



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2023 – 02:45 AM EDT

PDB ID : 3WCI
Title : The complex structure of HsSQS wtih ligand,BPH1325
Authors : Shang, N.; Li, Q.; Ko, T.P.; Chan, H.C.; Huang, C.H.; Ren, F.; Zheng, Y.;
Zhu, Z.; Chen, C.C.; Guo, R.T.
Deposited on : 2013-05-27
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

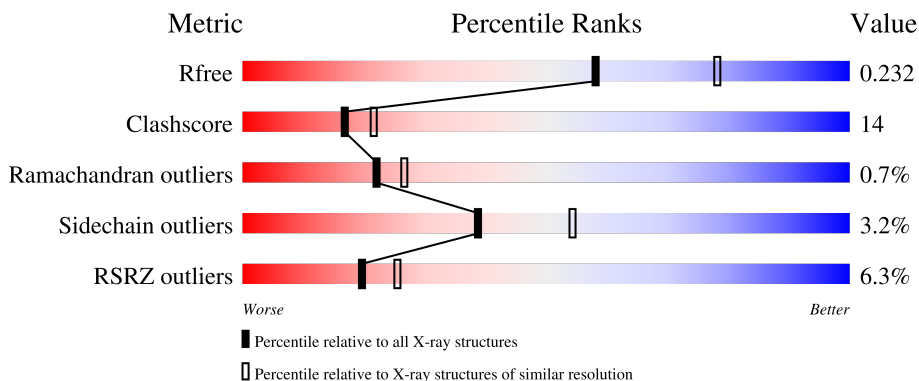
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	360	 3% 73% 19% • 7%
1	B	360	 4% 68% 23% • 7%
1	C	360	 4% 69% 22% • 7%
1	D	360	 9% 63% 27% • 7%
1	E	360	 4% 68% 22% • 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	360	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BH5	C	401	-	-	-	X
2	BH5	D	401	-	-	-	X
2	BH5	E	401	-	-	-	X
2	BH5	F	401	-	-	-	X

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17732 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 Squalene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2696	1717	458	503	18	0	0	0
1	B	334	2696	1717	458	503	18	0	0	0
1	C	334	2696	1717	458	503	18	0	0	0
1	D	334	2696	1717	458	503	18	0	0	0
1	E	334	2696	1717	458	503	18	0	0	0
1	F	334	2696	1717	458	503	18	0	0	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	expression tag	UNP P37268
A	12	GLY	-	expression tag	UNP P37268
A	13	SER	-	expression tag	UNP P37268
A	14	SER	-	expression tag	UNP P37268
A	15	HIS	-	expression tag	UNP P37268
A	16	HIS	-	expression tag	UNP P37268
A	17	HIS	-	expression tag	UNP P37268
A	18	HIS	-	expression tag	UNP P37268
A	19	HIS	-	expression tag	UNP P37268
A	20	HIS	-	expression tag	UNP P37268
A	21	SER	-	expression tag	UNP P37268
A	22	SER	-	expression tag	UNP P37268
A	23	GLY	-	expression tag	UNP P37268
A	24	LEU	-	expression tag	UNP P37268
A	25	VAL	-	expression tag	UNP P37268
A	26	PRO	-	expression tag	UNP P37268
A	27	ARG	-	expression tag	UNP P37268

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLY	-	expression tag	UNP P37268
A	29	SER	-	expression tag	UNP P37268
A	30	HIS	-	expression tag	UNP P37268
A	248	LEU	LYS	engineered mutation	UNP P37268
A	315	LEU	LYS	engineered mutation	UNP P37268
A	318	LEU	LYS	engineered mutation	UNP P37268
A	353	ASN	ASP	SEE REMARK 999	UNP P37268
B	11	MET	-	expression tag	UNP P37268
B	12	GLY	-	expression tag	UNP P37268
B	13	SER	-	expression tag	UNP P37268
B	14	SER	-	expression tag	UNP P37268
B	15	HIS	-	expression tag	UNP P37268
B	16	HIS	-	expression tag	UNP P37268
B	17	HIS	-	expression tag	UNP P37268
B	18	HIS	-	expression tag	UNP P37268
B	19	HIS	-	expression tag	UNP P37268
B	20	HIS	-	expression tag	UNP P37268
B	21	SER	-	expression tag	UNP P37268
B	22	SER	-	expression tag	UNP P37268
B	23	GLY	-	expression tag	UNP P37268
B	24	LEU	-	expression tag	UNP P37268
B	25	VAL	-	expression tag	UNP P37268
B	26	PRO	-	expression tag	UNP P37268
B	27	ARG	-	expression tag	UNP P37268
B	28	GLY	-	expression tag	UNP P37268
B	29	SER	-	expression tag	UNP P37268
B	30	HIS	-	expression tag	UNP P37268
B	248	LEU	LYS	engineered mutation	UNP P37268
B	315	LEU	LYS	engineered mutation	UNP P37268
B	318	LEU	LYS	engineered mutation	UNP P37268
B	353	ASN	ASP	SEE REMARK 999	UNP P37268
C	11	MET	-	expression tag	UNP P37268
C	12	GLY	-	expression tag	UNP P37268
C	13	SER	-	expression tag	UNP P37268
C	14	SER	-	expression tag	UNP P37268
C	15	HIS	-	expression tag	UNP P37268
C	16	HIS	-	expression tag	UNP P37268
C	17	HIS	-	expression tag	UNP P37268
C	18	HIS	-	expression tag	UNP P37268
C	19	HIS	-	expression tag	UNP P37268
C	20	HIS	-	expression tag	UNP P37268
C	21	SER	-	expression tag	UNP P37268

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	22	SER	-	expression tag	UNP P37268
C	23	GLY	-	expression tag	UNP P37268
C	24	LEU	-	expression tag	UNP P37268
C	25	VAL	-	expression tag	UNP P37268
C	26	PRO	-	expression tag	UNP P37268
C	27	ARG	-	expression tag	UNP P37268
C	28	GLY	-	expression tag	UNP P37268
C	29	SER	-	expression tag	UNP P37268
C	30	HIS	-	expression tag	UNP P37268
C	248	LEU	LYS	engineered mutation	UNP P37268
C	315	LEU	LYS	engineered mutation	UNP P37268
C	318	LEU	LYS	engineered mutation	UNP P37268
C	353	ASN	ASP	SEE REMARK 999	UNP P37268
D	11	MET	-	expression tag	UNP P37268
D	12	GLY	-	expression tag	UNP P37268
D	13	SER	-	expression tag	UNP P37268
D	14	SER	-	expression tag	UNP P37268
D	15	HIS	-	expression tag	UNP P37268
D	16	HIS	-	expression tag	UNP P37268
D	17	HIS	-	expression tag	UNP P37268
D	18	HIS	-	expression tag	UNP P37268
D	19	HIS	-	expression tag	UNP P37268
D	20	HIS	-	expression tag	UNP P37268
D	21	SER	-	expression tag	UNP P37268
D	22	SER	-	expression tag	UNP P37268
D	23	GLY	-	expression tag	UNP P37268
D	24	LEU	-	expression tag	UNP P37268
D	25	VAL	-	expression tag	UNP P37268
D	26	PRO	-	expression tag	UNP P37268
D	27	ARG	-	expression tag	UNP P37268
D	28	GLY	-	expression tag	UNP P37268
D	29	SER	-	expression tag	UNP P37268
D	30	HIS	-	expression tag	UNP P37268
D	248	LEU	LYS	engineered mutation	UNP P37268
D	315	LEU	LYS	engineered mutation	UNP P37268
D	318	LEU	LYS	engineered mutation	UNP P37268
D	353	ASN	ASP	SEE REMARK 999	UNP P37268
E	11	MET	-	expression tag	UNP P37268
E	12	GLY	-	expression tag	UNP P37268
E	13	SER	-	expression tag	UNP P37268
E	14	SER	-	expression tag	UNP P37268
E	15	HIS	-	expression tag	UNP P37268

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	16	HIS	-	expression tag	UNP P37268
E	17	HIS	-	expression tag	UNP P37268
E	18	HIS	-	expression tag	UNP P37268
E	19	HIS	-	expression tag	UNP P37268
E	20	HIS	-	expression tag	UNP P37268
E	21	SER	-	expression tag	UNP P37268
E	22	SER	-	expression tag	UNP P37268
E	23	GLY	-	expression tag	UNP P37268
E	24	LEU	-	expression tag	UNP P37268
E	25	VAL	-	expression tag	UNP P37268
E	26	PRO	-	expression tag	UNP P37268
E	27	ARG	-	expression tag	UNP P37268
E	28	GLY	-	expression tag	UNP P37268
E	29	SER	-	expression tag	UNP P37268
E	30	HIS	-	expression tag	UNP P37268
E	248	LEU	LYS	engineered mutation	UNP P37268
E	315	LEU	LYS	engineered mutation	UNP P37268
E	318	LEU	LYS	engineered mutation	UNP P37268
E	353	ASN	ASP	SEE REMARK 999	UNP P37268
F	11	MET	-	expression tag	UNP P37268
F	12	GLY	-	expression tag	UNP P37268
F	13	SER	-	expression tag	UNP P37268
F	14	SER	-	expression tag	UNP P37268
F	15	HIS	-	expression tag	UNP P37268
F	16	HIS	-	expression tag	UNP P37268
F	17	HIS	-	expression tag	UNP P37268
F	18	HIS	-	expression tag	UNP P37268
F	19	HIS	-	expression tag	UNP P37268
F	20	HIS	-	expression tag	UNP P37268
F	21	SER	-	expression tag	UNP P37268
F	22	SER	-	expression tag	UNP P37268
F	23	GLY	-	expression tag	UNP P37268
F	24	LEU	-	expression tag	UNP P37268
F	25	VAL	-	expression tag	UNP P37268
F	26	PRO	-	expression tag	UNP P37268
F	27	ARG	-	expression tag	UNP P37268
F	28	GLY	-	expression tag	UNP P37268
F	29	SER	-	expression tag	UNP P37268
F	30	HIS	-	expression tag	UNP P37268
F	248	LEU	LYS	engineered mutation	UNP P37268
F	315	LEU	LYS	engineered mutation	UNP P37268
F	318	LEU	LYS	engineered mutation	UNP P37268

Continued on next page...

