB-CA-C	-5.06	102.25	110.85
1	B	207	MET	CG-SD-CE	5.05	112.01	100.90
1	B	123	GLN	CB-CA-C	5.05	118.07	109.84
1	G	225	ASP	CA-CB-CG	5.04	117.64	112.60
1	E	359	ASP	CA-CB-CG	5.04	117.64	112.60
1	E	157	PHE	CB-CA-C	5.02	118.88	111.65
1	K	48	ASP	CB-CA-C	5.02	118.61	110.22
1	L	283[A]	ASP	CA-CB-CG	5.02	117.62	112.60
1	L	283[B]	ASP	CA-CB-CG	5.02	117.62	112.60
1	A	248	MET	CG-SD-CE	5.02	111.94	100.90
1	D	306	GLU	CB-CA-C	-5.02	100.92	109.65
1	A	147	PRO	CA-C-N	-5.01	118.97	123.33
1	A	147	PRO	C-N-CA	-5.01	118.97	123.33
1	H	85	ARG	N-CA-CB	5.01	117.59	110.03
1	D	55	ARG	CB-CA-C	5.01	118.01	109.75

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	ARG	Sidechain
1	A	265	ARG	Sidechain
1	A	91	ARG	Sidechain
1	C	212	ARG	Sidechain
1	C	233	ARG	Sidechain
1	D	212	ARG	Sidechain
1	D	233	ARG	Sidechain
1	D	265	ARG	Sidechain
1	D	85	ARG	Sidechain
1	E	350	ASP	Peptide
1	F	212	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	F	233	ARG	Sidechain
1	G	110	ARG	Sidechain
1	G	265	ARG	Sidechain
1	H	203	ARG	Sidechain
1	H	233	ARG	Sidechain
1	H	323	ASN	Peptide
1	H	54	ARG	Peptide
1	J	212	ARG	Sidechain
1	J	35	ARG	Sidechain
1	K	265	ARG	Sidechain
1	K	316	ARG	Sidechain
1	K	54	ARG	Sidechain
1	L	203	ARG	Sidechain
1	L	212	ARG	Sidechain
1	L	91	ARG	Sidechain

## 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	2706	0	2650	28	0
1	B	2692	0	2635	25	0
1	C	2703	0	2644	22	0
1	D	2715	0	2656	19	0
1	E	2693	0	2636	20	0
1	F	2703	0	2645	34	0
1	G	2703	0	2644	29	0
1	H	2698	0	2641	21	0
1	I	2711	0	2656	26	0
1	J	2709	0	2653	23	0
1	K	2697	0	2638	21	0
1	L	2715	0	2656	22	0
2	A	62	0	49	6	0
2	B	62	0	49	0	0
2	C	62	0	49	1	0
2	D	62	0	49	2	0
2	E	62	0	49	2	0
2	F	62	0	49	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	62	0	49	0	0
2	H	62	0	49	1	0
2	I	62	0	49	1	0
2	J	62	0	49	3	0
2	K	62	0	49	0	0
2	L	62	0	49	2	0
3	A	99	0	0	1	0
3	B	103	0	0	2	0
3	C	105	0	0	2	0
3	D	106	0	0	0	0
3	E	108	0	0	1	0
3	F	104	0	0	0	0
3	G	92	0	0	1	0
3	H	101	0	0	0	0
3	I	110	0	0	0	0
3	J	121	0	0	1	0
3	K	114	0	0	2	0
3	L	101	0	0	0	0
All	All	34453	0	32342	261	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 (261) 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:B:138:HIS:O	1:B:212:ARG:HD3	1.60	1.01
1:L:88:VAL:O	1:L:92:LEU:HD12	1.76	0.85
1:G:259:LEU:HD22	1:G:274:LEU:HD13	1.60	0.83
1:H:79:VAL:HG22	1:H:107:ILE:HB	1.63	0.79
1:A:291:PHE:O	1:A:294:SER:HB3	1.84	0.77
1:A:80:LEU:HD23	1:A:108:TYR:CE2	2.21	0.75
1:H:80:LEU:HD23	1:H:108:TYR:CE2	2.23	0.74
1:L:80:LEU:HD23	1:L:108:TYR:CE1	2.23	0.74
1:D:80:LEU:HD23	1:D:108:TYR:CE2	2.22	0.73
1:K:196:ILE:HG13	1:L:153:LEU:HD21	1.72	0.72
1:I:118:GLY:O	1:I:121:SER:OG	2.10	0.69
1:G:80:LEU:HD23	1:G:108:TYR:CE1	2.28	0.69
1:E:80:LEU:HD23	1:E:108:TYR:CE2	2.27	0.69
1:I:80:LEU:HD23	1:I:108:TYR:CE2	2.27	0.68
1:E:78:ASP:OD1	1:E:175:ARG:NH2	2.18	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:LEU:HD23	1:B:108:TYR:CE2	2.33	0.63
1:A:41:SER:O	1:A:42:VAL:C	2.41	0.63
1:F:85:ARG:CD	2:F:401:SFC:O2A	2.48	0.61
1:F:80:LEU:HD23	1:F:108:TYR:CE2	2.37	0.60
1:A:38:ARG:NH2	2:A:401:SFC:O4B	2.36	0.59
1:C:138:HIS:HD2	3:C:529:HOH:O	1.84	0.59
1:G:28:ASP:HA	1:G:53:ASN:ND2	2.18	0.58
1:G:79:VAL:HG22	1:G:107:ILE:HB	1.84	0.58
1:J:28:ASP:HA	1:J:53:ASN:ND2	2.18	0.58
1:G:28:ASP:HA	1:G:53:ASN:HD22	1.68	0.58
1:F:85:ARG:HD3	2:F:401:SFC:O2A	2.02	0.58
1:E:225:ASP:OD2	1:E:272:ARG:NH1	2.37	0.57
1:J:28:ASP:HA	1:J:53:ASN:HD22	1.69	0.57
1:L:145:GLU:O	1:L:212:ARG:NH1	2.31	0.57
1:D:37:ASP:O	1:D:58:THR:HA	2.04	0.57
1:E:336:ARG:NH2	1:F:180:LYS:HB2	2.19	0.56
1:F:181:GLY:O	1:F:182:GLN:HB3	2.04	0.56
1:H:291:PHE:O	1:H:294:SER:HB3	2.05	0.56
1:J:126:HIS:ND1	2:J:401:SFC:H2	2.20	0.56
1:C:80:LEU:HD23	1:C:108:TYR:CE2	2.40	0.56
1:K:51:LEU:HA	1:K:54:ARG:NH1	2.21	0.56
1:G:51:LEU:HA	1:G:54:ARG:NH1	2.20	0.55
1:B:291:PHE:O	1:B:294:SER:HB3	2.07	0.55
1:D:78:ASP:OD1	1:D:175:ARG:NH2	2.36	0.55
1:A:346:ALA:O	1:A:347:ALA:O	2.23	0.55
1:F:80:LEU:CD2	1:F:108:TYR:CE2	2.90	0.55
1:C:176:GLN:HA	1:C:176:GLN:HE21	1.71	0.55
1:G:55:ARG:HD2	1:G:349:ILE:HD12	1.88	0.55
1:A:259:LEU:HD22	1:A:274:LEU:HD13	1.88	0.55
1:E:126:HIS:ND1	2:E:401:SFC:H2	2.22	0.54
1:K:60:ASP:O	1:K:66:GLY:HA3	2.07	0.54
1:C:80:LEU:CD2	1:C:108:TYR:CE2	2.91	0.54
1:K:80:LEU:HD23	1:K:108:TYR:CE2	2.43	0.54
1:C:60:ASP:O	1:C:66:GLY:HA3	2.08	0.53
1:I:80:LEU:CD2	1:I:108:TYR:CE2	2.91	0.53
1:L:126:HIS:ND1	2:L:401:SFC:H2	2.23	0.53
1:C:55:ARG:HD2	1:C:349:ILE:HD12	1.89	0.53
1:F:113:GLY:HA3	1:F:130:TYR:CZ	2.43	0.53
1:F:291:PHE:O	1:F:292:ALA:C	2.52	0.53
1:I:51:LEU:HA	1:I:54:ARG:NH1	2.23	0.53
1:F:322:ALA:O	1:F:323:ASN:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:259:LEU:HD22	1:I:274:LEU:HD13	1.90	0.53
1:G:163:PHE:O	1:H:332:PRO:HG3	2.08	0.53
1:C:135:GLY:HA2	1:D:302:LEU:O	2.10	0.52
1:H:225:ASP:OD2	1:H:272:ARG:NH1	2.42	0.52
1:J:225:ASP:OD2	1:J:272:ARG:NH1	2.42	0.52
1:A:2:ALA:HB3	1:A:340:SER:OG	2.10	0.52
1:A:346:ALA:O	1:A:347:ALA:C	2.53	0.52
1:A:180:LYS:O	1:B:336:ARG:NH2	2.43	0.52
1:B:138:HIS:O	1:B:212:ARG:CD	2.46	0.52
1:K:259:LEU:HD22	1:K:274:LEU:HD13	1.92	0.52
1:F:40:SER:O	1:F:41:SER:HB3	2.10	0.51
1:I:198:MET:HB2	1:J:50:MET:HE1	1.92	0.51
1:G:105:ARG:HH11	1:G:105:ARG:HG2	1.73	0.51
1:G:102:VAL:O	1:G:103:ASN:HB2	2.10	0.51
1:H:126:HIS:ND1	2:H:401:SFC:H2	2.25	0.51
1:K:181:GLY:O	1:K:182:GLN:HB3	2.10	0.51
1:F:85:ARG:HD2	2:F:401:SFC:O2A	2.10	0.51
1:K:138:HIS:HD2	3:K:552:HOH:O	1.94	0.51
1:J:60:ASP:O	1:J:66:GLY:HA3	2.11	0.51
1:C:152:ASN:HD22	2:C:401:SFC:H132	1.75	0.50
1:F:10:VAL:HG22	1:F:79:VAL:HB	1.93	0.50
1:C:19:GLY:N	1:C:20:PRO:CD	2.75	0.50
1:G:302:LEU:O	1:H:135:GLY:HA2	2.12	0.50
1:J:80:LEU:HD23	1:J:108:TYR:CE2	2.46	0.50
1:K:336:ARG:HH11	1:K:336:ARG:HG2	1.76	0.50
1:G:347:ALA:O	1:G:349:ILE:N	2.45	0.50
1:F:113:GLY:HA3	1:F:130:TYR:CE1	2.47	0.50
1:E:117:THR:O	1:F:316:ARG:HD2	2.12	0.50
1:F:55:ARG:HD2	1:F:349:ILE:HD11	1.94	0.49
1:J:291:PHE:O	1:J:294:SER:HB3	2.12	0.49
1:E:11:VAL:O	1:E:80:LEU:HD12	2.12	0.49
1:E:259:LEU:HD22	1:E:274:LEU:HD13	1.93	0.49
1:E:105:ARG:HG2	1:E:179:GLY:O	2.12	0.49
1:A:138:HIS:HD2	3:A:534:HOH:O	1.95	0.49
1:J:113:GLY:HA3	1:J:130:TYR:CE1	2.47	0.49
1:A:126:HIS:ND1	2:A:401:SFC:H2	2.28	0.48
1:L:111:MET:HE3	1:L:186:ALA:O	2.13	0.48
1:F:329:MET:HE3	1:F:330:PRO:HD2	1.95	0.48
1:I:225:ASP:OD2	1:I:272:ARG:NH1	2.45	0.48
1:B:61:LEU:HD22	1:B:94:LEU:HD11	1.95	0.48
1:C:336:ARG:NH2	1:D:180:LYS:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:175:ARG:O	1:G:175:ARG:HG2	2.13	0.48
1:L:320:TYR:CE2	1:L:322:ALA:HB2	2.48	0.48
1:I:8:LEU:HD11	1:I:172:LEU:HD11	1.96	0.48
1:A:51:LEU:HA	1:A:54:ARG:NH1	2.28	0.47
1:H:349:ILE:HD11	1:H:354:VAL:HG22	1.96	0.47
1:C:9:ARG:HG2	1:C:358:TRP:CZ2	2.50	0.47
1:E:28:ASP:HA	1:E:53:ASN:ND2	2.29	0.47
1:A:153:LEU:HD21	1:B:196:ILE:HG13	1.96	0.47
2:A:401:SFC:O9P	2:A:401:SFC:CEP	2.62	0.47
1:D:39:PRO:O	1:D:42:VAL:HB	2.15	0.47
1:J:48:ASP:OD1	1:J:50:MET:N	2.38	0.47
1:H:105:ARG:HG2	1:H:179:GLY:O	2.15	0.47
1:E:1:MET:O	1:E:6:SER:OG	2.27	0.47
1:F:60:ASP:O	1:F:66:GLY:HA3	2.15	0.47
1:H:231:ASP:OD2	1:H:233:ARG:NH1	2.43	0.47
1:J:107:ILE:HD12	1:J:171:ALA:HB1	1.97	0.47
1:B:114:TRP:CZ3	1:B:133:LEU:HD22	2.50	0.46
1:F:196:ILE:HG12	1:F:199:MET:HB2	1.97	0.46
1:G:93:GLY:C	3:G:545:HOH:O	2.58	0.46
1:K:346:ALA:O	1:K:347:ALA:C	2.58	0.46
1:E:244:PHE:HB3	1:E:295:ASP:O	2.15	0.46
1:F:76:LYS:NZ	1:F:359:ASP:HB2	2.30	0.46
1:H:320:TYR:HE2	1:H:322:ALA:HB2	1.79	0.46
1:J:322:ALA:O	1:J:323:ASN:C	2.58	0.46
2:A:401:SFC:H6	1:B:198:MET:HE1	1.97	0.46
1:F:114:TRP:CZ3	1:F:133:LEU:HD22	2.51	0.46
1:I:117:THR:O	1:J:316:ARG:HD2	2.16	0.46
1:I:198:MET:HE1	2:J:401:SFC:H6	1.97	0.46
1:D:113:GLY:HA3	1:D:130:TYR:CE1	2.51	0.46
1:E:10:VAL:HG22	1:E:79:VAL:HB	1.98	0.46
1:G:117:THR:O	1:H:316:ARG:HD2	2.15	0.46
1:C:358:TRP:O	1:C:359:ASP:HB2	2.15	0.46
1:J:111:MET:HE3	1:J:186:ALA:O	2.16	0.45
1:L:4:PRO:HG3	1:L:334:PHE:CZ	2.50	0.45
1:D:106:LEU:O	1:D:181:GLY:HA3	2.15	0.45
1:D:268:TRP:N	1:D:269:PRO:CD	2.79	0.45
1:I:268:TRP:N	1:I:269:PRO:CD	2.78	0.45
1:J:243[A]:GLN:HG2	3:J:512:HOH:O	2.16	0.45
1:K:244:PHE:CD1	1:K:295:ASP:HB3	2.52	0.45
1:A:58:THR:O	1:A:59:ALA:HB2	2.16	0.45
1:K:136:ILE:HG12	1:K:196:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:85:ARG:NH1	1:E:122:GLN:O	2.45	0.45
1:E:19:GLY:N	1:E:20:PRO:HD2	2.32	0.45
1:A:39:PRO:HB3	1:A:58:THR:HG23	1.98	0.45
1:A:78:ASP:OD1	1:A:175:ARG:NH2	2.26	0.45
1:A:140:ILE:CD1	1:B:151:LEU:HG	2.46	0.45
1:B:181:GLY:O	1:B:182:GLN:HB3	2.17	0.45
1:B:225:ASP:OD2	1:B:272:ARG:NH1	2.49	0.45
1:H:248:MET:O	1:H:248:MET:HG2	2.17	0.45
1:I:135:GLY:HA2	1:J:302:LEU:O	2.17	0.45
1:I:248:MET:HE3	1:I:249:LEU:HD23	1.99	0.45
1:L:85:ARG:NH2	2:L:401:SFC:O4A	2.43	0.45
1:D:126:HIS:ND1	2:D:401:SFC:H2	2.31	0.45
1:G:322:ALA:HB1	1:G:323:ASN:HD22	1.82	0.45
1:C:295:ASP:CG	1:D:85:ARG:HH22	2.25	0.44
1:G:336:ARG:HG2	1:G:336:ARG:HH11	1.82	0.44
1:F:142:ARG:O	1:F:212:ARG:HD2	2.17	0.44
1:B:212:ARG:CG	1:B:212:ARG:NH1	2.74	0.44
1:D:294:SER:HB2	1:L:293:ASN:O	2.17	0.44
1:H:6:SER:HA	1:H:30:GLY:O	2.17	0.44
1:A:196:ILE:HG12	1:A:199:MET:HB2	2.00	0.44
1:L:1:MET:HE2	1:L:343:ARG:NH1	2.33	0.44
1:I:163:PHE:O	1:J:332:PRO:HG3	2.18	0.44
1:C:225:ASP:OD2	1:C:272:ARG:NH1	2.51	0.44
1:I:176:GLN:HE21	1:I:176:GLN:HA	1.83	0.44
1:I:224:TYR:HA	1:I:237:VAL:O	2.18	0.43
1:L:79:VAL:HG22	1:L:107:ILE:HB	1.99	0.43
1:C:346:ALA:O	1:C:347:ALA:C	2.60	0.43
1:A:113:GLY:HA3	1:A:130:TYR:CE1	2.53	0.43
1:F:177:SER:O	1:F:177:SER:OG	2.36	0.43
2:A:401:SFC:H6	1:B:198:MET:CE	2.48	0.43
1:C:196:ILE:HG12	1:C:199:MET:HB2	2.00	0.43
1:K:148:VAL:HG21	1:L:141:GLY:HA2	2.00	0.43
1:F:268:TRP:N	1:F:269:PRO:CD	2.81	0.43
1:H:196:ILE:HG12	1:H:199:MET:HB2	2.00	0.43
1:B:9:ARG:HD3	1:B:358:TRP:CD2	2.53	0.43
1:D:113:GLY:HA2	1:D:188:MET:HB2	2.00	0.43
2:E:401:SFC:H22	2:E:401:SFC:O5P	2.18	0.43
1:F:224:TYR:HA	1:F:237:VAL:O	2.19	0.43
1:J:113:GLY:HA2	1:J:188:MET:HB2	2.00	0.43
1:E:138:HIS:HD2	3:E:564:HOH:O	2.02	0.43
1:A:176:GLN:NE2	1:B:176:GLN:HG2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:85:ARG:NH1	2:F:401:SFC:O5A	2.51	0.43
1:G:336:ARG:NH2	1:H:180:LYS:HB2	2.33	0.43
1:A:223:TYR:O	1:A:237:VAL:HG12	2.19	0.42
1:B:19:GLY:N	1:B:20:PRO:CD	2.82	0.42
1:D:293:ASN:O	1:L:294:SER:HB2	2.19	0.42
1:E:135:GLY:HA2	1:F:302:LEU:O	2.19	0.42
1:K:302:LEU:O	1:L:135:GLY:HA2	2.19	0.42
1:D:126:HIS:O	1:D:127:ASP:C	2.61	0.42
1:G:180:LYS:HB2	1:H:336:ARG:NH2	2.34	0.42
1:A:28:ASP:HA	1:A:53:ASN:ND2	2.33	0.42
1:B:212:ARG:NH1	1:B:212:ARG:HG2	2.34	0.42
1:E:302:LEU:O	1:F:135:GLY:HA2	2.18	0.42
1:I:111:MET:HE3	1:I:186:ALA:O	2.20	0.42
1:B:326:TRP:HD1	3:B:571:HOH:O	2.02	0.42
1:C:92:LEU:O	3:C:501:HOH:O	2.22	0.42
1:G:1:MET:O	1:G:6:SER:OG	2.23	0.42
1:G:24:MET:HB3	1:G:24:MET:HE2	1.87	0.42
1:K:316:ARG:O	1:K:333:ARG:NH1	2.43	0.42
1:K:347:ALA:O	1:K:348:THR:C	2.62	0.42
1:G:22:ALA:O	1:G:165:LEU:HD21	2.19	0.42
1:H:28:ASP:CG	1:H:52:ARG:HH21	2.26	0.42
1:H:349:ILE:HD11	1:H:354:VAL:CG2	2.49	0.42
1:G:291:PHE:O	1:G:292:ALA:C	2.62	0.42
1:I:23:ALA:HB3	1:I:54:ARG:HH21	1.85	0.42
1:D:80:LEU:CD2	1:D:108:TYR:CE2	2.98	0.42
1:I:198:MET:HE3	1:J:157:PHE:HZ	1.84	0.42
1:G:113:GLY:HA3	1:G:130:TYR:CZ	2.55	0.42
1:I:198:MET:CE	2:J:401:SFC:H6	2.49	0.42
1:B:245:TYR:CE2	1:B:249:LEU:HD11	2.55	0.42
1:C:113:GLY:HA3	1:C:130:TYR:CZ	2.55	0.42
1:L:80:LEU:CD2	1:L:108:TYR:CE1	3.00	0.42
1:F:69:LEU:HD13	1:F:351:ILE:HG23	2.02	0.41
1:K:157:PHE:HA	1:K:161:SER:OG	2.20	0.41
1:B:310:GLU:OE2	3:B:501:HOH:O	2.22	0.41
1:K:196:ILE:HG23	1:K:196:ILE:O	2.19	0.41
1:F:51:LEU:HA	1:F:54:ARG:NH1	2.35	0.41
1:I:126:HIS:ND1	2:I:401:SFC:H2	2.35	0.41
1:K:316:ARG:HD2	1:L:117:THR:O	2.20	0.41
1:B:113:GLY:HA3	1:B:130:TYR:CE1	2.56	0.41
2:F:401:SFC:O9P	2:F:401:SFC:CEP	2.69	0.41
1:G:61:LEU:HD13	1:G:94:LEU:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:259:LEU:CD2	1:G:274:LEU:HD13	2.43	0.41
1:D:18:PRO:HB2	1:D:111:MET:HG2	2.02	0.41
1:F:75:ALA:HA	1:F:103:ASN:HB2	2.01	0.41
1:K:60:ASP:OD1	1:K:62:LYS:HB2	2.20	0.41
1:C:28:ASP:HA	1:C:53:ASN:ND2	2.36	0.41
1:I:241:GLU:HB2	1:I:244:PHE:CD2	2.56	0.41
1:L:358:TRP:O	1:L:359:ASP:HB2	2.20	0.41
1:A:224:TYR:HA	1:A:237:VAL:O	2.20	0.41
1:A:341:GLN:HA	1:A:342:PRO:HD3	1.96	0.41
1:C:113:GLY:HA3	1:C:130:TYR:CE1	2.56	0.41
1:D:156:ASP:OD2	2:D:401:SFC:H132	2.20	0.41
1:E:106:LEU:O	1:E:181:GLY:HA3	2.21	0.41
1:H:268:TRP:N	1:H:269:PRO:CD	2.83	0.41
1:A:183:VAL:HB	1:B:335:SER:OG	2.20	0.41
1:L:61:LEU:HD13	1:L:94:LEU:CD1	2.51	0.41
1:G:196:ILE:HG12	1:G:199:MET:HB2	2.03	0.41
1:G:268:TRP:N	1:G:269:PRO:CD	2.84	0.41
1:A:50:MET:HE1	1:B:198:MET:HB2	2.03	0.40
1:C:302:LEU:O	1:D:135:GLY:HA2	2.21	0.40
1:F:106:LEU:O	1:F:181:GLY:HA3	2.21	0.40
1:K:91:ARG:NH1	3:K:512:HOH:O	2.50	0.40
1:E:241:GLU:HB2	1:E:244:PHE:CD2	2.55	0.40
1:F:127:ASP:OD2	1:F:155:GLY:N	2.53	0.40
1:F:288:GLY:O	1:F:292:ALA:HB2	2.22	0.40
1:I:322:ALA:C	1:I:323:ASN:CG	2.88	0.40
1:J:102:VAL:O	1:J:103:ASN:HB2	2.20	0.40
1:J:316:ARG:O	1:J:317:ASN:C	2.64	0.40
1:B:17:GLY:O	1:B:20:PRO:HD2	2.20	0.40
1:C:106:LEU:O	1:C:181:GLY:HA3	2.22	0.40
1:I:316:ARG:HD2	1:J:117:THR:O	2.22	0.40
1:L:113:GLY:CA	1:L:188:MET:HE3	2.52	0.40
1:L:222:PRO:O	1:L:227:TYR:OH	2.37	0.40
1:G:113:GLY:HA2	1:G:188:MET:HB2	2.02	0.40
1:H:199:MET:O	1:H:203:ARG:HB2	2.21	0.40
1:I:28:ASP:HA	1:I:53:ASN:ND2	2.36	0.40
1:K:111:MET:HE3	1:K:186:ALA:O	2.21	0.40
1:A:38:ARG:HG2	2:A:401:SFC:C6A	2.52	0.40
1:A:244:PHE:HB3	1:A:295:ASP:O	2.21	0.40
1:F:79:VAL:HG22	1:F:107:ILE:HB	2.02	0.40
1:I:162:MET:HB3	1:J:162:MET:HB3	2.04	0.40
1:L:114:TRP:CZ3	1:L:133:LEU:HD22	2.56	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	355/364 (98%)	333 (94%)	17 (5%)	5 (1%)	9	6
1	B	353/364 (97%)	337 (96%)	13 (4%)	3 (1%)	16	15
1	C	355/364 (98%)	333 (94%)	19 (5%)	3 (1%)	16	15
1	D	356/364 (98%)	331 (93%)	23 (6%)	2 (1%)	22	21
1	E	353/364 (97%)	332 (94%)	20 (6%)	1 (0%)	37	40
1	F	354/364 (97%)	327 (92%)	18 (5%)	9 (2%)	4	2
1	G	355/364 (98%)	324 (91%)	24 (7%)	7 (2%)	6	3
1	H	354/364 (97%)	331 (94%)	20 (6%)	3 (1%)	16	15
1	I	355/364 (98%)	336 (95%)	16 (4%)	3 (1%)	16	15
1	J	355/364 (98%)	335 (94%)	19 (5%)	1 (0%)	37	40
1	K	354/364 (97%)	330 (93%)	19 (5%)	5 (1%)	9	6
1	L	356/364 (98%)	336 (94%)	19 (5%)	1 (0%)	37	40
All	All	4255/4368 (97%)	3985 (94%)	227 (5%)	43 (1%)	13	11