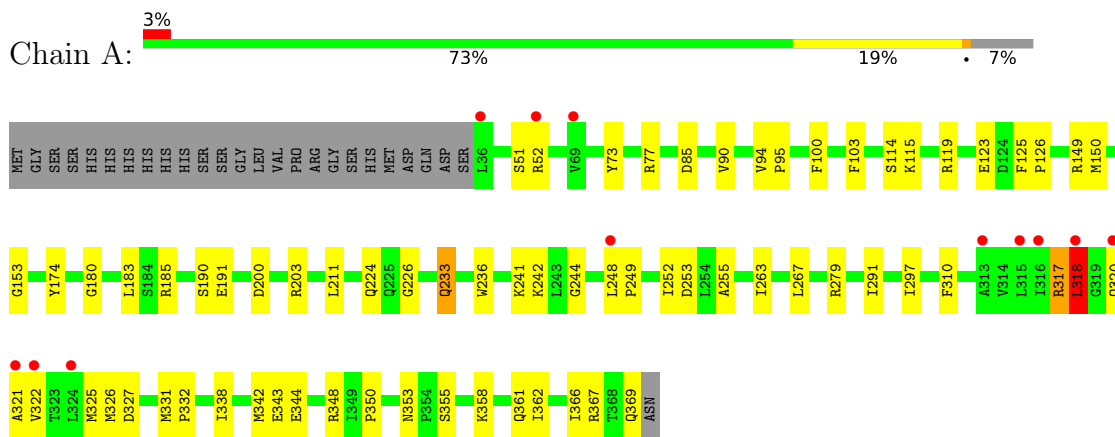
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	278	Total 278	O 278	0	0
3	D	177	Total 177	O 177	0	0
3	E	185	Total 185	O 185	0	0
3	F	156	Total 156	O 156	0	0

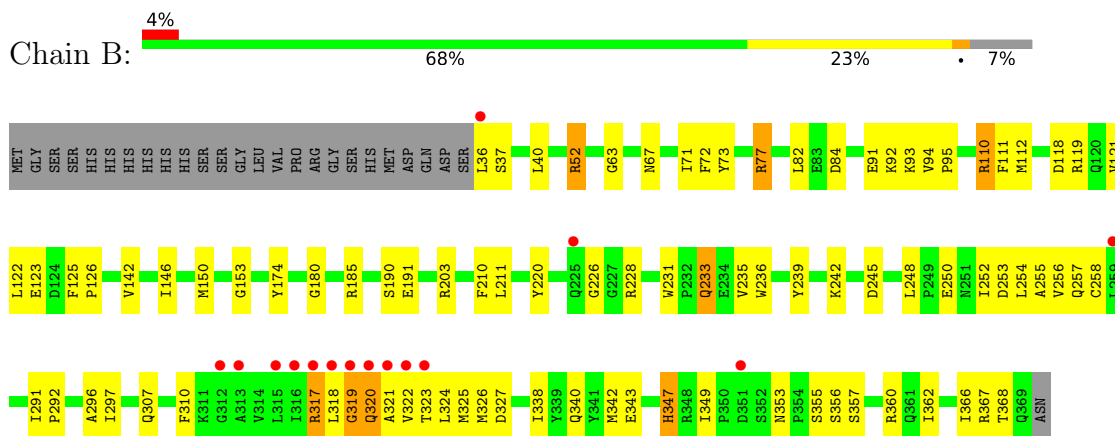
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

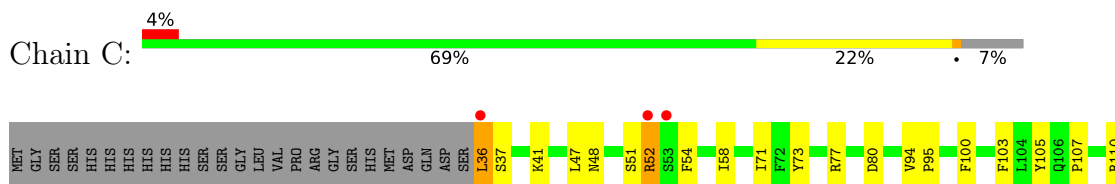
- Molecule 1: Squalene synthase

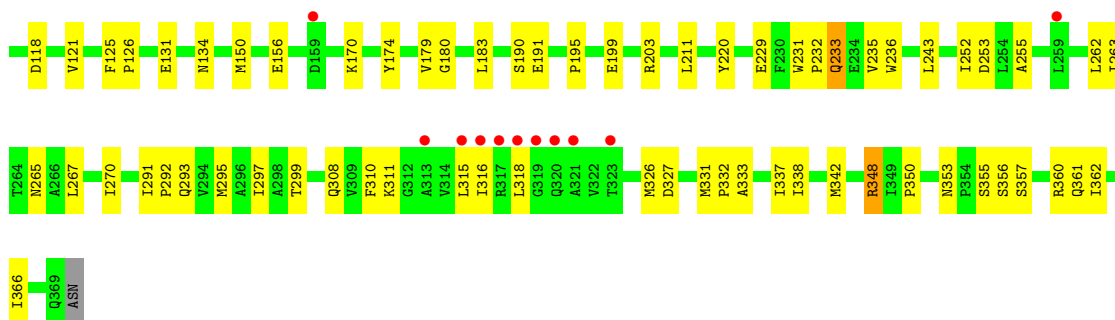


- Molecule 1: Squalene synthase

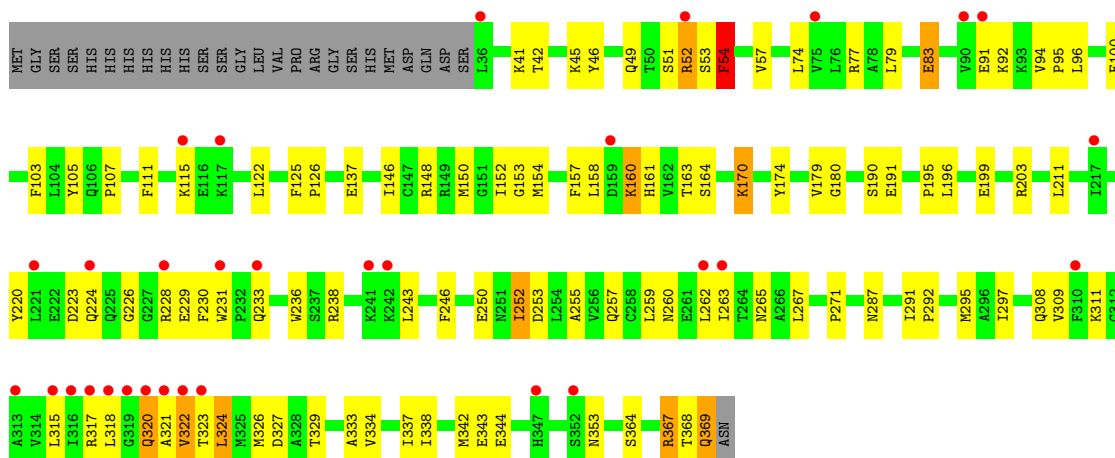


- Molecule 1: Squalene synthase

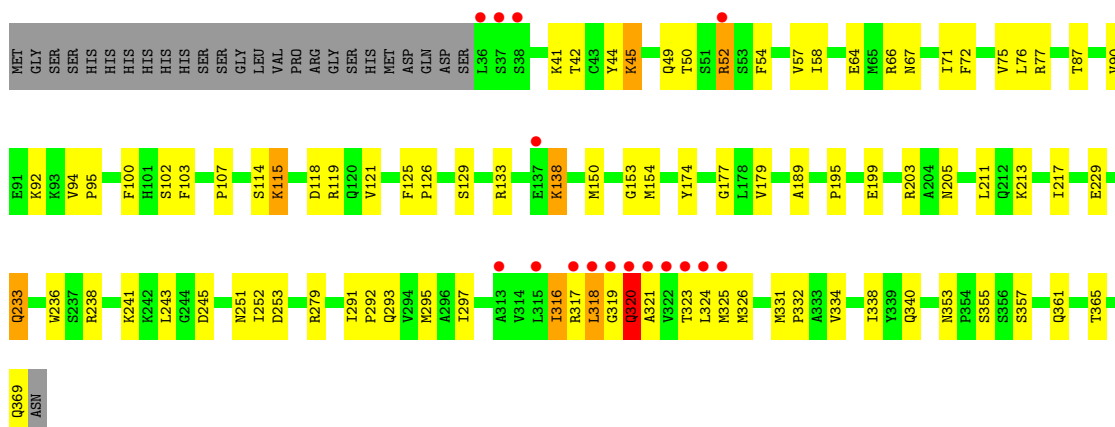




- Molecule 1: Squalene synthase

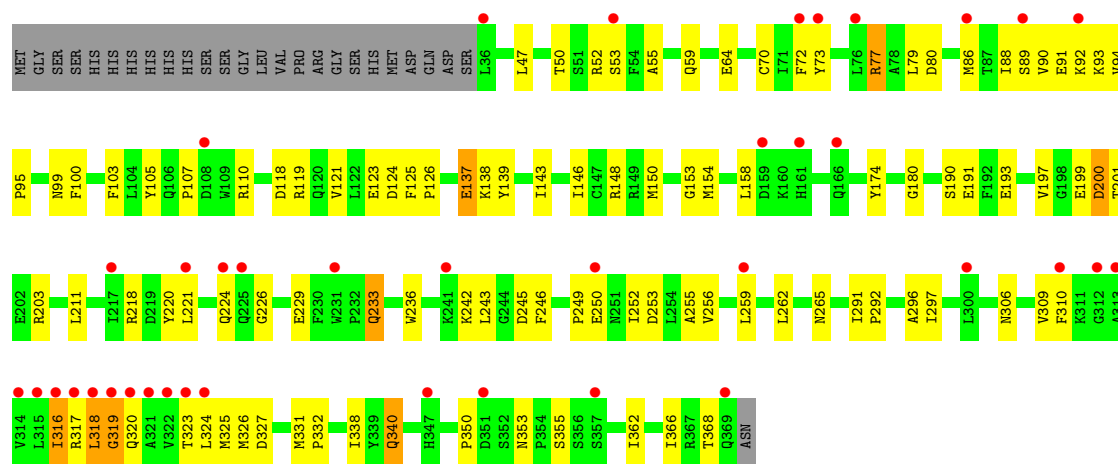


- Molecule 1: Squalene synthase



- Molecule 1: Squalene synthase





4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.38Å 153.62Å 91.16Å 90.00° 90.82° 90.00°	Depositor
Resolution (Å)	25.00 – 2.30 24.87 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.30) 95.3 (24.87-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 2.31Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.217 , 0.265 0.185 , 0.232	Depositor DCC
R_{free} test set	4949 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtrriage
Anisotropy	0.613	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 57.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17732	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BH5