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	ASN
1	A	347	ALA
1	C	347	ALA
1	E	323	ASN
1	F	41	SER
1	F	348	THR
1	G	103	ASN
1	G	292	ALA
1	G	348	THR

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Mol	Chain	Res	Type
1	H	347	ALA
1	K	103	ASN
1	K	347	ALA
1	B	103	ASN
1	B	347	ALA
1	C	103	ASN
1	F	42	VAL
1	F	103	ASN
1	G	347	ALA
1	D	59	ALA
1	D	103	ASN
1	F	292	ALA
1	I	40	SER
1	J	103	ASN
1	K	40	SER
1	L	103	ASN
1	A	59	ALA
1	B	59	ALA
1	G	101	LYS
1	H	348	THR
1	I	103	ASN
1	K	348	THR
1	A	40	SER
1	A	41	SER
1	F	178	SER
1	F	323	ASN
1	G	59	ALA
1	I	42	VAL
1	K	182	GLN
1	F	59	ALA
1	F	151	LEU
1	G	175	ARG
1	H	39	PRO
1	C	66	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	276/277 (100%)	270 (98%)	6 (2%)	47	58
1	B	274/277 (99%)	269 (98%)	5 (2%)	54	66
1	C	275/277 (99%)	267 (97%)	8 (3%)	37	46
1	D	277/277 (100%)	268 (97%)	9 (3%)	34	42
1	E	274/277 (99%)	265 (97%)	9 (3%)	33	41
1	F	275/277 (99%)	266 (97%)	9 (3%)	33	41
1	G	275/277 (99%)	262 (95%)	13 (5%)	22	26
1	H	274/277 (99%)	266 (97%)	8 (3%)	37	46
1	I	276/277 (100%)	267 (97%)	9 (3%)	33	41
1	J	275/277 (99%)	270 (98%)	5 (2%)	54	66
1	K	275/277 (99%)	265 (96%)	10 (4%)	30	37
1	L	277/277 (100%)	270 (98%)	7 (2%)	42	53
All	All	3303/3324 (99%)	3205 (97%)	98 (3%)	36	45

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	34	VAL
1	A	54	ARG
1	A	199	MET
1	A	294	SER
1	A	359	ASP
1	B	6	SER
1	B	335	SER
1	B	342	PRO
1	B	351	ILE
1	B	356	THR
1	C	6	SER
1	C	40	SER
1	C	54	ARG
1	C	176	GLN
1	C	207	MET
1	C	294	SER
1	C	349	ILE
1	C	351	ILE
1	D	6	SER
1	D	45	ILE
1	D	56	ILE

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Mol	Chain	Res	Type
1	D	85	ARG
1	D	148	VAL
1	D	199	MET
1	D	248	MET
1	D	294	SER
1	D	350	ASP
1	E	6	SER
1	E	54	ARG
1	E	72	LYS
1	E	144	ASP
1	E	199	MET
1	E	207	MET
1	E	248	MET
1	E	323	ASN
1	E	350	ASP
1	F	6	SER
1	F	42	VAL
1	F	43	ASP
1	F	56	ILE
1	F	85	ARG
1	F	173	TRP
1	F	176	GLN
1	F	199	MET
1	F	277	GLU
1	G	6	SER
1	G	40	SER
1	G	54	ARG
1	G	58	THR
1	G	76	LYS
1	G	140	ILE
1	G	255	ASP
1	G	258	GLU
1	G	293	ASN
1	G	321	GLU
1	G	323	ASN
1	G	349	ILE
1	G	351	ILE
1	H	6	SER
1	H	45	ILE
1	H	104	ASP
1	H	117	THR
1	H	199	MET

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Mol	Chain	Res	Type
1	H	294	SER
1	H	348	THR
1	H	349	ILE
1	I	6	SER
1	I	42	VAL
1	I	43	ASP
1	I	54	ARG
1	I	58	THR
1	I	76	LYS
1	I	91	ARG
1	I	121	SER
1	I	323	ASN
1	J	58	THR
1	J	176	GLN
1	J	199	MET
1	J	243[A]	GLN
1	J	243[B]	GLN
1	K	6	SER
1	K	38	ARG
1	K	40	SER
1	K	54	ARG
1	K	58	THR
1	K	176	GLN
1	K	196	ILE
1	K	199	MET
1	K	265	ARG
1	K	349	ILE
1	L	40	SER
1	L	45	ILE
1	L	68	GLU
1	L	199	MET
1	L	258	GLU
1	L	294	SER
1	L	323	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	176	GLN
1	A	263	ASN
1	A	286	HIS

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Mol	Chain	Res	Type
1	A	323	ASN
1	A	327	GLN
1	B	116	GLN
1	B	286	HIS
1	B	323	ASN
1	C	138	HIS
1	C	176	GLN
1	C	263	ASN
1	C	282	HIS
1	C	327	GLN
1	D	282	HIS
1	D	308	HIS
1	E	138	HIS
1	E	176	GLN
1	E	263	ASN
1	E	293	ASN
1	F	116	GLN
1	F	176	GLN
1	F	282	HIS
1	F	286	HIS
1	F	293	ASN
1	G	116	GLN
1	G	138	HIS
1	G	176	GLN
1	G	263	ASN
1	G	308	HIS
1	G	323	ASN
1	G	327	GLN
1	H	286	HIS
1	I	138	HIS
1	I	176	GLN
1	I	327	GLN
1	J	176	GLN
1	J	286	HIS
1	J	308	HIS
1	J	323	ASN
1	K	138	HIS
1	K	176	GLN
1	K	282	HIS
1	K	327	GLN
1	L	122	GLN
1	L	176	GLN

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Mol	Chain	Res	Type
1	L	323	ASN

### 5.3.3 RNA [i](#)

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](#)

12 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	SFC	E	401	-	57,65,65	1.58	2 (3%)	73,96,96	1.71	9 (12%)
2	SFC	B	401	-	57,65,65	1.02	2 (3%)	73,96,96	1.18	6 (8%)
2	SFC	C	401	-	57,65,65	0.85	2 (3%)	73,96,96	1.29	11 (15%)
2	SFC	D	401	-	57,65,65	0.71	1 (1%)	73,96,96	1.21	6 (8%)
2	SFC	A	401	-	57,65,65	0.82	2 (3%)	73,96,96	1.35	7 (9%)
2	SFC	H	401	-	57,65,65	1.80	3 (5%)	73,96,96	1.31	9 (12%)
2	SFC	J	401	-	57,65,65	0.83	1 (1%)	73,96,96	1.23	10 (13%)
2	SFC	G	401	-	57,65,65	0.72	1 (1%)	73,96,96	1.48	8 (10%)
2	SFC	L	401	-	57,65,65	0.83	2 (3%)	73,96,96	1.19	10 (13%)
2	SFC	K	401	-	57,65,65	0.84	2 (3%)	73,96,96	1.38	11 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SFC	F	401	-	57,65,65	0.87	4 (7%)	73,96,96	1.40	10 (13%)
2	SFC	I	401	-	57,65,65	0.90	2 (3%)	73,96,96	1.20	8 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SFC	E	401	-	-	25/59/79/79	0/4/4/4
2	SFC	B	401	-	-	8/59/79/79	0/4/4/4
2	SFC	C	401	-	-	18/59/79/79	0/4/4/4
2	SFC	D	401	-	-	9/59/79/79	0/4/4/4
2	SFC	A	401	-	-	16/59/79/79	0/4/4/4
2	SFC	H	401	-	-	20/59/79/79	0/4/4/4
2	SFC	J	401	-	-	11/59/79/79	0/4/4/4
2	SFC	G	401	-	-	8/59/79/79	0/4/4/4
2	SFC	L	401	-	-	19/59/79/79	0/4/4/4
2	SFC	K	401	-	-	8/59/79/79	0/4/4/4
2	SFC	F	401	-	-	17/59/79/79	0/4/4/4
2	SFC	I	401	-	-	9/59/79/79	0/4/4/4

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	401	SFC	C2-C1	11.67	1.62	1.53
2	E	401	SFC	C2-C1	10.34	1.61	1.53
2	B	401	SFC	C2-C1	4.76	1.57	1.53
2	H	401	SFC	O1-C1	4.25	1.27	1.20
2	J	401	SFC	C2-C1	-3.53	1.50	1.53
2	I	401	SFC	C2-C1	3.31	1.56	1.53
2	L	401	SFC	O1-C1	3.17	1.25	1.20
2	I	401	SFC	O1-C1	3.12	1.25	1.20
2	C	401	SFC	C2-C1	3.05	1.56	1.53
2	E	401	SFC	O1-C1	3.00	1.25	1.20
2	K	401	SFC	C2-C1	2.92	1.55	1.53
2	B	401	SFC	O1-C1	2.90	1.25	1.20
2	C	401	SFC	O1-C1	2.79	1.24	1.20
2	F	401	SFC	C2-C1	2.72	1.55	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	SFC	P3B-O3B	2.63	1.64	1.59
2	A	401	SFC	O1-C1	2.58	1.24	1.20
2	K	401	SFC	O1-C1	2.56	1.24	1.20
2	F	401	SFC	O1-C1	2.46	1.24	1.20
2	L	401	SFC	O5P-C5P	2.31	1.28	1.23
2	F	401	SFC	O5P-C5P	2.25	1.27	1.23
2	H	401	SFC	P3B-O3B	2.17	1.63	1.59
2	G	401	SFC	O1-C1	2.17	1.24	1.20
2	D	401	SFC	O1-C1	2.16	1.24	1.20
2	F	401	SFC	P3B-O3B	2.04	1.63	1.59