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	0.37	0/2751	0.57	0/3724
1	B	0.35	0/2751	0.57	1/3724 (0.0%)
1	C	0.34	0/2751	0.54	0/3724
1	D	0.32	0/2751	0.52	0/3724
1	E	0.31	0/2751	0.53	0/3724
1	F	0.31	0/2751	0.55	2/3724 (0.1%)
All	All	0.33	0/16506	0.55	3/22344 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	319	GLY	N-CA-C	6.18	128.55	113.10
1	F	319	GLY	N-CA-C	-5.81	98.58	113.10
1	F	318	LEU	N-CA-C	5.04	124.60	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2696	0	2676	55	0
1	B	2696	0	2676	81	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2696	0	2676	61	0
1	D	2696	0	2676	110	0
1	E	2696	0	2676	81	0
1	F	2696	0	2676	94	0
2	A	31	0	40	8	0
2	B	31	0	40	11	0
2	C	31	0	40	11	0
2	D	31	0	40	6	0
2	E	31	0	40	6	0
2	F	31	0	40	5	0
3	A	283	0	0	3	0
3	B	291	0	0	8	0
3	C	278	0	0	1	0
3	D	177	0	0	2	0
3	E	185	0	0	4	0
3	F	156	0	0	3	0
All	All	17732	0	16296	461	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (461) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:229:GLU:HG2	1:D:243:LEU:HD23	1.45	0.97
1:A:317:ARG:HG3	1:A:318:LEU:H	1.32	0.94
1:D:52:ARG:HH21	1:D:52:ARG:HB3	1.32	0.93
1:F:233:GLN:HA	1:F:236:TRP:NE1	1.85	0.90
1:D:322:VAL:HG12	1:D:323:THR:H	1.39	0.86
1:B:233:GLN:HA	1:B:236:TRP:NE1	1.93	0.83
1:A:317:ARG:HG3	1:A:318:LEU:N	1.91	0.82
1:D:260:ASN:HD22	1:D:353:ASN:ND2	1.79	0.80
1:D:115:LYS:HA	1:D:115:LYS:HE2	1.65	0.78
1:D:324:LEU:HD11	1:E:318:LEU:HD21	1.67	0.76
1:D:326:MET:HE1	1:D:333:ALA:HA	1.67	0.76
1:B:77:ARG:NH1	2:B:401:BH5:H11	2.01	0.76
1:F:316:ILE:HD12	1:F:316:ILE:H	1.51	0.75
1:B:319:GLY:HA3	1:B:324:LEU:HD11	1.68	0.74
1:F:150:MET:HG3	1:F:174:TYR:O	1.88	0.74
1:D:220:TYR:HB2	1:D:231:TRP:CZ2	2.24	0.73
1:B:226:GLY:HA3	1:B:228:ARG:HH12	1.54	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:179:VAL:HG21	2:D:401:BH5:H19	1.70	0.72
1:D:233:GLN:HA	1:D:236:TRP:NE1	2.05	0.72
1:D:321:ALA:O	1:D:324:LEU:HD22	1.90	0.72
1:D:291:ILE:HB	1:D:292:PRO:HD3	1.72	0.71
1:D:291:ILE:HD12	1:F:325:MET:HB3	1.71	0.71
1:D:322:VAL:HG12	1:D:323:THR:N	2.04	0.71
1:A:317:ARG:CG	1:A:318:LEU:H	2.02	0.71
1:F:252:ILE:HG13	1:F:253:ASP:N	2.06	0.70
1:F:100:PHE:HA	1:F:103:PHE:CD2	2.25	0.70
1:B:52:ARG:HG3	2:B:401:BH5:OAE	1.91	0.70
1:B:77:ARG:HD3	2:B:401:BH5:CAY	2.22	0.69
1:E:87:THR:HG21	1:E:115:LYS:HG3	1.74	0.69
1:B:318:LEU:HD22	3:B:684:HOH:O	1.92	0.69
1:E:195:PRO:O	1:E:199:GLU:HG3	1.93	0.69
1:A:224:GLN:NE2	1:A:244:GLY:HA2	2.08	0.69
1:B:36:LEU:HD12	1:B:37:SER:H	1.58	0.69
1:F:89:SER:OG	1:F:91:GLU:HG2	1.93	0.69
1:B:326:MET:HE3	1:C:291:ILE:HD11	1.75	0.69
1:C:150:MET:HG3	1:C:174:TYR:O	1.92	0.69
1:B:368:THR:HG21	1:C:41:LYS:HA	1.75	0.68
1:C:156:GLU:OE1	1:C:170:LYS:HE2	1.93	0.68
1:F:211:LEU:HD12	2:F:401:BH5:H30	1.76	0.68
1:F:252:ILE:HG13	1:F:253:ASP:H	1.58	0.68
1:D:322:VAL:O	1:D:324:LEU:N	2.26	0.68
1:D:150:MET:HG3	1:D:174:TYR:O	1.93	0.68
1:E:211:LEU:HD12	2:E:401:BH5:H30	1.75	0.68
1:A:325:MET:O	1:B:327:ASP:HB2	1.94	0.67
1:D:327:ASP:OD2	1:D:329:THR:HG23	1.95	0.67
1:E:94:VAL:HB	1:E:95:PRO:HD3	1.77	0.67
1:F:350:PRO:HG2	1:F:353:ASN:HB2	1.76	0.67
1:F:125:PHE:N	1:F:126:PRO:HD2	2.09	0.66
1:E:325:MET:O	1:F:327:ASP:HB2	1.94	0.66
1:B:77:ARG:HD3	2:B:401:BH5:H11	1.76	0.66
1:A:322:VAL:O	1:A:326:MET:HG2	1.96	0.66
1:E:129:SER:HB2	1:E:133:ARG:HH12	1.61	0.66
1:D:343:GLU:HG2	1:D:367:ARG:NH2	2.12	0.65
1:D:343:GLU:HG2	1:D:367:ARG:HH22	1.61	0.65
1:F:316:ILE:HD12	1:F:316:ILE:N	2.12	0.65
1:C:183:LEU:HD12	2:C:401:BH5:H35	1.78	0.65
1:F:353:ASN:HD21	1:F:355:SER:HB2	1.60	0.65
1:B:248:LEU:HB3	1:B:250:GLU:OE1	1.98	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:GLN:HE21	1:B:322:VAL:H	1.45	0.64
1:C:105:TYR:O	1:C:107:PRO:HD3	1.97	0.64
1:B:343:GLU:OE1	1:C:48:ASN:HB3	1.98	0.64
1:C:315:LEU:O	1:C:315:LEU:HD12	1.96	0.64
1:D:291:ILE:HG23	1:F:325:MET:HG3	1.79	0.64
1:C:297:ILE:CD1	1:C:338:ILE:HG12	2.28	0.64
1:D:287:ASN:O	1:D:291:ILE:HG12	1.98	0.64
1:B:320:GLN:HG2	1:B:340:GLN:NE2	2.13	0.64
1:A:242:LYS:NZ	1:A:242:LYS:HB2	2.13	0.63
1:A:350:PRO:HG2	1:A:353:ASN:HB2	1.79	0.63
1:E:229:GLU:HG2	1:E:243:LEU:HD23	1.80	0.63
1:C:195:PRO:O	1:C:199:GLU:HG3	1.98	0.62
1:B:77:ARG:HH11	2:B:401:BH5:H11	1.64	0.62
1:B:226:GLY:HA3	1:B:228:ARG:NH1	2.14	0.62
1:E:320:GLN:H	1:E:324:LEU:HG	1.64	0.62
1:B:343:GLU:OE1	1:B:367:ARG:NH2	2.33	0.62
1:F:249:PRO:O	1:F:252:ILE:HG23	2.00	0.62
1:B:349:ILE:HD12	1:B:360:ARG:HG2	1.82	0.61
1:F:221:LEU:HD13	1:F:310:PHE:O	2.00	0.61
1:F:93:LYS:HD2	1:F:158:LEU:HD11	1.82	0.61
2:B:401:BH5:H9	3:B:733:HOH:O	2.00	0.61
1:F:90:VAL:O	1:F:94:VAL:HG23	1.99	0.61
1:E:317:ARG:O	1:E:317:ARG:HG3	1.99	0.61
1:C:297:ILE:HD13	1:C:338:ILE:HG12	1.83	0.61
1:C:353:ASN:ND2	1:C:355:SER:H	1.99	0.60
1:A:353:ASN:ND2	1:A:355:SER:H	2.00	0.60
1:C:52:ARG:HD3	2:C:401:BH5:PBD	2.41	0.60
1:D:100:PHE:HA	1:D:103:PHE:CD2	2.37	0.60
1:F:291:ILE:HB	1:F:292:PRO:HD3	1.84	0.60
1:E:100:PHE:HA	1:E:103:PHE:CD2	2.36	0.60
1:C:348:ARG:O	1:C:350:PRO:HD3	2.02	0.59
1:D:153:GLY:HA3	1:D:174:TYR:CD1	2.38	0.59
1:C:331:MET:HB3	1:C:332:PRO:HD3	1.85	0.59
1:A:51:SER:HB2	1:A:73:TYR:CZ	2.38	0.59
1:A:326:MET:HA	1:B:327:ASP:HB2	1.84	0.59
1:A:94:VAL:HB	1:A:95:PRO:HD3	1.85	0.59
1:E:115:LYS:NZ	1:E:115:LYS:HB3	2.18	0.59
1:A:211:LEU:HD12	2:A:401:BH5:H30	1.84	0.58
1:D:94:VAL:HB	1:D:95:PRO:HD3	1.84	0.58
1:C:36:LEU:N	1:C:36:LEU:HD22	2.17	0.58
1:E:45:LYS:O	1:E:49:GLN:HG3	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:211:LEU:HD12	2:C:401:BH5:H30	1.84	0.58