All (105) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	SFC	C2-C1-S1P	7.45	119.90	111.81
2	G	401	SFC	C2-C1-S1P	6.12	118.45	111.81
2	E	401	SFC	O1-C1-S1P	-5.87	115.90	123.80
2	B	401	SFC	C2-C1-S1P	5.39	117.67	111.81
2	F	401	SFC	C2-C1-S1P	5.37	117.64	111.81
2	K	401	SFC	C2-C1-S1P	5.29	117.56	111.81
2	A	401	SFC	CEP-CBP-CCP	-5.07	99.96	108.23
2	E	401	SFC	C3-C2-C1	4.67	119.98	109.90
2	G	401	SFC	O4A-P2A-O5A	4.57	134.84	112.24
2	I	401	SFC	C2-C1-S1P	4.08	116.24	111.81
2	D	401	SFC	O4A-P2A-O5A	4.04	132.19	112.24
2	L	401	SFC	C3-C2-C1	4.00	118.52	109.90
2	E	401	SFC	O8A-P3B-O7A	3.99	122.89	107.64
2	C	401	SFC	C3-C2-C1	3.98	118.49	109.90
2	K	401	SFC	O8A-P3B-O3B	-3.89	88.56	105.99
2	F	401	SFC	O8A-P3B-O7A	3.89	122.49	107.64
2	H	401	SFC	C3-C2-C1	3.88	118.27	109.90
2	A	401	SFC	C2-C1-S1P	3.83	115.97	111.81
2	J	401	SFC	C2-C1-S1P	3.77	115.90	111.81
2	H	401	SFC	C2-C1-S1P	3.75	115.88	111.81
2	G	401	SFC	O8A-P3B-O7A	3.69	121.75	107.64
2	G	401	SFC	O8A-P3B-O9A	-3.62	96.50	110.68
2	A	401	SFC	CDP-CBP-CCP	3.62	114.13	108.23
2	K	401	SFC	O8A-P3B-O9A	3.59	124.75	110.68
2	B	401	SFC	O1-C1-S1P	-3.54	119.03	123.80
2	H	401	SFC	O1-C1-S1P	-3.43	119.18	123.80
2	J	401	SFC	O8A-P3B-O7A	3.39	120.61	107.64
2	E	401	SFC	O7A-P3B-O3B	-3.37	90.89	105.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	SFC	CEP-CBP-CCP	-3.36	102.75	108.23
2	A	401	SFC	C3-C2-C1	3.36	117.14	109.90
2	K	401	SFC	O8A-P3B-O7A	3.22	119.93	107.64
2	G	401	SFC	O6A-P2A-O5A	-3.22	96.50	109.07
2	A	401	SFC	O4A-P2A-O5A	3.18	127.95	112.24
2	D	401	SFC	C2-C1-S1P	3.18	115.26	111.81
2	E	401	SFC	C3P-N4P-C5P	3.16	128.70	122.84
2	J	401	SFC	CDP-CBP-CAP	3.09	114.18	108.82
2	E	401	SFC	C2P-S1P-C1	3.07	110.98	101.75
2	K	401	SFC	O6A-P2A-O5A	-3.06	97.11	109.07
2	J	401	SFC	O8A-P3B-O9A	3.01	122.48	110.68
2	L	401	SFC	O4A-P2A-O5A	3.01	127.12	112.24
2	L	401	SFC	CDP-CBP-CAP	2.98	113.98	108.82
2	F	401	SFC	O4A-P2A-O5A	2.96	126.89	112.24
2	F	401	SFC	CEP-CBP-CAP	2.92	113.89	108.82
2	L	401	SFC	CDP-CBP-CCP	-2.91	103.48	108.23
2	I	401	SFC	C3-C2-C1	2.87	116.09	109.90
2	I	401	SFC	O4A-P2A-O5A	2.86	126.36	112.24
2	J	401	SFC	C3-C2-C1	2.85	116.04	109.90
2	J	401	SFC	O7A-P3B-O9A	-2.80	99.71	110.68
2	I	401	SFC	C5A-C6A-N6A	2.79	124.60	120.35
2	C	401	SFC	O8A-P3B-O7A	2.79	118.30	107.64
2	J	401	SFC	O8A-P3B-O3B	-2.79	93.50	105.99
2	K	401	SFC	O4A-P2A-O5A	2.78	125.98	112.24
2	C	401	SFC	CEP-CBP-CAP	2.74	113.56	108.82
2	H	401	SFC	CDP-CBP-CCP	2.71	112.66	108.23
2	G	401	SFC	C5A-C6A-N6A	2.69	124.44	120.35
2	F	401	SFC	CEP-CBP-CCP	-2.69	103.85	108.23
2	H	401	SFC	C7P-C6P-C5P	2.61	116.71	112.36
2	A	401	SFC	CEP-CBP-CAP	2.60	113.34	108.82
2	B	401	SFC	C3-C2-C1	2.59	115.48	109.90
2	H	401	SFC	O4B-C1B-C2B	-2.58	103.15	106.93
2	F	401	SFC	O2B-C2B-C3B	2.58	118.48	111.17
2	F	401	SFC	C5A-C6A-N6A	2.57	124.25	120.35
2	E	401	SFC	O2B-C2B-C3B	2.54	118.37	111.17
2	E	401	SFC	C5A-C6A-N6A	2.53	124.20	120.35
2	H	401	SFC	C5A-C6A-N6A	2.50	124.15	120.35
2	H	401	SFC	P2A-O3A-P1A	2.41	141.11	132.83
2	L	401	SFC	C5A-C6A-N6A	2.39	123.98	120.35
2	K	401	SFC	C13-C2-C3	2.38	118.62	112.92
2	J	401	SFC	C5A-C6A-N6A	2.37	123.95	120.35
2	I	401	SFC	O8A-P3B-O7A	2.34	116.57	107.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	SFC	C2-C1-S1P	2.33	114.35	111.81
2	J	401	SFC	O1-C1-C2	-2.33	120.38	124.12
2	C	401	SFC	C5A-C6A-N6A	2.32	123.88	120.35
2	L	401	SFC	C2-C1-S1P	2.32	114.33	111.81
2	K	401	SFC	C5A-C6A-N6A	2.31	123.87	120.35
2	F	401	SFC	O8A-P3B-O9A	-2.31	101.63	110.68
2	A	401	SFC	C5A-C6A-N6A	2.30	123.84	120.35
2	G	401	SFC	O1-C1-S1P	-2.29	120.72	123.80
2	K	401	SFC	O1-C1-C2	-2.27	120.47	124.12
2	L	401	SFC	O6A-P2A-O5A	-2.27	100.20	109.07
2	C	401	SFC	O7A-P3B-O3B	-2.26	95.87	105.99
2	C	401	SFC	O4A-P2A-O5A	2.25	123.36	112.24
2	C	401	SFC	OAP-CAP-CBP	2.23	115.50	110.25
2	D	401	SFC	CEP-CBP-CCP	2.22	111.86	108.23
2	L	401	SFC	O3B-P3B-O9A	-2.21	100.88	109.39
2	D	401	SFC	C3P-N4P-C5P	-2.20	118.76	122.84
2	L	401	SFC	O1-C1-C2	-2.20	120.59	124.12
2	C	401	SFC	CDP-CBP-CCP	2.19	111.80	108.23
2	H	401	SFC	O6A-CCP-CBP	2.16	114.02	110.55
2	G	401	SFC	O1-C1-C2	-2.16	120.65	124.12
2	K	401	SFC	O3B-C3B-C2B	-2.16	103.87	111.68
2	I	401	SFC	O3B-P3B-O9A	-2.13	101.15	109.39
2	B	401	SFC	O8A-P3B-O9A	2.13	119.01	110.68
2	J	401	SFC	O4A-P2A-O5A	2.11	122.69	112.24
2	I	401	SFC	CEP-CBP-CCP	2.11	111.67	108.23
2	I	401	SFC	O4A-P2A-O6A	-2.09	98.03	107.75
2	D	401	SFC	C5A-C6A-N6A	2.07	123.49	120.35
2	B	401	SFC	O4A-P2A-O5A	2.05	122.39	112.24
2	F	401	SFC	O1-C1-S1P	-2.04	121.05	123.80
2	L	401	SFC	O8A-P3B-O9A	2.04	118.67	110.68
2	C	401	SFC	O8A-P3B-O3B	2.04	115.13	105.99
2	F	401	SFC	O7A-P3B-O3B	-2.03	96.89	105.99
2	K	401	SFC	C3-C2-C1	2.03	114.27	109.90
2	B	401	SFC	O2B-C2B-C3B	2.01	116.87	111.17
2	D	401	SFC	O3B-P3B-O9A	-2.01	101.64	109.39

There are no chirality outliers.

All (168) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	SFC	CCP-O6A-P2A-O4A
2	A	401	SFC	C9P-CAP-CBP-CCP

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Mol	Chain	Res	Type	Atoms
2	A	401	SFC	C9P-CAP-CBP-CDP
2	A	401	SFC	C9P-CAP-CBP-CEP
2	A	401	SFC	C5P-C6P-C7P-N8P
2	B	401	SFC	S1P-C1-C2-C3
2	B	401	SFC	O1-C1-C2-C3
2	B	401	SFC	C12-C10-C9-C7
2	C	401	SFC	C3B-O3B-P3B-O9A
2	C	401	SFC	CCP-O6A-P2A-O4A
2	C	401	SFC	CCP-O6A-P2A-O5A
2	C	401	SFC	C9P-CAP-CBP-CCP
2	C	401	SFC	C9P-CAP-CBP-CDP
2	C	401	SFC	C9P-CAP-CBP-CEP
2	C	401	SFC	S1P-C1-C2-C3
2	C	401	SFC	O1-C1-C2-C3
2	C	401	SFC	C11-C10-C9-C7
2	D	401	SFC	C3B-C4B-C5B-O5B
2	D	401	SFC	O4B-C4B-C5B-O5B
2	D	401	SFC	C5B-O5B-P1A-O2A
2	D	401	SFC	C5P-C6P-C7P-N8P
2	D	401	SFC	S1P-C1-C2-C3
2	D	401	SFC	O1-C1-C2-C3
2	D	401	SFC	C12-C10-C9-C7
2	E	401	SFC	C5B-O5B-P1A-O2A
2	E	401	SFC	CCP-O6A-P2A-O4A
2	E	401	SFC	CCP-O6A-P2A-O5A
2	E	401	SFC	C9P-CAP-CBP-CCP
2	E	401	SFC	C9P-CAP-CBP-CDP
2	E	401	SFC	C9P-CAP-CBP-CEP
2	E	401	SFC	C5P-C6P-C7P-N8P
2	E	401	SFC	C2P-C3P-N4P-C5P
2	E	401	SFC	C3P-C2P-S1P-C1
2	E	401	SFC	O1-C1-S1P-C2P
2	E	401	SFC	C2-C1-S1P-C2P
2	E	401	SFC	C12-C10-C9-C7
2	F	401	SFC	CCP-O6A-P2A-O5A
2	F	401	SFC	OAP-CAP-CBP-CCP
2	F	401	SFC	C9P-CAP-CBP-CCP
2	F	401	SFC	OAP-CAP-CBP-CDP
2	F	401	SFC	C9P-CAP-CBP-CDP
2	F	401	SFC	C9P-CAP-CBP-CEP
2	H	401	SFC	CCP-O6A-P2A-O4A
2	H	401	SFC	CCP-O6A-P2A-O5A

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Mol	Chain	Res	Type	Atoms
2	H	401	SFC	C9P-CAP-CBP-CCP
2	H	401	SFC	C9P-CAP-CBP-CEP
2	H	401	SFC	C5P-C6P-C7P-N8P
2	H	401	SFC	C2P-C3P-N4P-C5P
2	H	401	SFC	C2-C1-S1P-C2P
2	H	401	SFC	S1P-C1-C2-C3
2	H	401	SFC	O1-C1-C2-C3
2	I	401	SFC	S1P-C1-C2-C3
2	I	401	SFC	O1-C1-C2-C3
2	I	401	SFC	C12-C10-C9-C7
2	J	401	SFC	C12-C10-C9-C7
2	K	401	SFC	C5P-C6P-C7P-N8P
2	K	401	SFC	S1P-C1-C2-C3
2	K	401	SFC	C11-C10-C9-C7
2	L	401	SFC	C3B-O3B-P3B-O9A
2	L	401	SFC	C3B-O3B-P3B-O8A
2	L	401	SFC	C5B-O5B-P1A-O2A
2	L	401	SFC	C5B-O5B-P1A-O3A
2	L	401	SFC	CCP-O6A-P2A-O3A
2	L	401	SFC	C9P-CAP-CBP-CCP
2	L	401	SFC	C9P-CAP-CBP-CDP
2	L	401	SFC	C9P-CAP-CBP-CEP
2	L	401	SFC	C11-C10-C9-C7
2	A	401	SFC	C11-C10-C9-C7
2	C	401	SFC	C12-C10-C9-C7
2	C	401	SFC	C4B-C3B-O3B-P3B
2	B	401	SFC	C11-C10-C9-C7
2	D	401	SFC	C11-C10-C9-C7
2	E	401	SFC	C11-C10-C9-C7
2	I	401	SFC	C11-C10-C9-C7
2	J	401	SFC	C11-C10-C9-C7
2	K	401	SFC	C12-C10-C9-C7
2	L	401	SFC	C12-C10-C9-C7
2	C	401	SFC	C2B-C3B-O3B-P3B
2	A	401	SFC	C12-C10-C9-C7
2	K	401	SFC	O1-C1-C2-C3
2	L	401	SFC	O4B-C4B-C5B-O5B
2	B	401	SFC	C5P-C6P-C7P-N8P
2	C	401	SFC	C5P-C6P-C7P-N8P
2	G	401	SFC	C5P-C6P-C7P-N8P
2	I	401	SFC	C5P-C6P-C7P-N8P
2	J	401	SFC	C5P-C6P-C7P-N8P

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Mol	Chain	Res	Type	Atoms
2	F	401	SFC	C2-C1-S1P-C2P
2	G	401	SFC	C2-C1-S1P-C2P
2	I	401	SFC	C2-C1-S1P-C2P
2	J	401	SFC	C2-C1-S1P-C2P
2	L	401	SFC	C2-C1-S1P-C2P
2	A	401	SFC	OAP-CAP-CBP-CDP
2	A	401	SFC	OAP-CAP-CBP-CEP
2	C	401	SFC	OAP-CAP-CBP-CDP
2	C	401	SFC	OAP-CAP-CBP-CEP
2	E	401	SFC	OAP-CAP-CBP-CDP
2	E	401	SFC	OAP-CAP-CBP-CEP
2	F	401	SFC	OAP-CAP-CBP-CEP
2	H	401	SFC	OAP-CAP-CBP-CEP
2	L	401	SFC	OAP-CAP-CBP-CDP
2	L	401	SFC	OAP-CAP-CBP-CEP
2	I	401	SFC	C3B-O3B-P3B-O9A
2	A	401	SFC	CCP-O6A-P2A-O3A
2	J	401	SFC	C5B-O5B-P1A-O3A
2	A	401	SFC	CCP-O6A-P2A-O5A
2	F	401	SFC	CCP-O6A-P2A-O4A
2	L	401	SFC	CCP-O6A-P2A-O5A
2	H	401	SFC	O1-C1-S1P-C2P
2	A	401	SFC	C2-C1-S1P-C2P
2	A	401	SFC	OAP-CAP-CBP-CCP
2	C	401	SFC	OAP-CAP-CBP-CCP
2	E	401	SFC	OAP-CAP-CBP-CCP
2	H	401	SFC	OAP-CAP-CBP-CCP
2	L	401	SFC	OAP-CAP-CBP-CCP
2	A	401	SFC	O1-C1-C2-C3
2	E	401	SFC	O1-C1-C2-C3
2	F	401	SFC	O1-C1-C2-C3
2	G	401	SFC	O1-C1-C2-C3
2	J	401	SFC	O1-C1-C2-C3
2	L	401	SFC	O1-C1-C2-C3
2	B	401	SFC	O4B-C4B-C5B-O5B
2	F	401	SFC	CEP-CBP-CCP-O6A
2	D	401	SFC	P1A-O3A-P2A-O4A
2	J	401	SFC	P2A-O3A-P1A-O1A
2	H	401	SFC	O4B-C4B-C5B-O5B
2	I	401	SFC	O4B-C4B-C5B-O5B
2	E	401	SFC	S1P-C2P-C3P-N4P
2	B	401	SFC	CDP-CBP-CCP-O6A

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Mol	Chain	Res	Type	Atoms
2	F	401	SFC	CDP-CBP-CCP-O6A
2	H	401	SFC	N8P-C9P-CAP-CBP
2	A	401	SFC	S1P-C1-C2-C3
2	E	401	SFC	S1P-C1-C2-C3
2	F	401	SFC	S1P-C1-C2-C3
2	G	401	SFC	S1P-C1-C2-C3
2	J	401	SFC	S1P-C1-C2-C3
2	L	401	SFC	S1P-C1-C2-C3
2	K	401	SFC	C2-C1-S1P-C2P
2	E	401	SFC	P1A-O3A-P2A-O5A
2	G	401	SFC	C3B-O3B-P3B-O9A
2	F	401	SFC	C5P-C6P-C7P-N8P
2	L	401	SFC	C5P-C6P-C7P-N8P
2	H	401	SFC	C9P-CAP-CBP-CDP
2	B	401	SFC	C5B-O5B-P1A-O3A
2	C	401	SFC	CCP-O6A-P2A-O3A
2	E	401	SFC	CCP-O6A-P2A-O3A
2	F	401	SFC	CCP-O6A-P2A-O3A
2	H	401	SFC	CCP-O6A-P2A-O3A
2	H	401	SFC	OAP-CAP-CBP-CDP
2	I	401	SFC	C5B-O5B-P1A-O3A
2	G	401	SFC	O4B-C4B-C5B-O5B
2	K	401	SFC	O4B-C4B-C5B-O5B
2	E	401	SFC	P2A-O3A-P1A-O1A
2	E	401	SFC	P2A-O3A-P1A-O2A
2	E	401	SFC	P1A-O3A-P2A-O4A
2	F	401	SFC	P2A-O3A-P1A-O1A
2	G	401	SFC	P2A-O3A-P1A-O1A
2	G	401	SFC	P2A-O3A-P1A-O2A
2	H	401	SFC	P2A-O3A-P1A-O1A
2	H	401	SFC	P1A-O3A-P2A-O4A
2	J	401	SFC	P2A-O3A-P1A-O2A
2	K	401	SFC	P2A-O3A-P1A-O1A
2	J	401	SFC	C5B-O5B-P1A-O2A
2	A	401	SFC	O4B-C4B-C5B-O5B
2	C	401	SFC	O4B-C4B-C5B-O5B
2	E	401	SFC	O4B-C4B-C5B-O5B
2	F	401	SFC	O4B-C4B-C5B-O5B
2	J	401	SFC	O4B-C4B-C5B-O5B
2	H	401	SFC	O9P-C9P-CAP-CBP

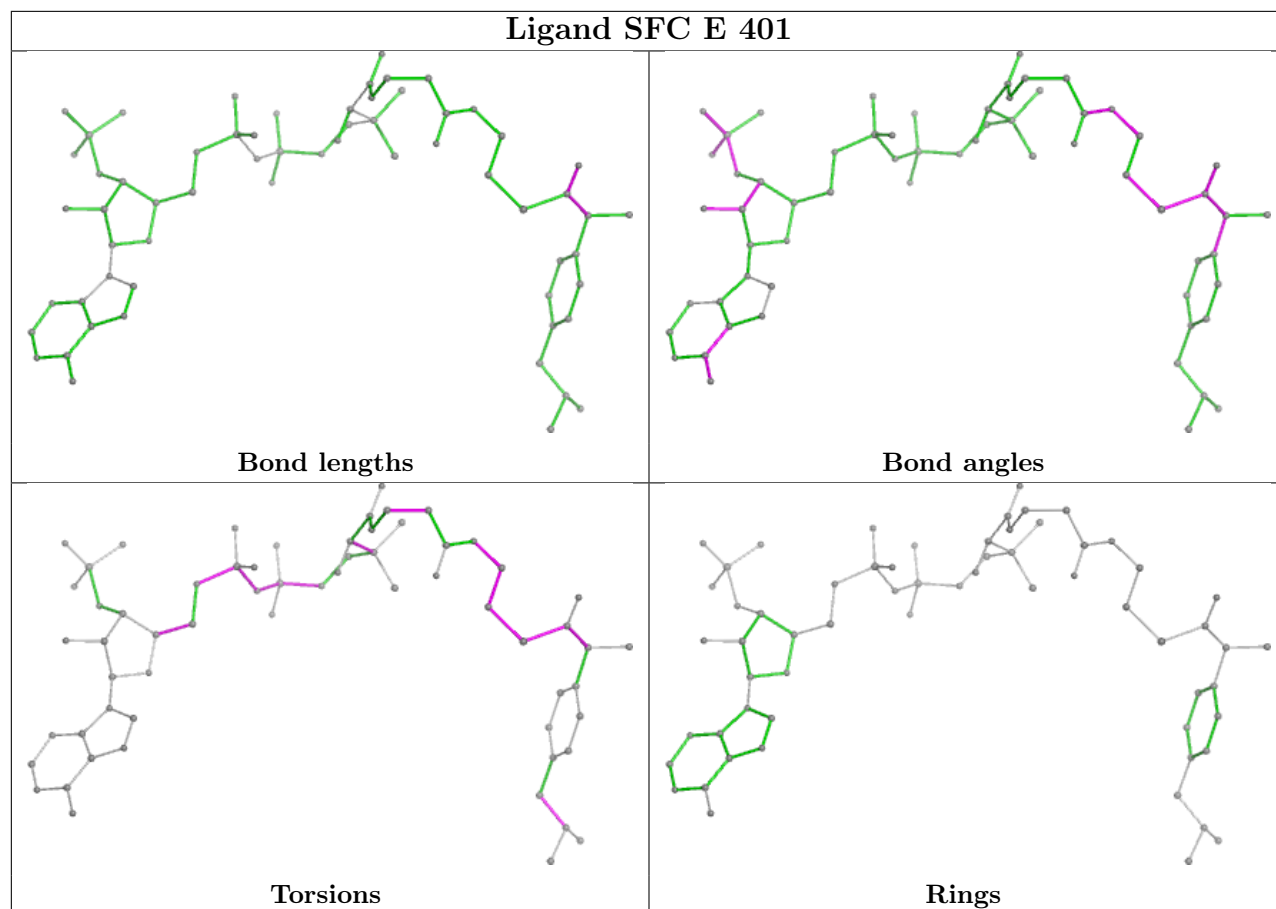
There are no ring outliers.

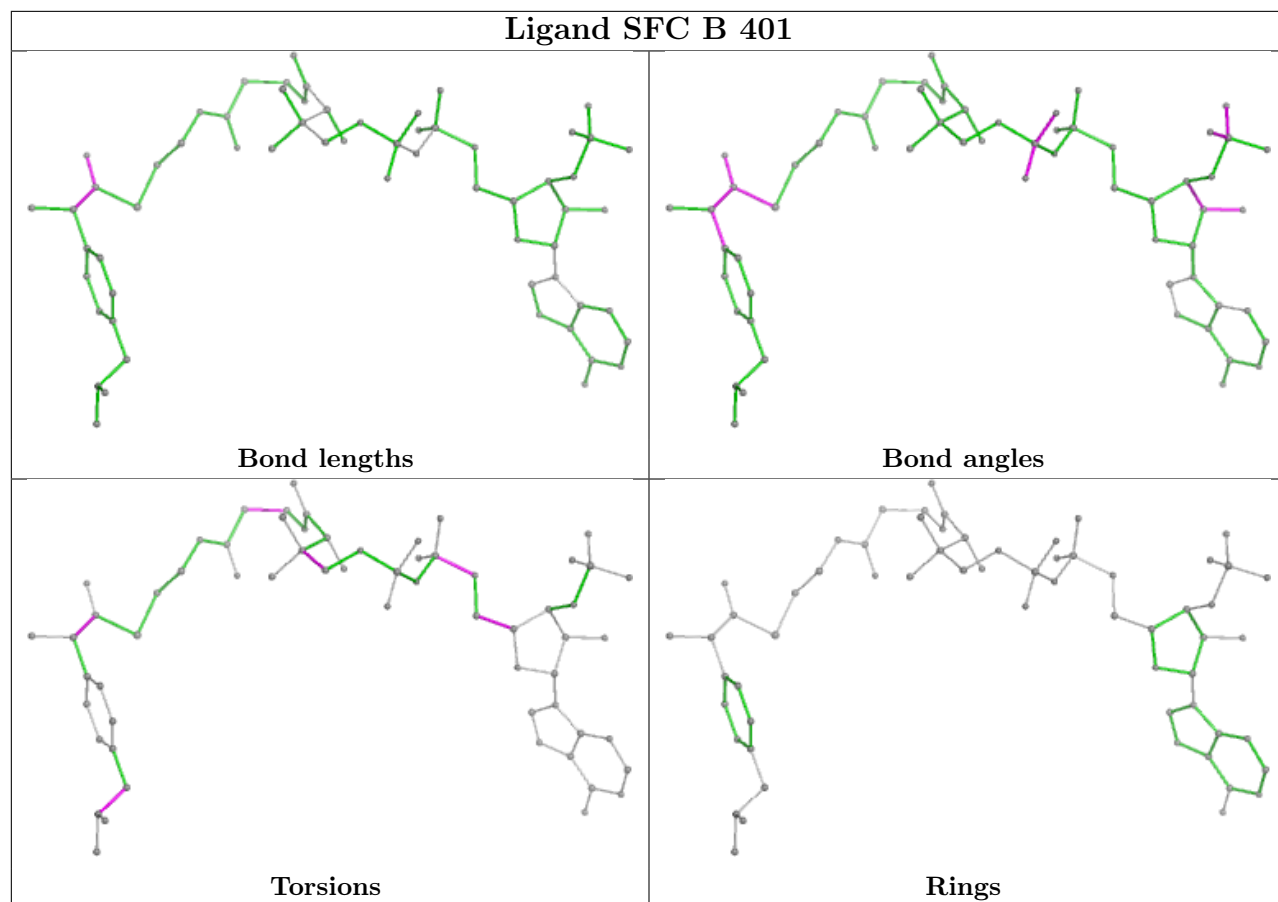
9 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	401	SFC	2	0
2	C	401	SFC	1	0
2	D	401	SFC	2	0
2	A	401	SFC	6	0
2	H	401	SFC	1	0
2	J	401	SFC	3	0
2	L	401	SFC	2	0
2	F	401	SFC	5	0
2	I	401	SFC	1	0

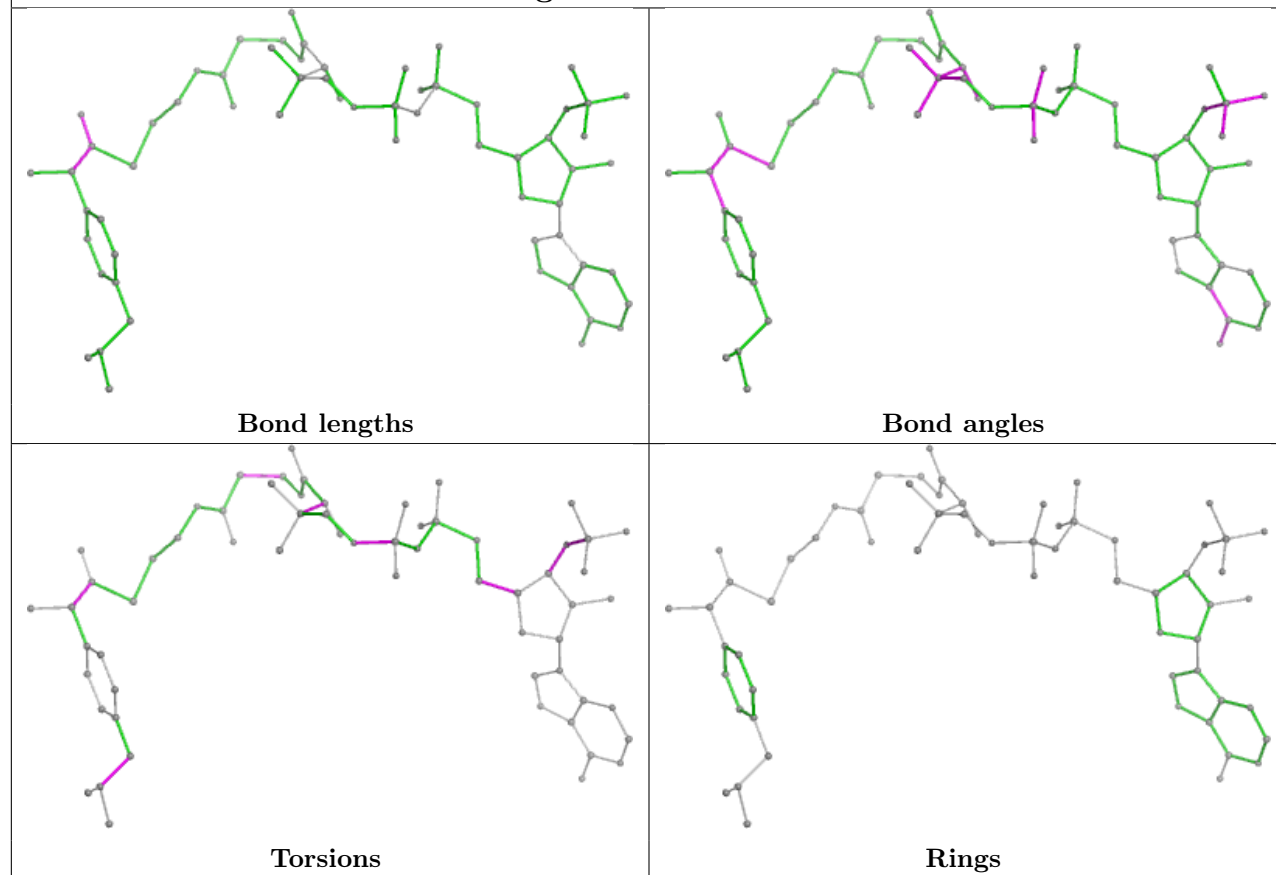
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