1:A:369:GLN:NE2	1:B:36:LEU:HB2	2.19	0.58
1:D:324:LEU:HD23	1:D:324:LEU:C	2.23	0.58
1:F:52:ARG:HG3	1:F:53:SER:H	1.69	0.58
1:E:150:MET:O	1:E:154:MET:HG3	2.04	0.58
1:E:233:GLN:HA	1:E:236:TRP:NE1	2.17	0.58
1:D:320:GLN:NE2	1:D:322:VAL:H	2.01	0.57
1:D:324:LEU:HD21	1:E:318:LEU:HD13	1.87	0.57
1:E:365:THR:O	1:E:369:GLN:HG3	2.04	0.57
1:F:233:GLN:HA	1:F:236:TRP:HE1	1.69	0.57
3:A:781:HOH:O	1:E:64:GLU:HG3	2.04	0.57
1:D:54:PHE:CE2	1:D:57:VAL:HG21	2.40	0.57
1:D:146:ILE:HG22	1:D:150:MET:HE3	1.86	0.57
1:D:364:SER:O	1:D:368:THR:HG23	2.03	0.57
1:B:233:GLN:HA	1:B:236:TRP:CD1	2.39	0.57
1:C:71:ILE:HD11	1:C:131:GLU:HB3	1.87	0.56
1:D:323:THR:O	1:D:326:MET:O	2.23	0.56
1:C:37:SER:O	1:C:41:LYS:HG3	2.05	0.56
1:D:51:SER:HA	2:D:401:BH5:OAB	2.04	0.56
1:F:324:LEU:HD13	1:F:324:LEU:O	2.05	0.56
1:B:94:VAL:HB	1:B:95:PRO:HD3	1.87	0.56
1:C:180:GLY:HA2	2:C:401:BH5:H36	1.87	0.56
1:D:368:THR:HG21	1:E:41:LYS:HA	1.87	0.56
1:E:325:MET:C	1:F:327:ASP:HB2	2.26	0.56
1:C:51:SER:HB2	1:C:73:TYR:CE1	2.39	0.56
1:D:320:GLN:NE2	1:D:321:ALA:N	2.54	0.56
1:F:297:ILE:CD1	1:F:338:ILE:HG12	2.35	0.56
1:E:323:THR:C	1:E:325:MET:H	2.08	0.56
1:D:324:LEU:HD11	1:E:318:LEU:HD11	1.87	0.56
1:C:51:SER:HB2	1:C:73:TYR:CZ	2.41	0.56
1:D:160:LYS:HG3	1:D:161:HIS:O	2.06	0.55
1:A:321:ALA:O	1:A:325:MET:N	2.39	0.55
1:C:293:GLN:O	1:C:297:ILE:HG13	2.06	0.55
1:D:252:ILE:HG22	1:D:253:ASP:N	2.21	0.55
1:E:316:ILE:HD12	1:E:316:ILE:H	1.72	0.55
1:F:91:GLU:OE1	1:F:91:GLU:N	2.33	0.54
1:F:229:GLU:HB3	1:F:243:LEU:HD23	1.89	0.54
1:C:94:VAL:HB	1:C:95:PRO:HD3	1.90	0.54
1:A:343:GLU:OE1	1:A:367:ARG:NH2	2.40	0.54
1:E:118:ASP:O	1:E:121:VAL:HG22	2.06	0.54
1:A:369:GLN:HG2	1:B:36:LEU:HD22	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:323:THR:HG22	1:F:340:GLN:OE1	2.08	0.54
1:C:338:ILE:O	1:C:342:MET:HG2	2.08	0.54
1:D:52:ARG:HH21	1:D:52:ARG:CB	2.13	0.54
1:F:353:ASN:ND2	1:F:355:SER:HB2	2.23	0.54
1:E:353:ASN:ND2	1:E:355:SER:H	2.05	0.53
1:A:343:GLU:HG2	3:B:758:HOH:O	2.07	0.53
1:D:291:ILE:HD12	1:F:325:MET:CB	2.37	0.53
1:D:297:ILE:HD13	1:D:338:ILE:HG23	1.91	0.53
1:E:52:ARG:HB2	2:E:401:BH5:OAH	2.08	0.53
1:E:57:VAL:HG22	3:E:520:HOH:O	2.08	0.53
1:E:324:LEU:HD12	3:E:685:HOH:O	2.09	0.53
1:A:358:LYS:HA	1:A:361:GLN:HG2	1.90	0.53
1:B:82:LEU:O	1:B:93:LYS:HE2	2.09	0.53
1:C:52:ARG:HD3	2:C:401:BH5:OAB	2.08	0.53
1:A:252:ILE:HG23	1:A:253:ASP:N	2.24	0.53
1:E:211:LEU:HD12	2:E:401:BH5:CAP	2.37	0.53
1:A:77:ARG:HD2	2:A:401:BH5:H11	1.91	0.53
1:D:324:LEU:CD1	1:E:318:LEU:HD21	2.38	0.53
1:F:86:MET:C	1:F:88:ILE:H	2.11	0.53
1:B:119:ARG:O	1:B:123:GLU:HG3	2.09	0.53
1:D:324:LEU:HD21	1:E:318:LEU:HD22	1.91	0.53
1:F:146:ILE:CG2	1:F:150:MET:HE3	2.38	0.53
1:B:73:TYR:OH	2:B:401:BH5:H8	2.09	0.52
1:C:211:LEU:HD12	2:C:401:BH5:CAP	2.39	0.52
2:C:401:BH5:OAG	2:C:401:BH5:H9	2.09	0.52
1:D:211:LEU:HD12	2:D:401:BH5:CAP	2.40	0.52
1:F:233:GLN:HA	1:F:236:TRP:CD1	2.44	0.52
1:E:316:ILE:H	1:E:316:ILE:CD1	2.22	0.52
1:B:77:ARG:HD3	2:B:401:BH5:H12	1.90	0.52
1:D:322:VAL:CG1	1:D:323:THR:H	2.16	0.52
1:F:224:GLN:C	1:F:226:GLY:H	2.13	0.52
1:A:242:LYS:HB2	1:A:242:LYS:HZ2	1.74	0.52
1:B:153:GLY:HA3	1:B:174:TYR:CG	2.45	0.52
1:D:320:GLN:HE21	1:D:322:VAL:H	1.56	0.52
1:F:353:ASN:ND2	1:F:355:SER:H	2.07	0.52
1:E:126:PRO:HA	1:E:129:SER:OG	2.09	0.52
1:E:297:ILE:HD12	1:E:338:ILE:HG12	1.92	0.52
1:B:220:TYR:HB2	1:B:231:TRP:CZ2	2.44	0.51
1:C:291:ILE:HB	1:C:292:PRO:HD3	1.91	0.51
1:F:255:ALA:HB1	1:F:310:PHE:CZ	2.44	0.51
1:B:150:MET:HG3	1:B:174:TYR:O	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:77:ARG:HE	1:F:77:ARG:HA	1.75	0.51
1:D:52:ARG:CD	1:D:52:ARG:H	2.23	0.51
1:F:55:ALA:O	1:F:59:GLN:HG3	2.10	0.51
1:B:36:LEU:CD1	1:B:37:SER:H	2.23	0.51
1:B:322:VAL:HB	1:B:340:GLN:HE22	1.75	0.51
1:F:297:ILE:HD12	1:F:338:ILE:HG12	1.93	0.51
1:B:190:SER:O	1:B:191:GLU:HB2	2.10	0.51
1:D:180:GLY:HA2	2:D:401:BH5:H36	1.92	0.51
1:C:270:ILE:HD13	1:C:342:MET:SD	2.50	0.51
1:D:344:GLU:HG2	3:D:634:HOH:O	2.10	0.51
1:A:119:ARG:O	1:A:123:GLU:HG3	2.11	0.51
2:E:401:BH5:CAK	2:E:401:BH5:OAB	2.59	0.51
1:E:297:ILE:CD1	1:E:338:ILE:HG12	2.41	0.50
1:A:211:LEU:HD12	2:A:401:BH5:CAP	2.41	0.50
1:A:233:GLN:HA	1:A:236:TRP:NE1	2.26	0.50
1:B:253:ASP:O	1:B:257:GLN:HG3	2.11	0.50
1:E:321:ALA:HA	3:E:685:HOH:O	2.11	0.50
1:A:190:SER:O	1:A:191:GLU:HB2	2.10	0.50
1:F:256:VAL:O	1:F:259:LEU:HB3	2.12	0.50
1:B:356:SER:O	1:B:360:ARG:HG3	2.11	0.50
1:E:318:LEU:HD12	1:E:319:GLY:N	2.26	0.50
1:F:150:MET:O	1:F:154:MET:HG3	2.12	0.50
1:D:52:ARG:H	1:D:52:ARG:HD2	1.76	0.50
1:D:83:GLU:HG3	1:D:154:MET:HB3	1.92	0.50
1:D:153:GLY:HA3	1:D:174:TYR:CG	2.45	0.50
1:A:180:GLY:HA2	2:A:401:BH5:H36	1.93	0.50
1:A:90:VAL:O	1:A:94:VAL:HG23	2.12	0.49
1:D:320:GLN:CD	1:D:321:ALA:H	2.16	0.49
1:C:233:GLN:HA	1:C:236:TRP:NE1	2.28	0.49
1:B:255:ALA:HB1	1:B:310:PHE:CZ	2.47	0.49
1:D:233:GLN:HA	1:D:236:TRP:CD1	2.47	0.49
1:D:246:PHE:CE1	1:D:255:ALA:HA	2.47	0.49
1:F:105:TYR:O	1:F:107:PRO:HD3	2.11	0.49
1:F:119:ARG:O	1:F:123:GLU:HG3	2.13	0.49
1:A:150:MET:HG3	1:A:174:TYR:O	2.13	0.49
1:C:232:PRO:HG2	1:C:235:VAL:HB	1.94	0.49
1:D:92:LYS:O	1:D:96:LEU:HG	2.12	0.49
1:E:138:LYS:HG3	1:E:189:ALA:HB1	1.94	0.49
2:A:401:BH5:H38	3:A:513:HOH:O	2.12	0.49
1:E:129:SER:HB2	1:E:133:ARG:NH1	2.26	0.49
1:F:137:GLU:HG3	3:F:521:HOH:O	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:153:GLY:HA3	1:F:174:TYR:CG	2.48	0.49