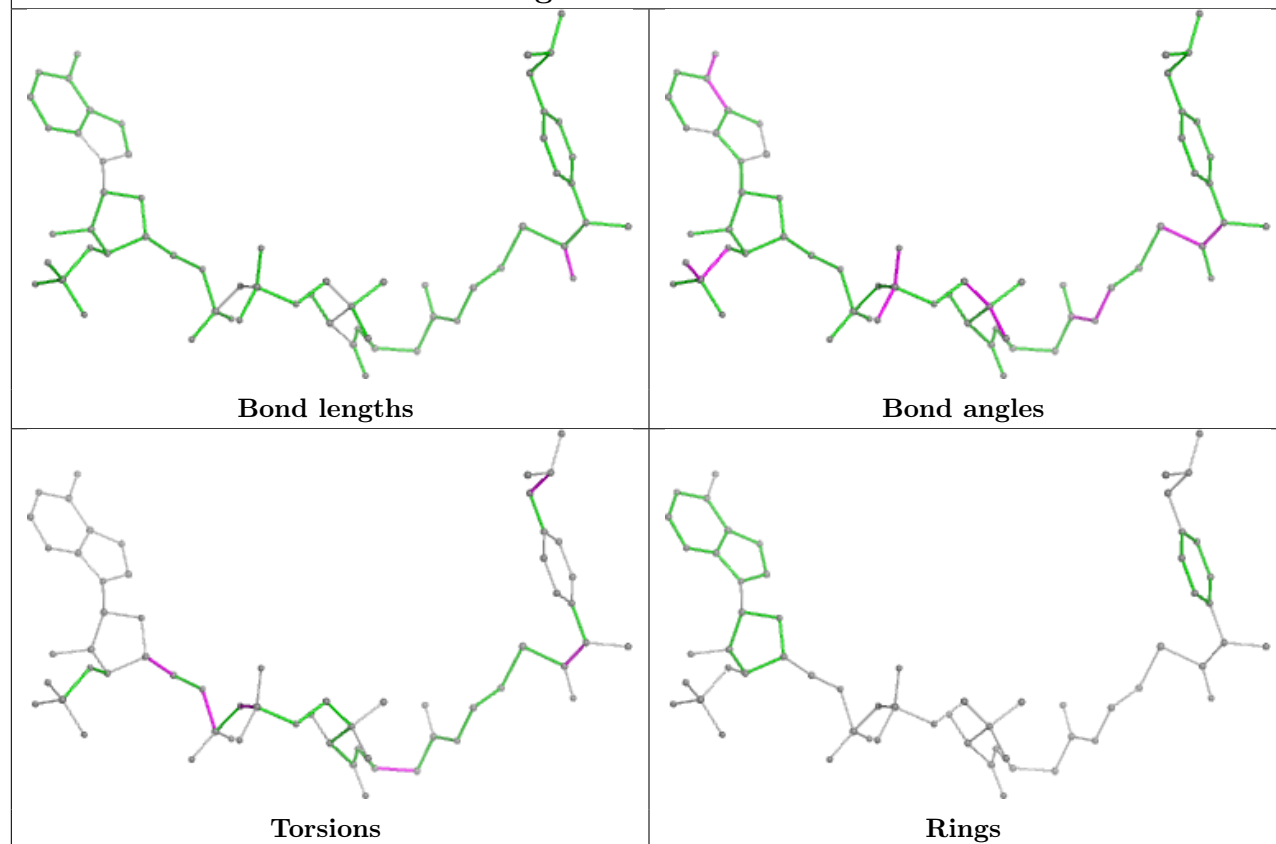




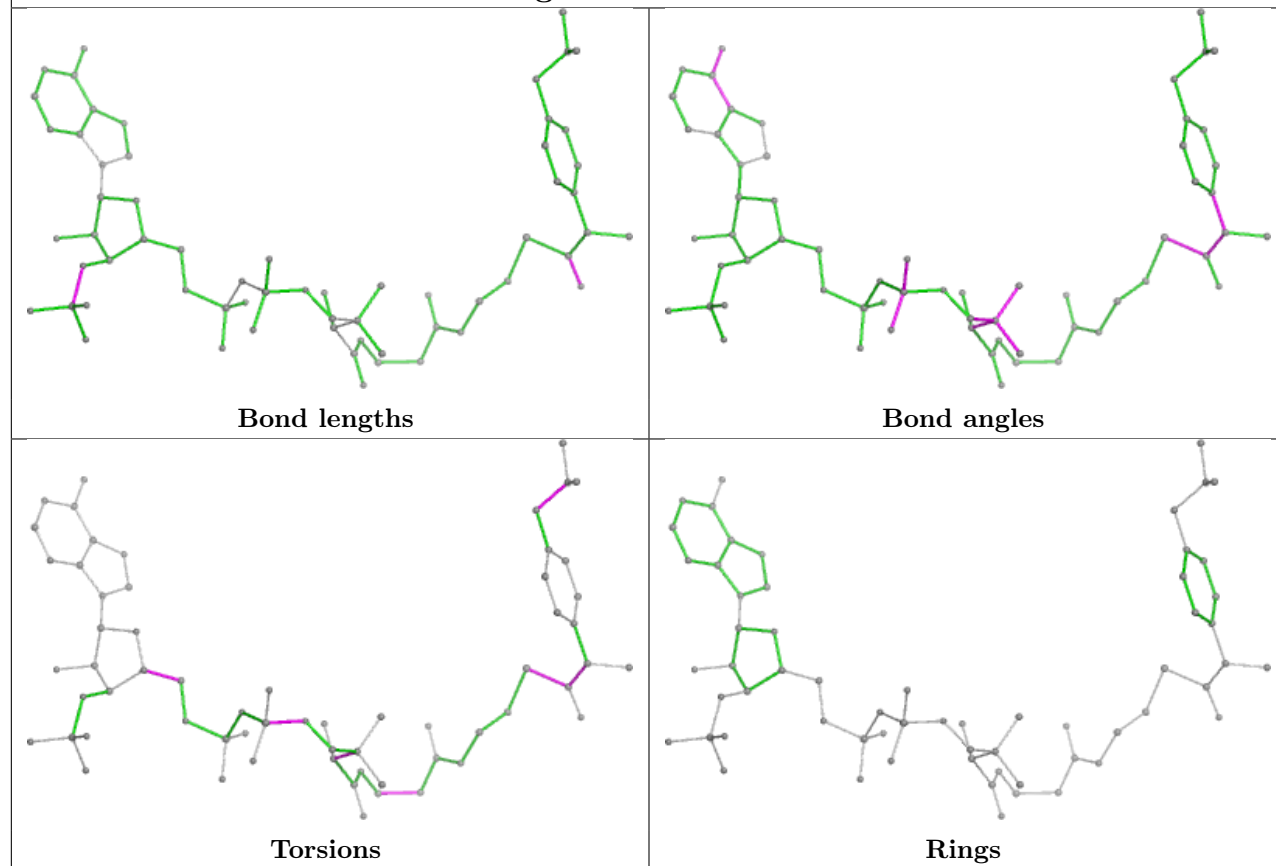
## Ligand SFC C 401



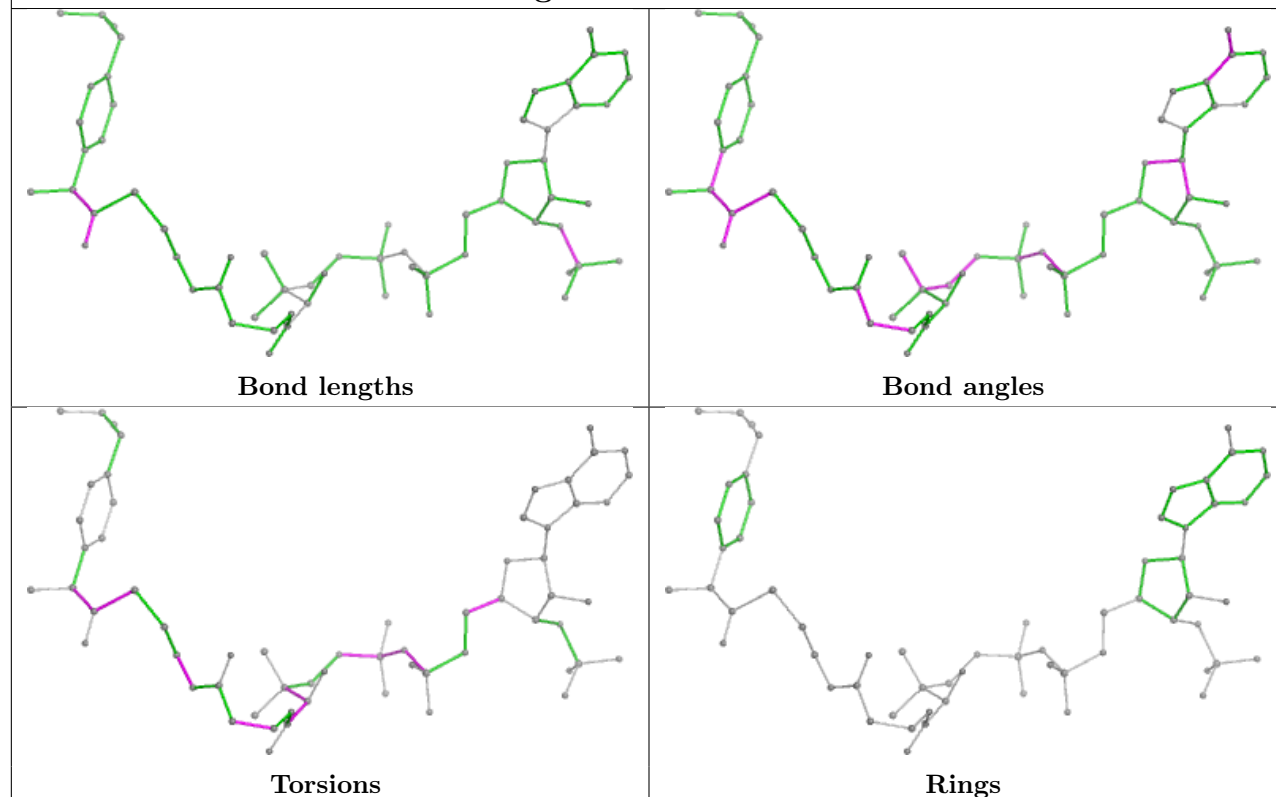
## Ligand SFC D 401



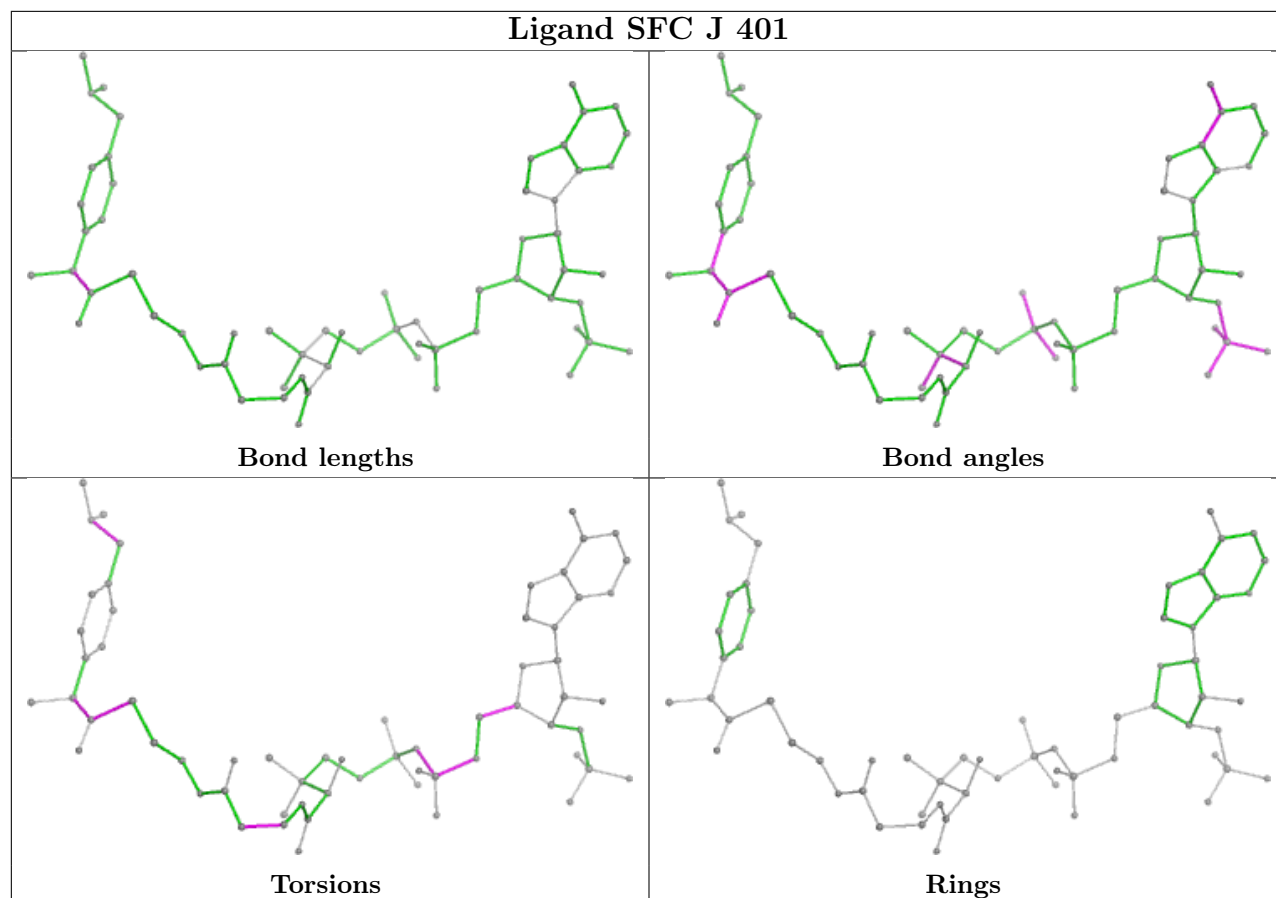
## Ligand SFC A 401



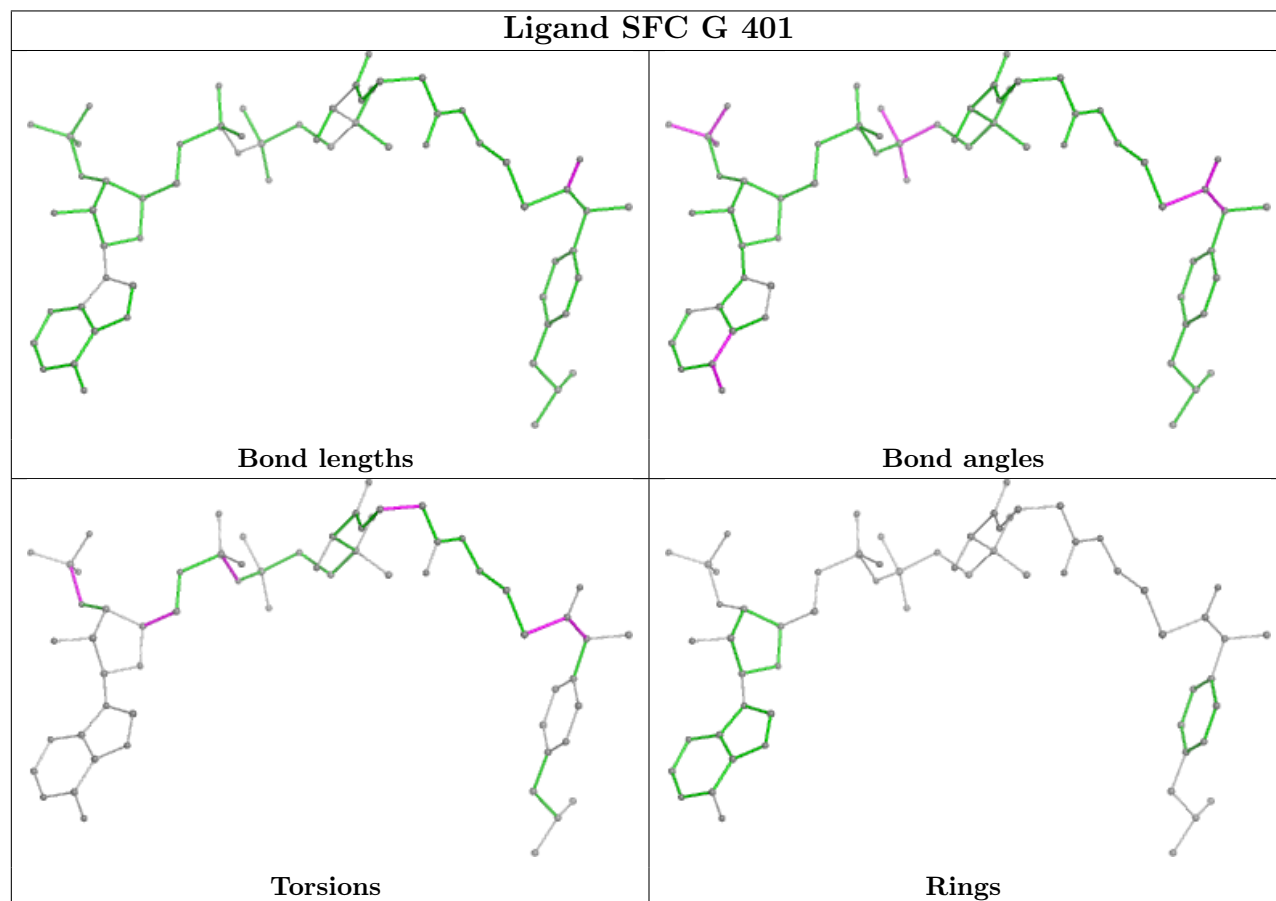
## Ligand SFC H 401



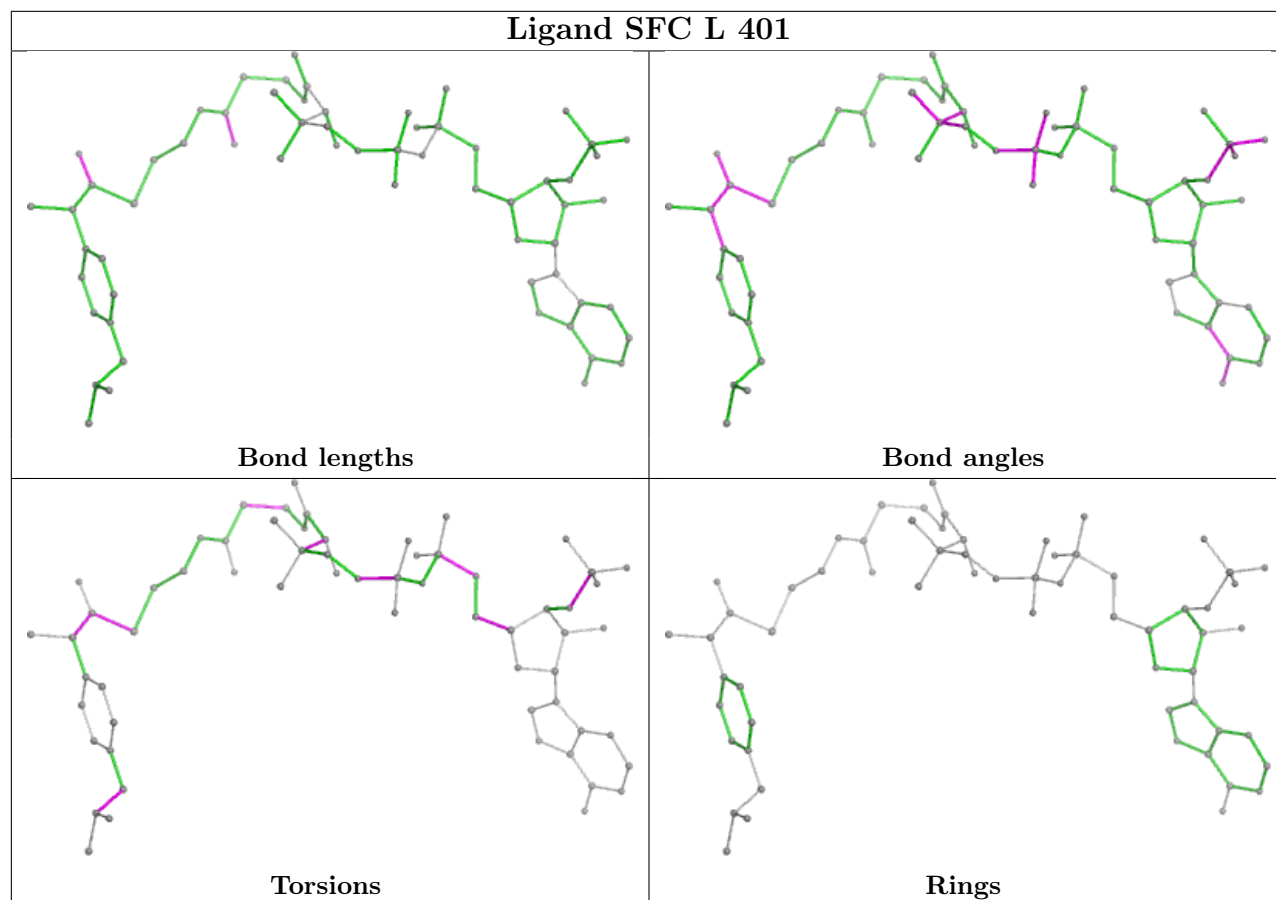
## Ligand SFC J 401



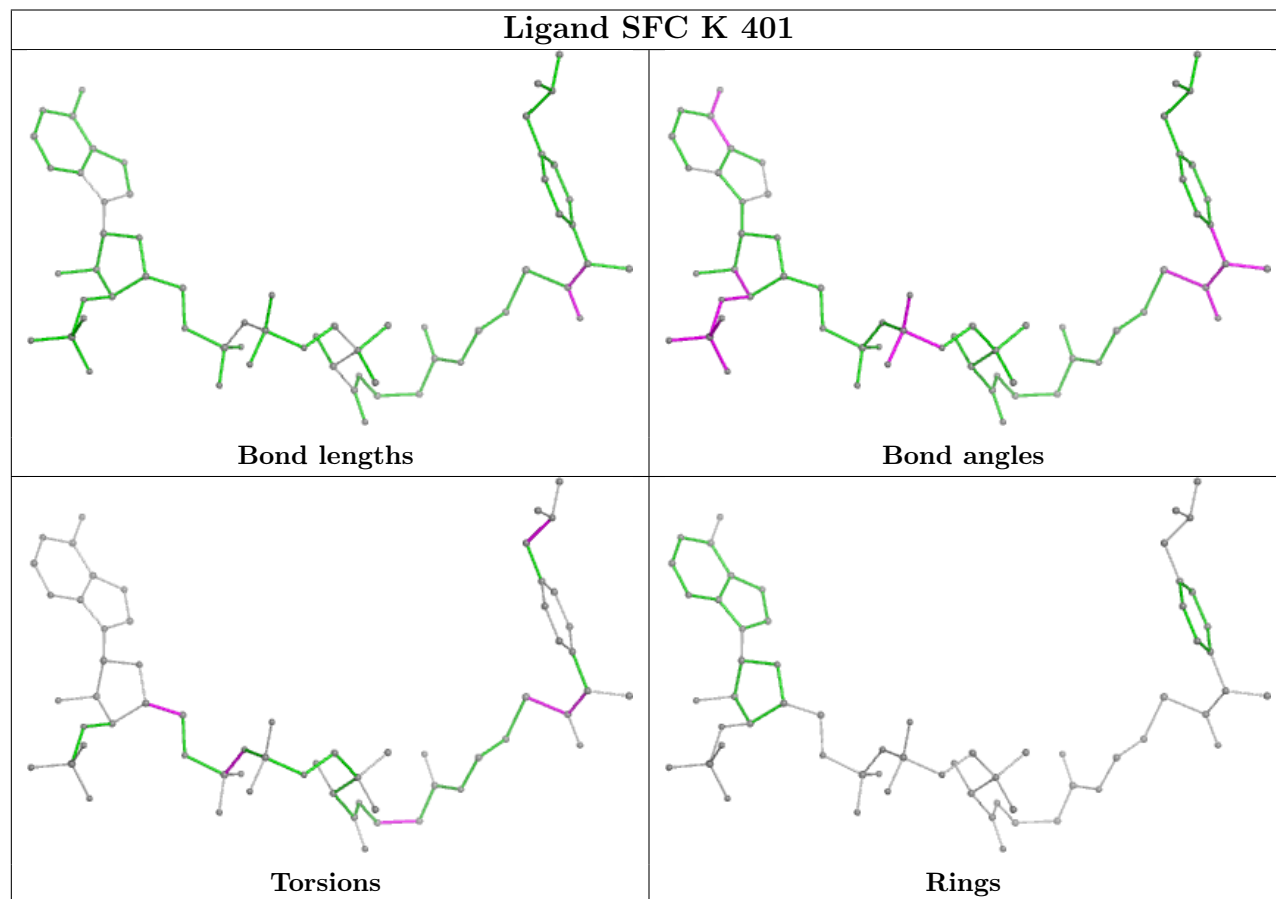
## Ligand SFC G 401

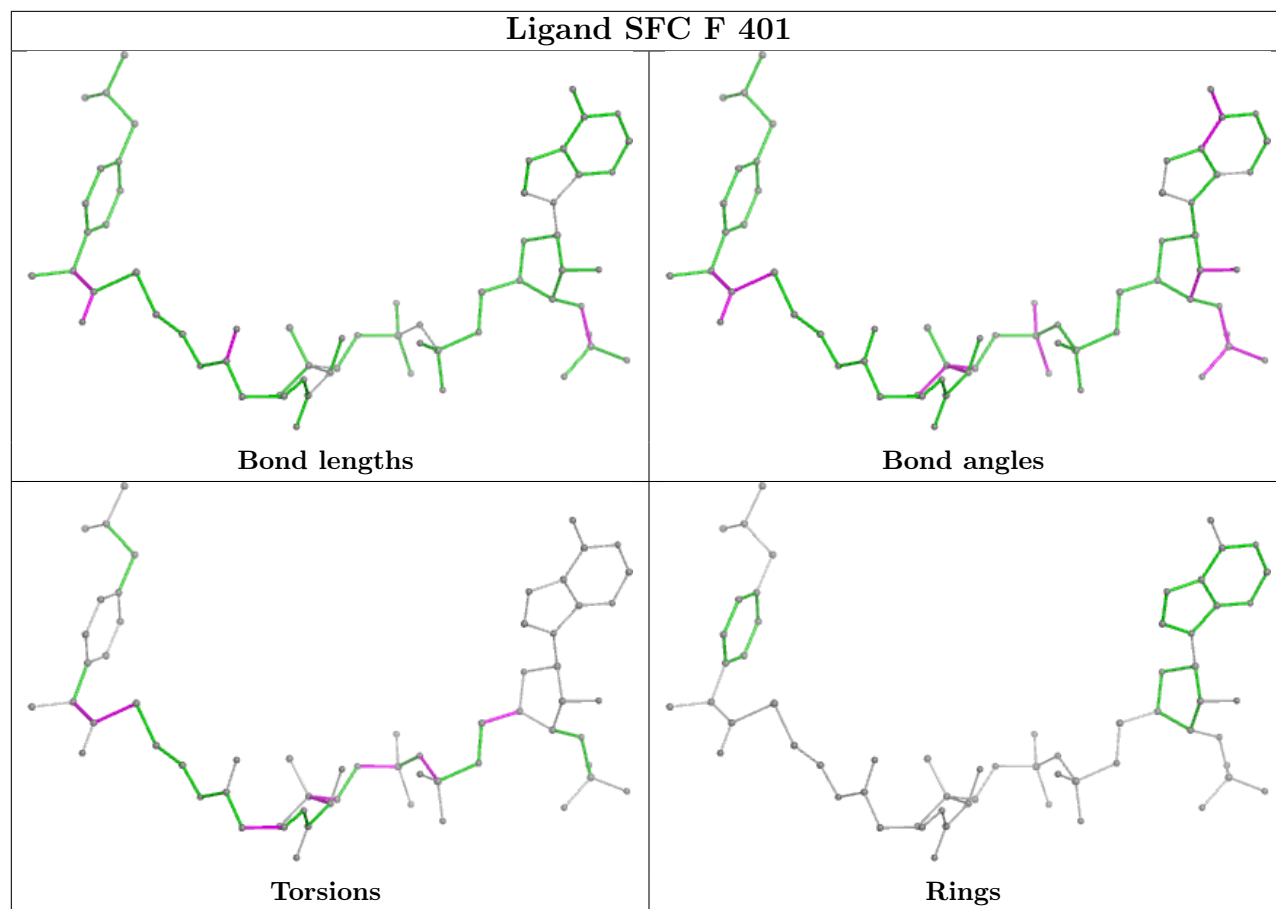


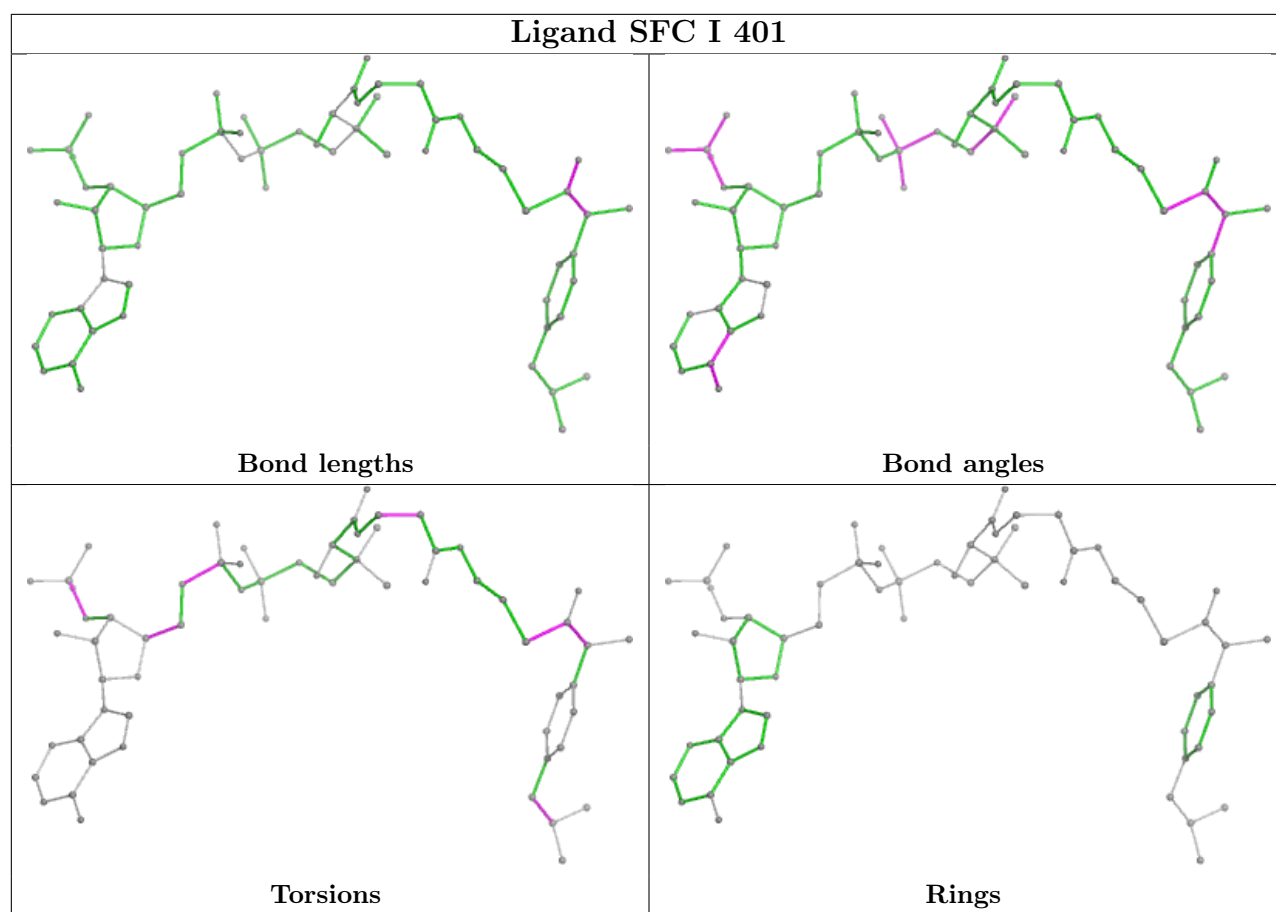
## Ligand SFC L 401



## Ligand SFC K 401







## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	357/364 (98%)	0.71	66 (18%) <b>4</b> <b>4</b>	27, 45, 93, 124	2 (0%)
1	B	354/364 (97%)	0.51	41 (11%) <b>11</b> <b>10</b>	22, 43, 90, 129	3 (0%)
1	C	357/364 (98%)	0.54	36 (10%) <b>14</b> <b>13</b>	26, 44, 91, 134	2 (0%)
1	D	358/364 (98%)	0.66	53 (14%) <b>7</b> <b>6</b>	26, 44, 94, 140	2 (0%)
1	E	355/364 (97%)	0.68	57 (16%) <b>5</b> <b>5</b>	28, 45, 94, 126	2 (0%)
1	F	357/364 (98%)	0.78	58 (16%) <b>5</b> <b>5</b>	28, 47, 95, 150	1 (0%)
1	G	357/364 (98%)	1.02	91 (25%) <b>2</b> <b>2</b>	27, 48, 103, 142	2 (0%)
1	H	356/364 (97%)	0.82	77 (21%) <b>3</b> <b>3</b>	26, 47, 99, 125	2 (0%)
1	I	358/364 (98%)	0.54	41 (11%) <b>11</b> <b>10</b>	28, 43, 89, 135	1 (0%)
1	J	357/364 (98%)	0.45	28 (7%) <b>20</b> <b>20</b>	17, 42, 86, 121	2 (0%)
1	K	355/364 (97%)	0.53	35 (9%) <b>14</b> <b>14</b>	22, 44, 90, 120	3 (0%)
1	L	358/364 (98%)	0.70	61 (17%) <b>5</b> <b>5</b>	27, 45, 94, 122	2 (0%)
All	All	4279/4368 (97%)	0.66	644 (15%) <b>6</b> <b>6</b>	17, 45, 94, 150	24 (0%)

All (644) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	42	VAL	9.4
1	D	42	VAL	8.4
1	J	346	ALA	8.2
1	D	45	ILE	7.7
1	H	45	ILE	7.7
1	L	45	ILE	7.7
1	A	346	ALA	7.2
1	H	346	ALA	7.0
1	L	180	LYS	6.9
1	I	45	ILE	6.6
1	E	349	ILE	6.4