1:A:100:PHE:HA	1:A:103:PHE:CD2	2.48	0.49
1:E:293:GLN:O	1:E:297:ILE:HG13	2.12	0.49
1:D:211:LEU:HD12	2:D:401:BH5:H30	1.94	0.48
1:D:327:ASP:OD2	1:F:326:MET:HA	2.13	0.48
1:A:125:PHE:N	1:A:126:PRO:CD	2.76	0.48
1:B:77:ARG:CD	2:B:401:BH5:H11	2.43	0.48
1:D:333:ALA:O	1:D:337:ILE:HG13	2.13	0.48
1:E:44:TYR:OH	1:E:66:ARG:HG2	2.13	0.48
1:F:246:PHE:CD1	1:F:255:ALA:HA	2.48	0.48
1:D:115:LYS:HA	1:D:115:LYS:CE	2.41	0.48
1:D:236:TRP:CG	1:D:243:LEU:HD13	2.49	0.48
1:E:229:GLU:CG	1:E:243:LEU:HD23	2.42	0.48
1:B:146:ILE:HG22	1:B:150:MET:HE3	1.95	0.48
1:F:124:ASP:C	1:F:126:PRO:HD2	2.34	0.48
1:F:221:LEU:O	1:F:224:GLN:HB3	2.12	0.48
1:F:89:SER:HG	1:F:91:GLU:HG2	1.76	0.48
1:D:53:SER:O	1:D:54:PHE:HB2	2.12	0.48
1:E:321:ALA:O	1:E:325:MET:HG2	2.13	0.48
1:F:79:LEU:HB2	1:F:100:PHE:CE2	2.48	0.48
1:D:260:ASN:HD22	1:D:353:ASN:HD22	1.61	0.48
1:F:118:ASP:O	1:F:121:VAL:HG22	2.14	0.48
1:D:238:ARG:HH11	1:D:238:ARG:HB2	1.79	0.48
1:E:92:LYS:O	1:E:95:PRO:HD2	2.13	0.48
1:A:297:ILE:CD1	1:A:338:ILE:HG12	2.44	0.48
1:D:238:ARG:HB2	1:D:238:ARG:NH1	2.29	0.48
1:B:67:ASN:O	1:B:71:ILE:HG12	2.14	0.47
1:D:190:SER:O	1:D:191:GLU:HB2	2.14	0.47
1:D:236:TRP:CD1	1:D:243:LEU:HD13	2.48	0.47
1:F:52:ARG:HG3	1:F:53:SER:N	2.29	0.47
1:D:150:MET:O	1:D:154:MET:HG3	2.13	0.47
1:B:185:ARG:HD2	3:B:510:HOH:O	2.14	0.47
1:C:255:ALA:HB1	1:C:310:PHE:CZ	2.49	0.47
1:E:72:PHE:O	1:E:75:VAL:HG22	2.14	0.47
1:D:105:TYR:O	1:D:107:PRO:HD3	2.13	0.47
1:F:72:PHE:CD1	1:F:143:ILE:HG23	2.49	0.47
1:F:200:ASP:OD2	1:F:203:ARG:HD2	2.15	0.47
1:C:333:ALA:O	1:C:337:ILE:HG13	2.15	0.47
1:C:190:SER:O	1:C:191:GLU:HB2	2.14	0.47
1:C:233:GLN:HG2	1:C:236:TRP:CZ2	2.50	0.47
1:D:41:LYS:HA	1:F:368:THR:OG1	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:362:ILE:O	1:F:366:ILE:HG13	2.15	0.47
1:B:36:LEU:HG	1:B:37:SER:N	2.29	0.47
1:B:125:PHE:N	1:B:126:PRO:CD	2.78	0.47
1:D:125:PHE:N	1:D:126:PRO:CD	2.78	0.47
1:E:42:THR:O	1:E:45:LYS:HB3	2.15	0.47
1:E:331:MET:HB3	1:E:332:PRO:HD3	1.97	0.47
1:A:297:ILE:HD12	1:A:338:ILE:HG12	1.97	0.47
1:E:233:GLN:HA	1:E:236:TRP:CE2	2.50	0.47
1:F:94:VAL:N	1:F:95:PRO:HD2	2.31	0.46
1:F:331:MET:HB3	1:F:332:PRO:HD3	1.97	0.46
1:B:92:LYS:HE2	3:B:786:HOH:O	2.15	0.46
1:B:362:ILE:O	1:B:366:ILE:HG13	2.15	0.46
1:E:320:GLN:HB3	1:E:323:THR:HG22	1.97	0.46
1:C:73:TYR:HB2	3:C:533:HOH:O	2.14	0.46
1:F:220:TYR:OH	1:F:246:PHE:HB2	2.15	0.46
1:D:334:VAL:O	1:D:338:ILE:HG13	2.16	0.46
1:C:179:VAL:HG21	2:C:401:BH5:H19	1.97	0.46
1:C:357:SER:O	1:C:361:GLN:HG3	2.16	0.46
1:E:291:ILE:O	1:E:295:MET:HG2	2.15	0.46
1:F:64:GLU:HG3	3:F:552:HOH:O	2.15	0.46
1:D:252:ILE:CG2	1:D:253:ASP:N	2.79	0.46
1:F:317:ARG:O	1:F:318:LEU:HB2	2.16	0.46
1:A:77:ARG:HD2	2:A:401:BH5:CAY	2.46	0.46
1:B:326:MET:CE	1:C:291:ILE:HD11	2.45	0.46
1:F:92:LYS:O	1:F:95:PRO:HG2	2.16	0.46
1:B:235:VAL:HG12	1:B:258:CYS:SG	2.56	0.46
1:D:170:LYS:HD3	1:D:174:TYR:HE2	1.80	0.46
1:A:183:LEU:HD12	2:A:401:BH5:H35	1.98	0.45
1:A:362:ILE:O	1:A:366:ILE:HG13	2.16	0.45
1:D:111:PHE:HB3	1:D:122:LEU:HB3	1.98	0.45
1:B:239:TYR:O	1:B:254:LEU:HD13	2.15	0.45
1:B:256:VAL:HG21	1:B:307:GLN:HG2	1.98	0.45
1:B:320:GLN:HG2	1:B:340:GLN:CD	2.36	0.45
1:E:326:MET:HA	1:F:327:ASP:HB2	1.99	0.45
1:A:153:GLY:HA3	1:A:174:TYR:CG	2.51	0.45
1:B:323:THR:OG1	1:B:340:GLN:HG2	2.17	0.45
1:B:347:HIS:O	1:B:347:HIS:CG	2.69	0.45
1:D:324:LEU:HD21	1:E:318:LEU:CD1	2.46	0.45
1:E:90:VAL:O	1:E:94:VAL:HG23	2.17	0.45
1:E:153:GLY:HA3	1:E:174:TYR:CG	2.51	0.45
1:E:241:LYS:HA	3:E:684:HOH:O	2.15	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:200:ASP:OD2	1:F:203:ARG:HB2	2.17	0.45
1:F:262:LEU:O	1:F:265:ASN:HB3	2.17	0.45
1:D:220:TYR:CZ	1:D:246:PHE:HB2	2.52	0.45
1:B:321:ALA:O	1:B:325:MET:HG2	2.17	0.45
1:B:338:ILE:O	1:B:342:MET:HG2	2.17	0.45
1:D:77:ARG:O	1:D:77:ARG:HD3	2.17	0.45
1:D:137:GLU:HB2	3:D:541:HOH:O	2.15	0.45
1:E:114:SER:HB3	1:E:119:ARG:HB2	1.99	0.45
1:F:73:TYR:CE2	2:F:401:BH5:H13	2.52	0.45
1:B:36:LEU:CG	1:B:37:SER:N	2.80	0.45
1:C:263:ILE:O	1:C:267:LEU:HG	2.17	0.45
1:C:125:PHE:N	1:C:126:PRO:CD	2.80	0.44
1:D:271:PRO:HA	1:D:369:GLN:HE22	1.81	0.44
1:D:157:PHE:CZ	1:D:170:LYS:HD2	2.52	0.44
1:E:233:GLN:HA	1:E:236:TRP:CD1	2.52	0.44
1:F:107:PRO:O	1:F:126:PRO:HB3	2.17	0.44
1:F:138:LYS:HE3	1:F:139:TYR:CZ	2.52	0.44
1:F:306:ASN:O	1:F:309:VAL:HG23	2.17	0.44
1:C:77:ARG:CZ	2:C:401:BH5:H11	2.47	0.44
1:F:95:PRO:O	1:F:99:ASN:ND2	2.51	0.44
1:F:323:THR:OG1	1:F:324:LEU:N	2.50	0.44
1:B:91:GLU:CD	1:B:91:GLU:H	2.21	0.44
1:B:291:ILE:HB	1:B:292:PRO:HD3	1.99	0.44
1:A:149:ARG:HH22	1:A:185:ARG:HH22	1.66	0.44
1:B:211:LEU:HD23	1:B:296:ALA:HB2	2.00	0.44
1:C:252:ILE:HG23	1:C:253:ASP:N	2.33	0.44
2:C:401:BH5:OAG	2:C:401:BH5:CAJ	2.66	0.44
1:E:320:GLN:HG3	1:E:340:GLN:HE21	1.83	0.44
1:A:331:MET:HB3	1:A:332:PRO:HD3	2.00	0.44
1:E:213:LYS:O	1:E:217:ILE:HG13	2.17	0.44
1:E:323:THR:C	1:E:325:MET:N	2.71	0.44
1:A:291:ILE:HD11	1:C:326:MET:HE3	2.00	0.43
1:F:190:SER:O	1:F:191:GLU:HB2	2.18	0.43
1:D:308:GLN:HA	1:D:308:GLN:NE2	2.33	0.43
1:D:327:ASP:CG	1:F:326:MET:HA	2.39	0.43
1:A:224:GLN:NE2	1:A:244:GLY:CA	2.78	0.43
1:B:210:PHE:CZ	1:B:297:ILE:HG12	2.53	0.43
1:D:148:ARG:O	1:D:152:ILE:HG12	2.18	0.43
1:A:255:ALA:HB1	1:A:310:PHE:CZ	2.53	0.43
1:A:327:ASP:HB3	1:C:326:MET:HA	2.01	0.43
1:B:153:GLY:HA3	1:B:174:TYR:CD1	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:291:ILE:HB	1:E:292:PRO:HD3	2.01	0.43