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Mol	Chain	Res	Type	RSRZ
1	A	45	ILE	6.3
1	H	39	PRO	6.2
1	B	346	ALA	6.1
1	D	346	ALA	6.0
1	K	346	ALA	5.9
1	F	42	VAL	5.9
1	I	346	ALA	5.8
1	G	45	ILE	5.8
1	C	346	ALA	5.8
1	H	355	LEU	5.8
1	E	45	ILE	5.7
1	G	346	ALA	5.5
1	J	45	ILE	5.5
1	F	346	ALA	5.4
1	K	324	GLY	5.3
1	D	348	THR	5.1
1	K	347	ALA	5.1
1	J	351	ILE	5.0
1	H	44	GLY	5.0
1	F	46	SER	5.0
1	I	42	VAL	5.0
1	I	349	ILE	4.9
1	E	346	ALA	4.9
1	G	347	ALA	4.9
1	J	347	ALA	4.9
1	F	347	ALA	4.9
1	G	349	ILE	4.9
1	B	347	ALA	4.9
1	C	349	ILE	4.9
1	G	355	LEU	4.9
1	C	45	ILE	4.8
1	D	347	ALA	4.8
1	E	39	PRO	4.8
1	I	47	ARG	4.8
1	J	324	GLY	4.8
1	H	34	VAL	4.8
1	B	40	SER	4.8
1	C	41	SER	4.8
1	F	349	ILE	4.7
1	G	44	GLY	4.7
1	L	349	ILE	4.7
1	B	46	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	D	324	GLY	4.6
1	G	179	GLY	4.6
1	F	323	ASN	4.6
1	K	349	ILE	4.5
1	F	49	ALA	4.5
1	L	324	GLY	4.5
1	G	102	VAL	4.5
1	K	180	LYS	4.4
1	D	351	ILE	4.4
1	C	324	GLY	4.4
1	G	324	GLY	4.4
1	H	72	LYS	4.4
1	E	40	SER	4.3
1	G	46	SER	4.3
1	G	351	ILE	4.3
1	G	10	VAL	4.3
1	G	34	VAL	4.3
1	F	101	LYS	4.3
1	G	348	THR	4.3
1	A	180	LYS	4.2
1	G	72	LYS	4.2
1	H	57	VAL	4.2
1	I	323	ASN	4.2
1	H	58	THR	4.2
1	J	323	ASN	4.2
1	B	47	ARG	4.2
1	J	345	PRO	4.2
1	F	47	ARG	4.1
1	B	349	ILE	4.1
1	K	41	SER	4.1
1	G	359	ASP	4.1
1	A	351	ILE	4.1
1	I	180	LYS	4.1
1	D	349	ILE	4.1
1	F	351	ILE	4.1
1	F	324	GLY	4.1
1	K	49	ALA	4.1
1	I	359	ASP	4.1
1	A	345	PRO	4.0
1	C	347	ALA	4.0
1	G	49	ALA	4.0
1	C	44	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	I	324	GLY	4.0
1	G	79	VAL	4.0
1	C	176	GLN	4.0
1	G	41	SER	3.9
1	B	359	ASP	3.9
1	G	101	LYS	3.9
1	I	41	SER	3.9
1	E	324	GLY	3.9
1	H	324	GLY	3.9
1	K	359	ASP	3.9
1	C	323	ASN	3.9
1	G	11	VAL	3.9
1	B	351	ILE	3.8
1	I	351	ILE	3.8
1	A	62	LYS	3.8
1	K	348	THR	3.8
1	A	101	LYS	3.8
1	L	43	ASP	3.8
1	E	355	LEU	3.8
1	L	46	SER	3.8
1	H	40	SER	3.8
1	F	355	LEU	3.8
1	F	348	THR	3.8
1	J	44	GLY	3.8
1	J	349	ILE	3.8
1	H	358	TRP	3.8
1	G	66	GLY	3.7
1	L	346	ALA	3.7
1	E	351	ILE	3.7
1	L	351	ILE	3.7
1	A	76	LYS	3.7
1	G	353	ALA	3.7
1	H	2	ALA	3.7
1	F	345	PRO	3.7
1	A	56	ILE	3.7
1	G	56	ILE	3.7
1	H	351	ILE	3.7
1	C	207	MET	3.7
1	D	323	ASN	3.7
1	A	355	LEU	3.7
1	F	76	LYS	3.7
1	G	180	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	49	ALA	3.7
1	G	292	ALA	3.7
1	G	1	MET	3.7
1	G	358	TRP	3.7
1	L	348	THR	3.7
1	H	59	ALA	3.7
1	L	353	ALA	3.7
1	A	41	SER	3.6
1	B	76	LYS	3.6
1	B	7	GLY	3.6
1	H	7	GLY	3.6
1	G	58	THR	3.6
1	E	1	MET	3.6
1	H	180	LYS	3.6
1	A	349	ILE	3.6
1	D	47	ARG	3.6
1	C	345	PRO	3.6
1	H	105	ARG	3.6
1	E	66	GLY	3.6
1	A	69	LEU	3.6
1	H	8	LEU	3.6
1	D	43	ASP	3.6
1	A	58	THR	3.6
1	L	347	ALA	3.6
1	J	72	LYS	3.6
1	B	356	THR	3.5
1	F	180	LYS	3.5
1	G	354	VAL	3.5
1	G	100	ALA	3.5
1	H	347	ALA	3.5
1	G	345	PRO	3.5
1	H	345	PRO	3.5
1	C	180	LYS	3.5
1	A	47	ARG	3.5
1	G	33	VAL	3.5
1	E	207	MET	3.5
1	E	359	ASP	3.5
1	H	173	TRP	3.5
1	F	322	ALA	3.4
1	B	324	GLY	3.4
1	K	76	LYS	3.4
1	A	347	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	359	ASP	3.4
1	F	48	ASP	3.4
1	F	354	VAL	3.4
1	F	359	ASP	3.4
1	G	48	ASP	3.4
1	H	76	LYS	3.4
1	F	258	GLU	3.4
1	E	47	ARG	3.4
1	G	47	ARG	3.4
1	H	47	ARG	3.4
1	B	358	TRP	3.4
1	E	58	THR	3.4
1	A	66	GLY	3.4
1	B	348	THR	3.4
1	D	56	ILE	3.4
1	G	107	ILE	3.4
1	L	62	LYS	3.4
1	B	350	ASP	3.3
1	F	43	ASP	3.3
1	H	178	SER	3.3
1	L	70	ALA	3.3
1	L	100	ALA	3.3
1	A	93	GLY	3.3
1	F	66	GLY	3.3
1	E	323	ASN	3.3
1	L	42	VAL	3.3
1	B	345	PRO	3.2
1	C	48	ASP	3.2
1	I	144	ASP	3.2
1	A	358	TRP	3.2
1	L	47	ARG	3.2
1	H	16	ILE	3.2
1	A	324	GLY	3.2
1	H	323	ASN	3.2
1	H	145	GLU	3.2
1	I	348	THR	3.2
1	G	73	LEU	3.2
1	H	144	ASP	3.2
1	H	349	ILE	3.2
1	A	72	LYS	3.2
1	E	176	GLN	3.2
1	G	71	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	59	ALA	3.2
1	A	68	GLU	3.2
1	B	1	MET	3.2
1	G	76	LYS	3.2
1	I	1	MET	3.2
1	C	358	TRP	3.1
1	G	69	LEU	3.1
1	H	66	GLY	3.1
1	H	56	ILE	3.1
1	G	7	GLY	3.1
1	G	99	CYS	3.1
1	A	348	THR	3.1
1	G	144	ASP	3.1
1	J	41	SER	3.1
1	J	350	ASP	3.1
1	L	359	ASP	3.1
1	G	352	GLU	3.1
1	H	1	MET	3.1
1	G	94	LEU	3.1
1	B	77	ALA	3.1
1	B	257	ALA	3.1
1	D	1	MET	3.1
1	J	1	MET	3.1
1	E	353	ALA	3.0
1	G	257	ALA	3.0
1	J	49	ALA	3.0
1	C	351	ILE	3.0
1	E	56	ILE	3.0
1	E	350	ASP	3.0
1	K	47	ARG	3.0
1	G	178	SER	3.0
1	A	1	MET	3.0
1	D	102	VAL	3.0
1	K	102	VAL	3.0
1	L	7	GLY	3.0
1	F	59	ALA	3.0
1	F	292	ALA	3.0
1	F	144	ASP	3.0
1	F	350	ASP	3.0
1	D	41	SER	3.0
1	B	30	GLY	3.0
1	G	323	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	65	GLN	3.0
1	F	73	LEU	3.0
1	F	106	LEU	3.0
1	F	176	GLN	3.0
1	L	61	LEU	3.0
1	L	69	LEU	3.0
1	A	173	TRP	3.0
1	E	358	TRP	3.0
1	F	255	ASP	3.0
1	J	144	ASP	3.0
1	A	34	VAL	3.0
1	G	183	VAL	3.0
1	D	355	LEU	3.0
1	E	347	ALA	3.0
1	G	77	ALA	3.0
1	L	75	ALA	3.0
1	B	72	LYS	3.0
1	L	72	LYS	3.0
1	K	50	MET	2.9
1	L	1	MET	2.9
1	A	178	SER	2.9
1	L	173	TRP	2.9
1	I	58	THR	2.9
1	G	57	VAL	2.9
1	L	79	VAL	2.9
1	G	67	LEU	2.9
1	D	107	ILE	2.9
1	E	356	THR	2.9
1	D	76	LYS	2.9
1	D	258	GLU	2.9
1	H	73	LEU	2.9
1	H	353	ALA	2.9
1	H	46	SER	2.9
1	L	30	GLY	2.9
1	C	1	MET	2.9
1	G	106	LEU	2.9
1	H	102	VAL	2.9
1	K	1	MET	2.9
1	G	357	ASP	2.9
1	J	322	ALA	2.9
1	G	63	SER	2.9
1	F	293	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	76	LYS	2.9
1	F	358	TRP	2.8
1	J	48	ASP	2.8
1	E	70	ALA	2.8
1	H	176	GLN	2.8
1	G	177	SER	2.8
1	H	38	ARG	2.8
1	K	351	ILE	2.8
1	I	350	ASP	2.8
1	L	102	VAL	2.8
1	I	347	ALA	2.8
1	C	47	ARG	2.8
1	E	46	SER	2.8
1	B	323	ASN	2.8
1	E	180	LYS	2.8
1	F	62	LYS	2.8
1	G	62	LYS	2.8
1	A	99	CYS	2.8
1	A	207	MET	2.8
1	E	104	ASP	2.8
1	E	173	TRP	2.8
1	G	8	LEU	2.8
1	H	69	LEU	2.8
1	H	106	LEU	2.8
1	A	102	VAL	2.8
1	A	40	SER	2.8
1	B	49	ALA	2.8
1	F	75	ALA	2.8
1	A	97	GLU	2.8
1	I	258	GLU	2.8
1	F	1	MET	2.8
1	H	337	THR	2.8
1	H	37	ASP	2.8
1	H	350	ASP	2.8
1	C	69	LEU	2.8
1	D	69	LEU	2.8
1	E	73	LEU	2.8
1	F	173	TRP	2.8
1	J	76	LYS	2.7
1	A	74	ILE	2.7
1	G	36	ILE	2.7
1	G	74	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	65	GLN	2.7
1	I	345	PRO	2.7
1	K	176	GLN	2.7
1	G	105	ARG	2.7
1	K	350	ASP	2.7
1	A	354	VAL	2.7
1	D	354	VAL	2.7
1	D	322	ALA	2.7
1	E	75	ALA	2.7
1	H	31	ALA	2.7
1	B	207	MET	2.7
1	E	16	ILE	2.7
1	L	101	LYS	2.7
1	F	207	MET	2.7
1	A	77	ALA	2.7
1	A	353	ALA	2.7
1	B	322	ALA	2.7
1	C	173	TRP	2.7
1	I	176	GLN	2.7
1	G	293	ASN	2.7
1	A	49	ALA	2.7
1	C	49	ALA	2.7
1	C	353	ALA	2.7
1	F	11	VAL	2.7
1	G	59	ALA	2.7
1	J	176	GLN	2.7
1	K	358	TRP	2.7
1	D	97	GLU	2.7
1	L	144	ASP	2.7
1	E	69	LEU	2.6
1	G	176	GLN	2.6
1	J	47	ARG	2.6
1	J	325	GLY	2.6
1	I	358	TRP	2.6
1	K	72	LYS	2.6
1	D	345	PRO	2.6
1	K	345	PRO	2.6
1	L	345	PRO	2.6
1	G	207	MET	2.6
1	H	207	MET	2.6
1	C	40	SER	2.6
1	C	66	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	59	ALA	2.6
1	G	70	ALA	2.6
1	C	350	ASP	2.6
1	E	72	LYS	2.6
1	I	173	TRP	2.6
1	G	40	SER	2.6
1	J	46	SER	2.6
1	G	172	LEU	2.6
1	I	61	LEU	2.6
1	A	7	GLY	2.6
1	H	352	GLU	2.6
1	E	322	ALA	2.6
1	L	2	ALA	2.6
1	J	102	VAL	2.6
1	H	357	ASP	2.6
1	K	48	ASP	2.6
1	F	56	ILE	2.6
1	D	105	ARG	2.6
1	G	343	ARG	2.6
1	A	176	GLN	2.6
1	D	2	ALA	2.5
1	F	102	VAL	2.5
1	I	354	VAL	2.5
1	H	107	ILE	2.5
1	L	41	SER	2.5
1	I	326	TRP	2.5
1	H	5	LEU	2.5
1	L	355	LEU	2.5
1	B	66	GLY	2.5
1	I	101	LYS	2.5
1	D	353	ALA	2.5
1	L	350	ASP	2.5
1	G	50	MET	2.5
1	G	108	TYR	2.5
1	L	323	ASN	2.5
1	L	56	ILE	2.5
1	B	180	LYS	2.5
1	E	61	LEU	2.5
1	E	106	LEU	2.5
1	I	69	LEU	2.5
1	B	50	MET	2.5
1	J	353	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	356	THR	2.5
1	L	34	VAL	2.5
1	D	39	PRO	2.5
1	A	98	GLU	2.5
1	H	6	SER	2.5
1	K	46	SER	2.5
1	E	93	GLY	2.5
1	K	355	LEU	2.5
1	E	144	ASP	2.5
1	E	77	ALA	2.5
1	H	100	ALA	2.5
1	E	34	VAL	2.5
1	C	101	LYS	2.4
1	F	107	ILE	2.4
1	B	144	ASP	2.4
1	G	2	ALA	2.4
1	G	31	ALA	2.4
1	A	10	VAL	2.4
1	I	102	VAL	2.4
1	D	180	LYS	2.4
1	F	72	LYS	2.4
1	I	76	LYS	2.4
1	A	94	LEU	2.4
1	D	65	GLN	2.4
1	F	65	GLN	2.4
1	B	75	ALA	2.4
1	G	322	ALA	2.4
1	H	322	ALA	2.4
1	K	173	TRP	2.4
1	H	354	VAL	2.4
1	H	63	SER	2.4
1	F	50	MET	2.4
1	F	69	LEU	2.4
1	I	2	ALA	2.4
1	F	356	THR	2.4
1	G	326	TRP	2.4
1	L	177	SER	2.4
1	G	55	ARG	2.4
1	C	7	GLY	2.4
1	I	43	ASP	2.4
1	L	181	GLY	2.4
1	A	61	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	106	LEU	2.3
1	L	80	LEU	2.3
1	C	72	LYS	2.3
1	A	59	ALA	2.3
1	A	356	THR	2.3
1	L	58	THR	2.3
1	A	46	SER	2.3
1	D	173	TRP	2.3
1	B	176	GLN	2.3
1	D	48	ASP	2.3
1	D	144	ASP	2.3
1	H	179	GLY	2.3
1	K	144	ASP	2.3
1	G	68	GLU	2.3
1	H	68	GLU	2.3
1	L	36	ILE	2.3
1	A	70	ALA	2.3
1	H	348	THR	2.3
1	I	49	ALA	2.3
1	E	91	ARG	2.3
1	K	343	ARG	2.3
1	E	79	VAL	2.3
1	D	358	TRP	2.3
1	L	358	TRP	2.3
1	K	258	GLU	2.3
1	L	315	GLU	2.3
1	G	91	ARG	2.3
1	G	75	ALA	2.3
1	H	49	ALA	2.3
1	H	75	ALA	2.3
1	A	177	SER	2.3
1	C	178	SER	2.3
1	D	34	VAL	2.3
1	K	34	VAL	2.3
1	A	64	ASP	2.3
1	E	7	GLY	2.3
1	B	62	LYS	2.3
1	H	108	TYR	2.3
1	A	105	ARG	2.3
1	I	353	ALA	2.3
1	D	46	SER	2.3
1	A	258	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	345	PRO	2.2
1	F	68	GLU	2.2
1	A	184	VAL	2.2
1	F	10	VAL	2.2
1	H	33	VAL	2.2
1	D	74	ILE	2.2
1	H	74	ILE	2.2
1	D	73	LEU	2.2
1	F	70	ALA	2.2
1	I	322	ALA	2.2
1	L	68	GLU	2.2
1	E	178	SER	2.2
1	B	39	PRO	2.2
1	J	344	PRO	2.2
1	E	10	VAL	2.2
1	D	92	LEU	2.2
1	B	353	ALA	2.2
1	F	353	ALA	2.2
1	K	322	ALA	2.2
1	G	350	ASP	2.2
1	H	342	PRO	2.2
1	F	99	CYS	2.2
1	H	325	GLY	2.2
1	C	105	ARG	2.2
1	K	38	ARG	2.2
1	H	334	PHE	2.2
1	D	352	GLU	2.2
1	G	277	GLU	2.2
1	I	315	GLU	2.2
1	J	352	GLU	2.2
1	L	352	GLU	2.2
1	H	80	LEU	2.2
1	D	178	SER	2.2
1	H	338	ALA	2.2
1	H	64	ASP	2.2
1	H	101	LYS	2.2
1	J	37	ASP	2.2
1	F	325	GLY	2.2
1	K	325	GLY	2.2
1	K	323	ASN	2.2
1	L	354	VAL	2.2
1	L	176	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	352	GLU	2.1
1	A	51	LEU	2.1
1	A	73	LEU	2.1
1	F	51	LEU	2.1
1	G	51	LEU	2.1
1	G	61	LEU	2.1
1	L	107	ILE	2.1
1	C	348	THR	2.1
1	B	178	SER	2.1
1	A	75	ALA	2.1
1	A	350	ASP	2.1
1	B	59	ALA	2.1
1	D	70	ALA	2.1
1	D	288	GLY	2.1
1	E	179	GLY	2.1
1	E	325	GLY	2.1
1	A	323	ASN	2.1
1	D	176	GLN	2.1
1	A	11	VAL	2.1
1	B	354	VAL	2.1
1	D	183	VAL	2.1
1	E	68	GLU	2.1
1	H	315	GLU	2.1
1	B	73	LEU	2.1
1	E	62	LYS	2.1
1	G	5	LEU	2.1
1	H	51	LEU	2.1
1	I	56	ILE	2.1
1	A	63	SER	2.1
1	L	105	ARG	2.1
1	A	322	ALA	2.1
1	J	257	ALA	2.1
1	C	39	PRO	2.1
1	E	108	TYR	2.1
1	G	93	GLY	2.1
1	H	65	GLN	2.1
1	I	99	CYS	2.1
1	A	79	VAL	2.1
1	F	79	VAL	2.1
1	H	79	VAL	2.1
1	L	10	VAL	2.1
1	B	48	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	106	LEU	2.1
1	K	71	LEU	2.1
1	L	67	LEU	2.1
1	L	71	LEU	2.1
1	L	106	LEU	2.1
1	C	46	SER	2.1
1	A	289	ALA	2.1
1	F	93	GLY	2.1
1	G	96	PRO	2.1
1	G	325	GLY	2.1
1	I	207	MET	2.1
1	G	173	TRP	2.1
1	C	68	GLU	2.1
1	D	315	GLU	2.1
1	E	11	VAL	2.1
1	E	33	VAL	2.1
1	F	33	VAL	2.1
1	H	183	VAL	2.1
1	L	184	VAL	2.1
1	D	55	ARG	2.1
1	A	37	ASP	2.1
1	C	355	LEU	2.1
1	C	322	ALA	2.0
1	D	179	GLY	2.0
1	I	87	GLY	2.0
1	E	76	LYS	2.0
1	E	101	LYS	2.0
1	L	76	LYS	2.0
1	K	11	VAL	2.0
1	H	359	ASP	2.0
1	L	357	ASP	2.0
1	D	8	LEU	2.0
1	G	26	LEU	2.0
1	H	71	LEU	2.0
1	L	50	MET	2.0
1	A	181	GLY	2.0
1	F	352	GLU	2.0
1	I	68	GLU	2.0
1	L	77	ALA	2.0
1	E	105	ARG	2.0
1	I	62	LYS	2.0
1	K	105	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	L	108	TYR	2.0
1	B	102	VAL	2.0
1	L	183	VAL	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

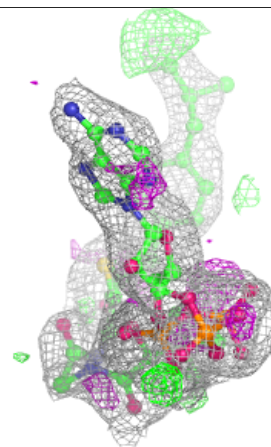
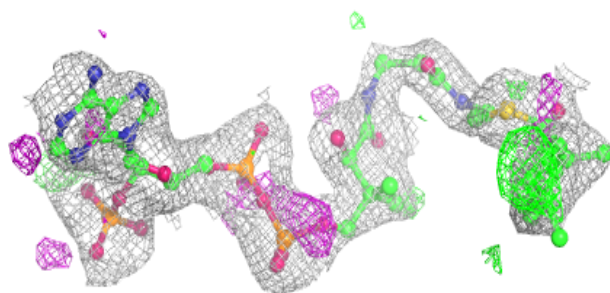
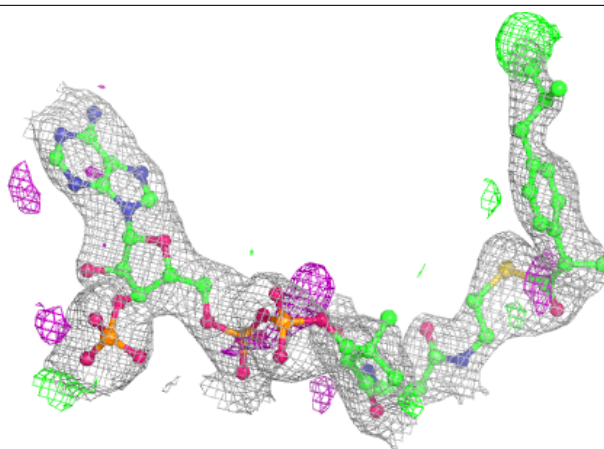
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SFC	E	401	62/62	0.87	0.17	61,77,93,113	0
2	SFC	H	401	62/62	0.87	0.17	56,82,96,106	0
2	SFC	A	401	62/62	0.94	0.12	39,61,89,97	0
2	SFC	F	401	62/62	0.94	0.11	36,53,75,89	0
2	SFC	C	401	62/62	0.94	0.11	42,60,73,87	0
2	SFC	L	401	62/62	0.94	0.11	37,59,79,83	0
2	SFC	D	401	62/62	0.95	0.10	33,53,73,91	0
2	SFC	I	401	62/62	0.95	0.10	35,53,72,77	0
2	SFC	K	401	62/62	0.95	0.10	37,54,72,91	0
2	SFC	G	401	62/62	0.95	0.11	35,54,81,86	0
2	SFC	B	401	62/62	0.96	0.10	38,55,84,95	0
2	SFC	J	401	62/62	0.96	0.10	33,47,68,86	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.

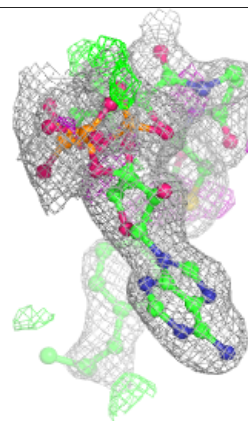
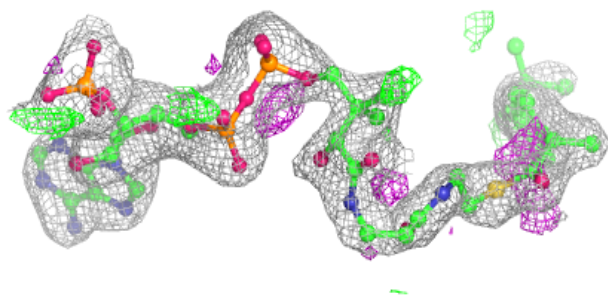
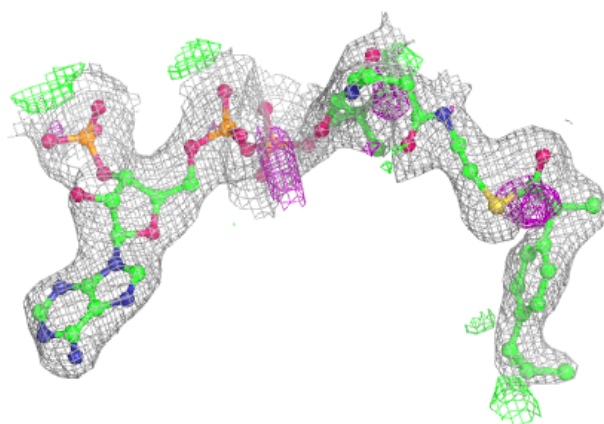
**Electron density around SFC E 401:**

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



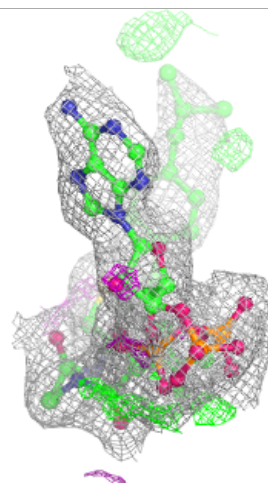
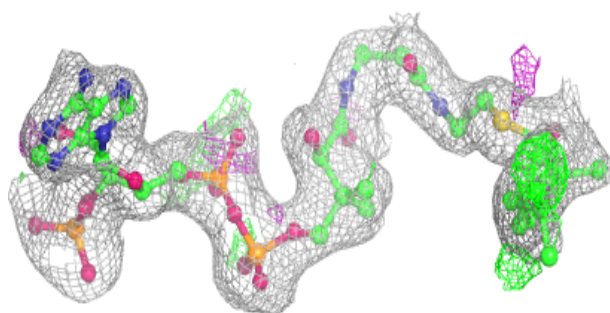
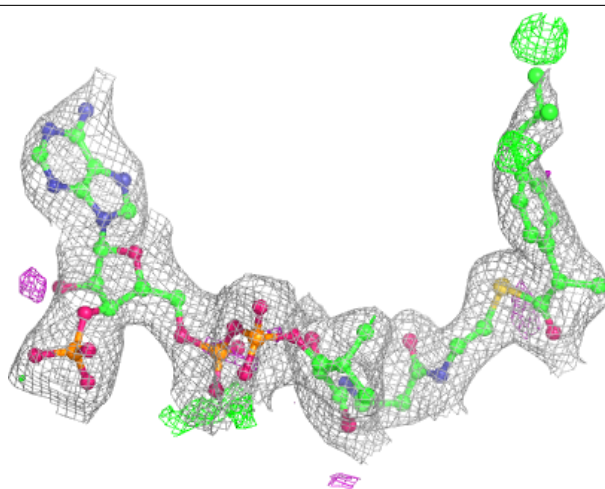
**Electron density around SFC H 401:**