1:F:211:LEU:HD12	2:F:401:BH5:CAP	2.46	0.43
1:F:211:LEU:HD23	1:F:296:ALA:HB2	2.01	0.43
1:A:317:ARG:O	1:A:318:LEU:CD1	2.66	0.43
1:E:75:VAL:HG23	1:E:76:LEU:N	2.34	0.43
1:C:100:PHE:HA	1:C:103:PHE:CD2	2.53	0.43
1:C:356:SER:O	1:C:360:ARG:HG3	2.19	0.43
1:F:319:GLY:O	1:F:320:GLN:HB2	2.18	0.43
1:A:52:ARG:NE	2:A:401:BH5:OAC	2.46	0.43
1:A:85:ASP:OD1	1:A:114:SER:HA	2.19	0.43
1:A:279:ARG:HD2	3:A:519:HOH:O	2.18	0.43
1:D:324:LEU:HD21	1:E:318:LEU:CD2	2.49	0.43
1:D:224:GLN:C	1:D:226:GLY:H	2.21	0.43
1:D:252:ILE:O	1:D:255:ALA:HB3	2.18	0.43
1:B:180:GLY:HA2	2:B:401:BH5:H36	2.01	0.43
1:D:195:PRO:O	1:D:199:GLU:HG3	2.19	0.43
1:A:248:LEU:HA	1:A:249:PRO:HD2	1.79	0.42
1:E:179:VAL:HG21	2:E:401:BH5:H19	2.01	0.42
1:A:263:ILE:O	1:A:267:LEU:HG	2.18	0.42
1:B:357:SER:HB3	3:B:752:HOH:O	2.19	0.42
1:C:229:GLU:HG2	1:C:243:LEU:HD23	2.01	0.42
1:C:262:LEU:O	1:C:265:ASN:HB3	2.19	0.42
1:F:89:SER:O	1:F:93:LYS:N	2.49	0.42
1:F:110:ARG:HD3	3:F:515:HOH:O	2.19	0.42
1:B:319:GLY:CA	1:B:324:LEU:HD21	2.49	0.42
1:C:54:PHE:O	1:C:58:ILE:HG13	2.19	0.42
1:C:353:ASN:HD22	1:C:355:SER:H	1.64	0.42
1:B:110:ARG:HG3	1:B:112:MET:SD	2.59	0.42
1:C:220:TYR:HB2	1:C:231:TRP:CZ2	2.54	0.42
1:D:246:PHE:CD1	1:D:255:ALA:HA	2.54	0.42
1:A:200:ASP:CG	1:A:203:ARG:HH21	2.22	0.42
1:A:348:ARG:O	1:A:350:PRO:HD3	2.20	0.42
1:B:297:ILE:HD13	1:B:338:ILE:HG23	2.00	0.42
1:D:338:ILE:O	1:D:342:MET:HG2	2.19	0.42
1:F:125:PHE:N	1:F:126:PRO:CD	2.77	0.42
1:F:193:GLU:HB3	1:F:197:VAL:HG21	2.00	0.42
1:B:142:VAL:O	1:B:146:ILE:HG12	2.20	0.42
1:B:252:ILE:HG23	1:B:253:ASP:N	2.34	0.42
1:D:308:GLN:NE2	1:D:311:LYS:HD2	2.34	0.42
1:F:199:GLU:O	1:F:201:THR:N	2.53	0.42
1:C:47:LEU:O	1:C:51:SER:HB3	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:THR:HB	1:E:77:ARG:HD2	2.02	0.42
1:E:177:GLY:HA3	1:E:205:ASN:OD1	2.20	0.42
2:E:401:BH5:H8	2:E:401:BH5:OAD	2.20	0.42
1:B:233:GLN:HE21	1:B:233:GLN:HB3	1.60	0.42
1:B:242:LYS:HB2	1:B:245:ASP:OD2	2.20	0.42
1:E:150:MET:HG3	1:E:174:TYR:O	2.19	0.42
1:B:250:GLU:CD	1:B:250:GLU:H	2.23	0.42
1:C:362:ILE:O	1:C:366:ILE:HG13	2.20	0.42
1:D:79:LEU:HD13	1:D:100:PHE:CG	2.55	0.42
1:F:153:GLY:HA3	1:F:174:TYR:CD1	2.55	0.42
1:A:200:ASP:OD2	1:A:203:ARG:HD2	2.19	0.42
1:B:317:ARG:NH1	3:B:665:HOH:O	2.53	0.42
1:D:238:ARG:HH11	1:D:238:ARG:CB	2.32	0.42
1:D:263:ILE:O	1:D:267:LEU:HG	2.20	0.42
1:D:295:MET:HG3	1:F:325:MET:HE2	2.02	0.42
1:E:115:LYS:HB3	1:E:115:LYS:HZ2	1.81	0.42
1:E:316:ILE:HD12	1:E:316:ILE:N	2.33	0.42
1:F:218:ARG:HD2	1:F:218:ARG:C	2.39	0.42
1:B:353:ASN:ND2	1:B:355:SER:H	2.18	0.41
1:D:228:ARG:HH11	1:D:228:ARG:HG3	1.84	0.41
1:E:129:SER:CB	1:E:133:ARG:HH12	2.30	0.41
1:D:53:SER:O	1:D:54:PHE:CB	2.66	0.41
1:F:47:LEU:HD22	1:F:70:CYS:SG	2.61	0.41
1:B:92:LYS:CE	3:B:786:HOH:O	2.67	0.41
1:D:220:TYR:OH	1:D:246:PHE:HB2	2.20	0.41
1:A:327:ASP:OD1	1:C:327:ASP:HB3	2.21	0.41
1:A:338:ILE:O	1:A:342:MET:HG2	2.21	0.41
1:D:259:LEU:HD21	1:D:309:VAL:HG21	2.02	0.41
2:D:401:BH5:H27	2:D:401:BH5:H22	1.90	0.41
1:E:67:ASN:O	1:E:71:ILE:HG12	2.21	0.41
1:F:236:TRP:HB2	1:F:246:PHE:CE2	2.56	0.41
1:E:54:PHE:O	1:E:58:ILE:HG13	2.20	0.41
1:F:180:GLY:HA2	2:F:401:BH5:H36	2.02	0.41
1:D:223:ASP:OD2	1:D:230:PHE:HD2	2.03	0.41
1:D:250:GLU:CD	1:D:250:GLU:H	2.24	0.41
1:D:262:LEU:O	1:D:265:ASN:HB3	2.21	0.41
1:E:252:ILE:HG23	1:E:253:ASP:N	2.36	0.41
1:F:148:ARG:HG2	1:F:148:ARG:HH21	1.86	0.41
1:A:252:ILE:CG2	1:A:253:ASP:N	2.84	0.41
1:B:77:ARG:NH1	1:B:77:ARG:HG2	2.36	0.41
1:C:183:LEU:CD1	2:C:401:BH5:H35	2.48	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLN:HA	1:C:236:TRP:CD1	2.56	0.41
1:D:322:VAL:C	1:D:324:LEU:N	2.73	0.41
1:E:319:GLY:O	1:E:320:GLN:HB2	2.19	0.41
1:F:50:THR:HB	1:F:77:ARG:CD	2.51	0.41
1:F:93:LYS:CD	1:F:158:LEU:HD11	2.50	0.41
1:B:77:ARG:CZ	2:B:401:BH5:H11	2.49	0.41
1:B:297:ILE:HD12	1:B:338:ILE:HG12	2.01	0.41
1:B:349:ILE:CD1	1:B:360:ARG:HG2	2.48	0.41
1:E:52:ARG:HG2	1:E:52:ARG:HH21	1.85	0.41
1:E:245:ASP:HB3	1:E:251:ASN:ND2	2.36	0.41
1:C:118:ASP:O	1:C:121:VAL:HG22	2.22	0.40
1:D:45:LYS:O	1:D:49:GLN:HG3	2.21	0.40
1:D:158:LEU:HD23	1:D:158:LEU:HA	1.93	0.40
1:E:50:THR:HB	1:E:77:ARG:CD	2.50	0.40
1:E:125:PHE:N	1:E:126:PRO:CD	2.84	0.40
1:E:320:GLN:CB	1:E:323:THR:HG22	2.51	0.40
1:E:334:VAL:O	1:E:338:ILE:HG13	2.22	0.40
1:F:242:LYS:HG3	1:F:245:ASP:OD2	2.21	0.40
1:B:36:LEU:HD21	1:B:40:LEU:HD23	2.03	0.40
1:D:320:GLN:HE21	1:D:320:GLN:HB3	1.71	0.40
1:D:326:MET:CE	1:D:333:ALA:HA	2.43	0.40
1:E:357:SER:O	1:E:361:GLN:HG3	2.21	0.40
1:B:111:PHE:HB3	1:B:122:LEU:HB3	2.04	0.40
1:C:299:THR:OG1	1:C:316:ILE:HD11	2.21	0.40
1:C:308:GLN:OE1	1:C:311:LYS:HD2	2.21	0.40
1:D:74:LEU:O	1:D:77:ARG:HB3	2.21	0.40
1:D:163:THR:OG1	1:D:164:SER:N	2.52	0.40
2:F:401:BH5:H27	2:F:401:BH5:H22	1.86	0.40
1:B:118:ASP:O	1:B:121:VAL:HG22	2.21	0.40
1:C:348:ARG:HH11	1:C:348:ARG:HB3	1.85	0.40
1:D:42:THR:HG22	1:D:46:TYR:CE2	2.57	0.40
1:D:253:ASP:O	1:D:257:GLN:HG3	2.21	0.40
1:F:146:ILE:HG23	1:F:150:MET:HE3	2.02	0.40
1:F:316:ILE:H	1:F:316:ILE:CD1	2.29	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	332/360 (92%)	316 (95%)	12 (4%)	4 (1%)	13	14
1	B	332/360 (92%)	318 (96%)	13 (4%)	1 (0%)	41	50
1	C	332/360 (92%)	323 (97%)	8 (2%)	1 (0%)	41	50
1	D	332/360 (92%)	308 (93%)	21 (6%)	3 (1%)	17	20
1	E	332/360 (92%)	316 (95%)	13 (4%)	3 (1%)	17	20
1	F	332/360 (92%)	305 (92%)	26 (8%)	1 (0%)	41	50
All	All	1992/2160 (92%)	1886 (95%)	93 (5%)	13 (1%)	22	26