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



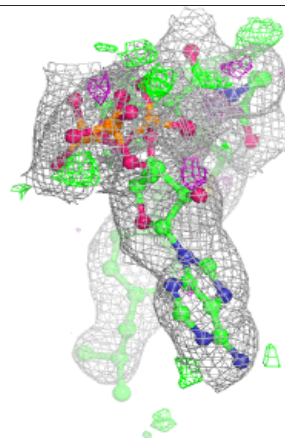
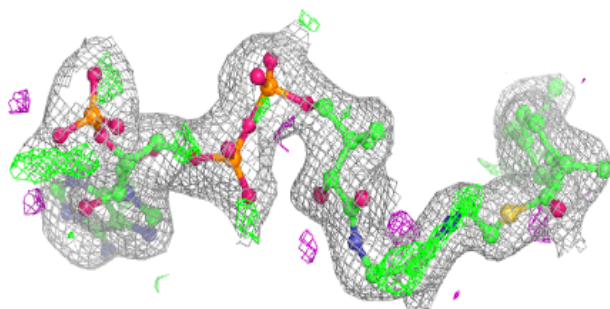
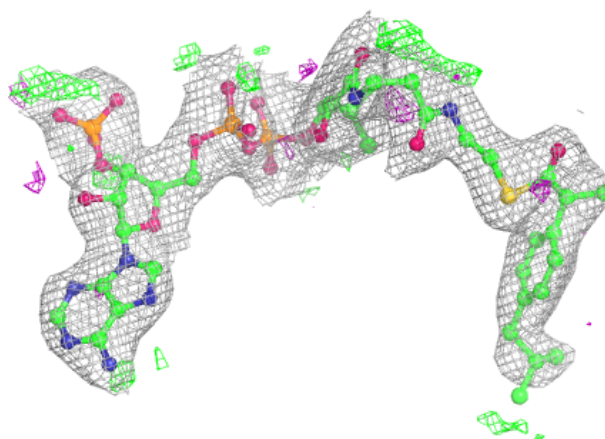
**Electron density around SFC A 401:**

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



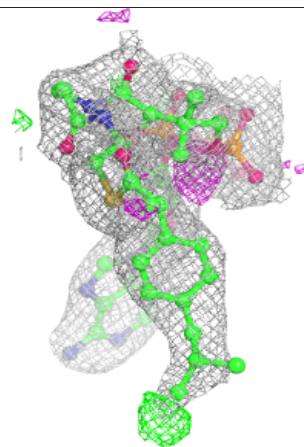
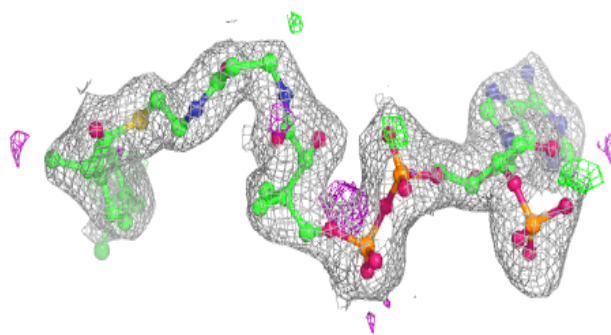
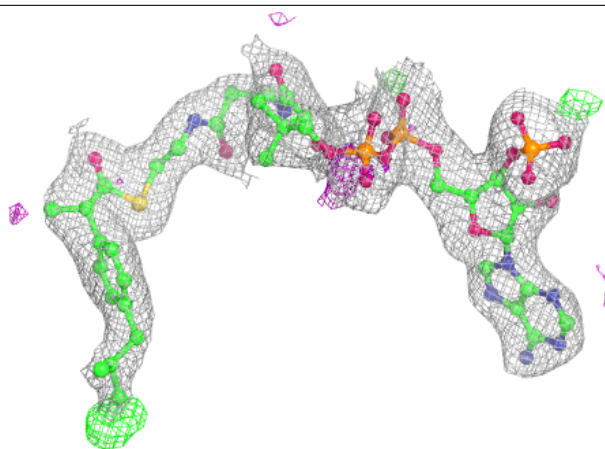
**Electron density around SFC F 401:**

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



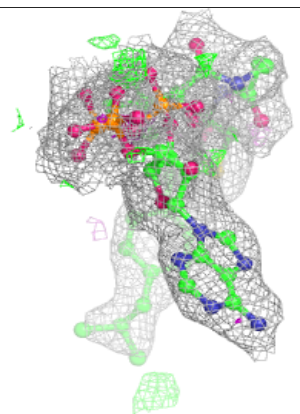
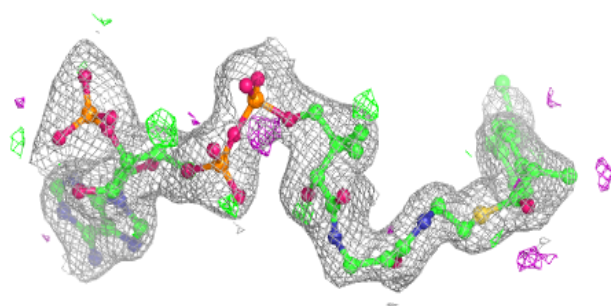
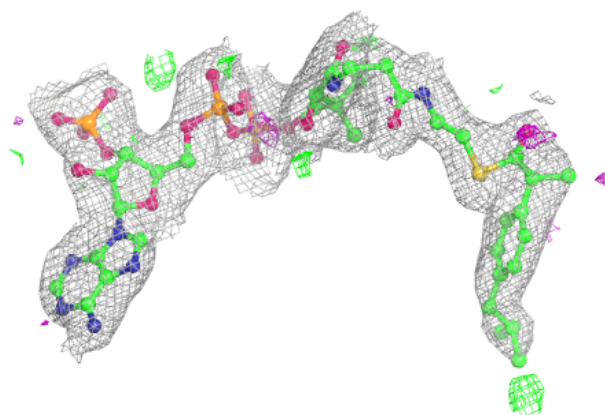
**Electron density around SFC C 401:**

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



**Electron density around SFC L 401:**

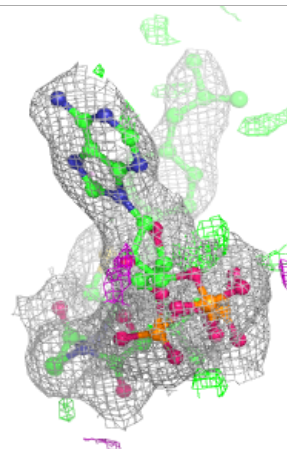
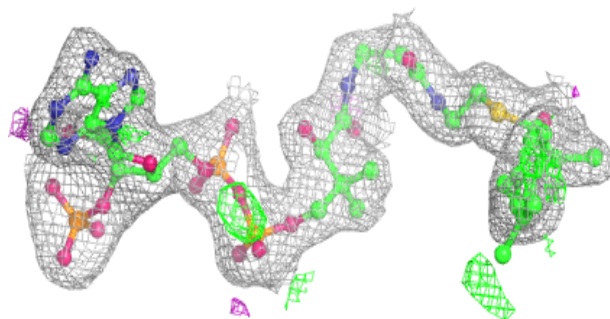
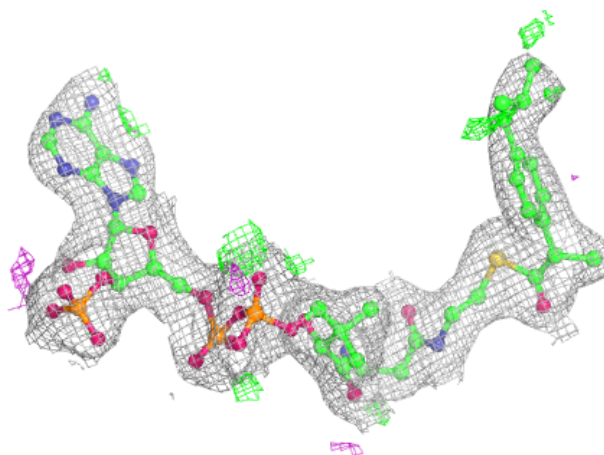
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around SFC D 401:**

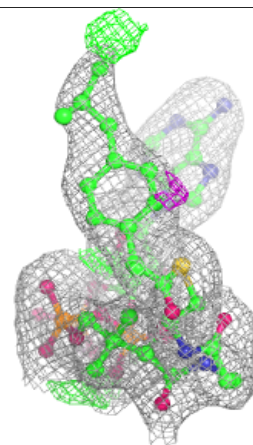
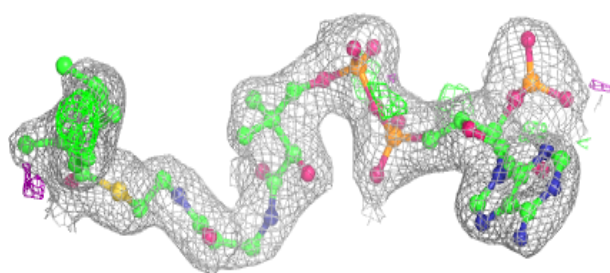
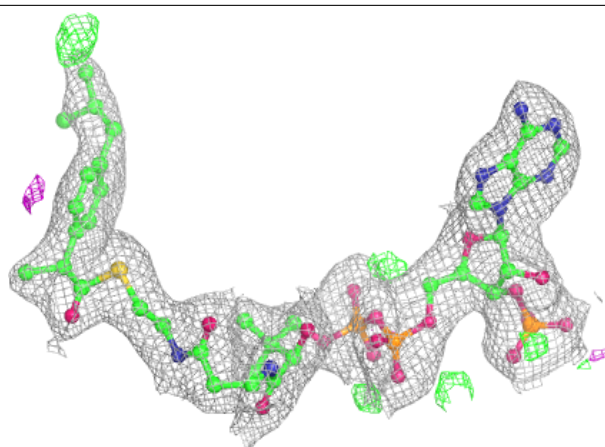
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



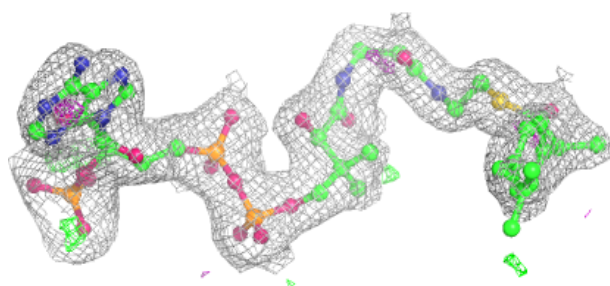
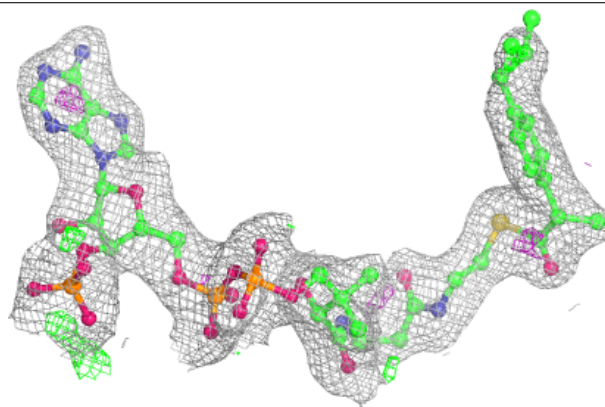


**Electron density around SFC I 401:**

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

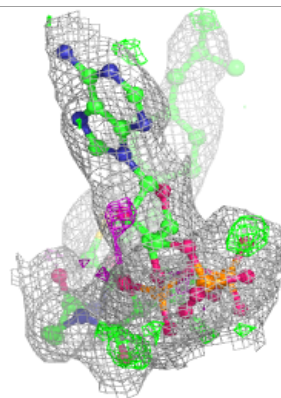
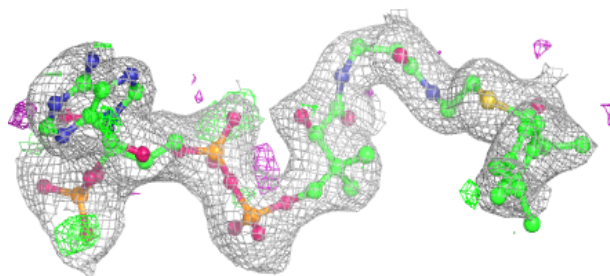
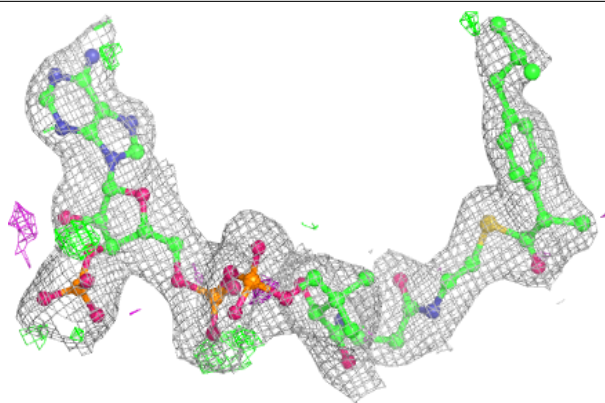
**Electron density around SFC K 401:**

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

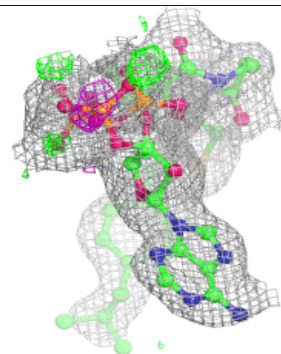
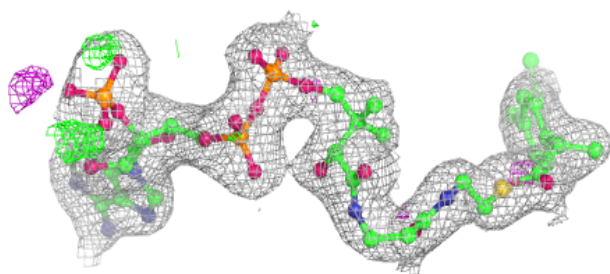
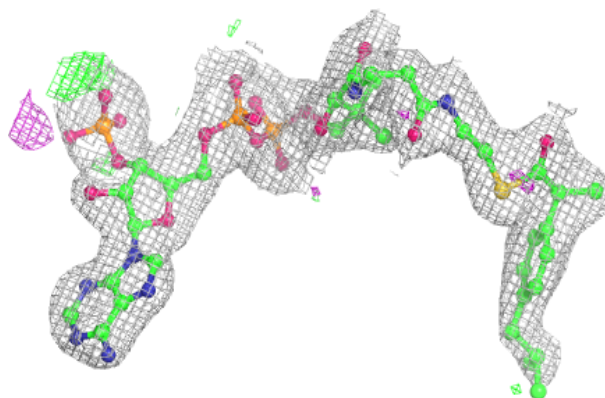


**Electron density around SFC G 401:**

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

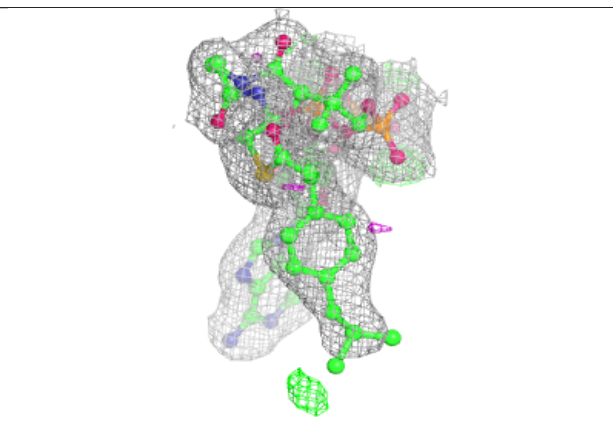
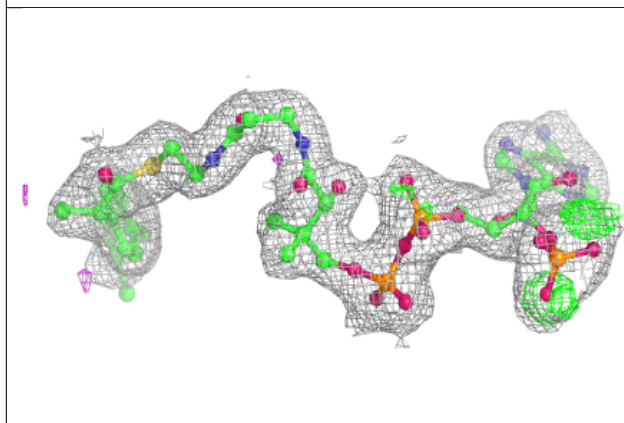
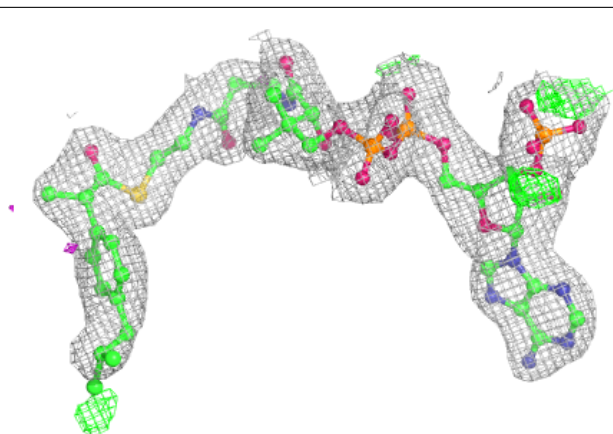
**Electron density around SFC B 401:**

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



**Electron density around SFC J 401:**

$2mF_o-DF_c$  (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.