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	317	ARG
1	A	320	GLN
1	D	54	PHE
1	D	318	LEU
1	C	318	LEU
1	E	318	LEU
1	A	226	GLY
1	A	318	LEU
1	E	320	GLN
1	F	200	ASP
1	D	322	VAL
1	B	63	GLY
1	E	107	PRO

5.3.2 Protein sidechains [i](#)

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	297/320 (93%)	292 (98%)	5 (2%)	60	76
1	B	297/320 (93%)	287 (97%)	10 (3%)	37	51
1	C	297/320 (93%)	288 (97%)	9 (3%)	41	57
1	D	297/320 (93%)	282 (95%)	15 (5%)	24	33
1	E	297/320 (93%)	286 (96%)	11 (4%)	34	48
1	F	297/320 (93%)	290 (98%)	7 (2%)	49	66
All	All	1782/1920 (93%)	1725 (97%)	57 (3%)	39	54

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LYS
1	A	233	GLN
1	A	241	LYS
1	A	318	LEU
1	A	344	GLU
1	B	52	ARG
1	B	72	PHE
1	B	77	ARG
1	B	84	ASP
1	B	110	ARG
1	B	203	ARG
1	B	233	GLN
1	B	317	ARG
1	B	320	GLN
1	B	347	HIS
1	C	36	LEU
1	C	52	ARG
1	C	80	ASP
1	C	110	ARG
1	C	134	ASN
1	C	203	ARG
1	C	233	GLN
1	C	295	MET
1	C	348	ARG
1	D	52	ARG
1	D	54	PHE
1	D	83	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	91	GLU
1	D	160	LYS
1	D	170	LYS
1	D	196	LEU
1	D	203	ARG
1	D	252	ILE
1	D	315	LEU
1	D	317	ARG
1	D	320	GLN
1	D	324	LEU
1	D	367	ARG
1	D	369	GLN
1	E	45	LYS
1	E	52	ARG
1	E	102	SER
1	E	115	LYS
1	E	138	LYS
1	E	203	ARG
1	E	233	GLN
1	E	238	ARG
1	E	279	ARG
1	E	316	ILE
1	E	320	GLN
1	F	77	ARG
1	F	80	ASP
1	F	137	GLU
1	F	233	GLN
1	F	250	GLU
1	F	316	ILE
1	F	340	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	224	GLN
1	A	225	GLN
1	A	233	GLN
1	A	251	ASN
1	A	257	GLN
1	A	369	GLN
1	B	101	HIS
1	B	120	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	225	GLN
1	B	233	GLN
1	B	251	ASN
1	B	320	GLN
1	B	340	GLN
1	C	48	ASN
1	C	59	GLN
1	C	101	HIS
1	C	120	GLN
1	C	225	GLN
1	C	233	GLN
1	C	251	ASN
1	C	257	GLN
1	C	293	GLN
1	C	361	GLN
1	D	106	GLN
1	D	224	GLN
1	D	225	GLN
1	D	257	GLN
1	D	308	GLN
1	D	320	GLN
1	D	353	ASN
1	D	369	GLN
1	E	233	GLN
1	E	257	GLN
1	E	320	GLN
1	E	340	GLN
1	E	361	GLN
1	F	99	ASN
1	F	161	HIS
1	F	225	GLN
1	F	233	GLN
1	F	257	GLN

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 monosaccharides 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
2	BH5	F	401	-	30,31,31	2.10	9 (30%)	37,42,42	1.27	4 (10%)
2	BH5	E	401	-	30,31,31	2.09	9 (30%)	37,42,42	1.38	5 (13%)
2	BH5	A	401	-	30,31,31	2.20	9 (30%)	37,42,42	1.47	5 (13%)
2	BH5	D	401	-	30,31,31	2.11	9 (30%)	37,42,42	1.22	4 (10%)
2	BH5	C	401	-	30,31,31	2.10	9 (30%)	37,42,42	1.20	5 (13%)
2	BH5	B	401	-	30,31,31	2.09	9 (30%)	37,42,42	1.27	5 (13%)

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	BH5	F	401	-	-	15/38/38/38	0/1/1/1
2	BH5	E	401	-	-	4/38/38/38	0/1/1/1
2	BH5	A	401	-	-	13/38/38/38	0/1/1/1
2	BH5	D	401	-	-	20/38/38/38	0/1/1/1
2	BH5	C	401	-	-	14/38/38/38	0/1/1/1
2	BH5	B	401	-	-	10/38/38/38	0/1/1/1

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	BH5	PBD-OAE	7.11	1.61	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	BH5	PBD-OAE	7.05	1.61	1.50
2	D	401	BH5	PBD-OAE	7.03	1.61	1.50
2	C	401	BH5	PBD-OAE	6.99	1.61	1.50
2	E	401	BH5	PBD-OAE	6.99	1.61	1.50
2	B	401	BH5	PBD-OAE	6.98	1.61	1.50
2	A	401	BH5	PBD-CBC	4.05	1.88	1.85
2	A	401	BH5	PBE-OAG	3.76	1.61	1.54
2	A	401	BH5	PBE-OAH	3.70	1.61	1.54
2	F	401	BH5	PBD-OAF	3.69	1.61	1.54
2	C	401	BH5	PBD-OAF	3.68	1.61	1.54
2	F	401	BH5	PBE-OAG	3.68	1.61	1.54
2	D	401	BH5	PBD-OAF	3.68	1.61	1.54
2	C	401	BH5	PBE-OAH	3.67	1.61	1.54
2	E	401	BH5	PBE-OAH	3.67	1.61	1.54
2	D	401	BH5	PBE-OAH	3.67	1.61	1.54
2	F	401	BH5	PBE-OAH	3.66	1.61	1.54
2	B	401	BH5	PBE-OAG	3.66	1.61	1.54
2	D	401	BH5	PBE-OAG	3.65	1.61	1.54
2	E	401	BH5	PBE-OAG	3.65	1.61	1.54
2	A	401	BH5	PBD-OAF	3.64	1.61	1.54
2	B	401	BH5	PBE-OAH	3.63	1.61	1.54
2	C	401	BH5	PBE-OAG	3.63	1.61	1.54
2	B	401	BH5	PBD-OAF	3.61	1.61	1.54
2	E	401	BH5	PBD-OAF	3.60	1.61	1.54
2	D	401	BH5	PBD-OAB	-3.51	1.48	1.54
2	C	401	BH5	PBD-OAB	-3.45	1.48	1.54
2	B	401	BH5	PBD-OAB	-3.44	1.48	1.54
2	F	401	BH5	PBD-OAB	-3.44	1.48	1.54
2	E	401	BH5	PBD-OAB	-3.41	1.48	1.54
2	A	401	BH5	PBE-CBC	3.40	1.87	1.85
2	A	401	BH5	PBD-OAB	-3.30	1.48	1.54
2	C	401	BH5	PBE-CBC	2.99	1.87	1.85
2	E	401	BH5	PBD-CBC	2.94	1.87	1.85
2	D	401	BH5	PBD-CBC	2.93	1.87	1.85
2	B	401	BH5	PBE-CBC	2.90	1.87	1.85
2	F	401	BH5	PBD-CBC	2.80	1.87	1.85
2	D	401	BH5	PBE-CBC	2.80	1.87	1.85
2	B	401	BH5	PBD-CBC	2.72	1.87	1.85
2	F	401	BH5	PBE-CBC	2.60	1.87	1.85
2	E	401	BH5	PBE-CBC	2.57	1.87	1.85
2	C	401	BH5	PBD-CBC	2.53	1.87	1.85
2	E	401	BH5	CAI-NBA	-2.40	1.33	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	BH5	CAJ-NBB	-2.36	1.33	1.37
2	A	401	BH5	CAJ-NBB	-2.32	1.33	1.37
2	B	401	BH5	CAI-NBA	-2.32	1.33	1.37
2	F	401	BH5	CAJ-NBB	-2.31	1.33	1.37
2	D	401	BH5	CAI-NBA	-2.30	1.33	1.37
2	F	401	BH5	CAI-NBA	-2.29	1.33	1.37
2	E	401	BH5	CAJ-NBB	-2.25	1.33	1.37
2	D	401	BH5	CAJ-NBB	-2.25	1.33	1.37
2	B	401	BH5	CAJ-NBB	-2.25	1.33	1.37
2	A	401	BH5	CAI-NBA	-2.23	1.33	1.37
2	C	401	BH5	CAI-NBA	-2.22	1.33	1.37

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	BH5	OAF-PBD-OAE	-4.78	102.32	113.06
2	E	401	BH5	OAB-PBD-CBC	3.66	114.37	106.17
2	A	401	BH5	OAB-PBD-CBC	3.61	114.27	106.17
2	A	401	BH5	PBD-CBC-OAD	3.52	115.30	107.30
2	E	401	BH5	OAF-PBD-OAE	-3.44	105.33	113.06
2	D	401	BH5	OAF-PBD-OAE	-3.26	105.74	113.06
2	F	401	BH5	OAF-PBD-OAE	-3.14	106.00	113.06
2	F	401	BH5	OAB-PBD-CBC	3.12	113.17	106.17
2	B	401	BH5	OAF-PBD-OAE	-3.07	106.17	113.06
2	B	401	BH5	OAB-PBD-CBC	3.02	112.93	106.17
2	D	401	BH5	OAB-PBD-CBC	3.00	112.89	106.17
2	E	401	BH5	PBD-CBC-OAD	3.00	114.11	107.30
2	E	401	BH5	PBE-CBC-OAD	2.91	113.92	107.30
2	C	401	BH5	OAF-PBD-OAE	-2.87	106.61	113.06
2	F	401	BH5	PBD-CBC-OAD	2.78	113.63	107.30
2	C	401	BH5	PBE-CBC-OAD	2.77	113.60	107.30
2	B	401	BH5	PBD-CBC-OAD	2.75	113.56	107.30
2	B	401	BH5	PBE-CBC-OAD	2.60	113.21	107.30
2	F	401	BH5	PBE-CBC-OAD	2.57	113.14	107.30
2	D	401	BH5	PBE-CBC-OAD	2.47	112.93	107.30
2	C	401	BH5	PBD-CBC-OAD	2.47	112.93	107.30
2	E	401	BH5	PBE-CBC-PBD	-2.46	108.41	112.81
2	D	401	BH5	PBD-CBC-OAD	2.40	112.75	107.30
2	C	401	BH5	OAB-PBD-CBC	2.37	111.48	106.17
2	A	401	BH5	OAC-PBE-CBC	2.27	115.79	109.86
2	A	401	BH5	PBE-CBC-OAD	2.23	112.38	107.30
2	C	401	BH5	PBE-CBC-PBD	-2.14	108.97	112.81

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^o)	Ideal(^o)
2	B	401	BH5	PBE-CBC-PBD	-2.07	109.10	112.81

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	BH5	PBE-CBC-PBD-OAE
2	A	401	BH5	OAD-CBC-PBD-OAE
2	A	401	BH5	CAZ-CBC-PBD-OAE
2	A	401	BH5	PBE-CBC-PBD-OAF
2	A	401	BH5	OAD-CBC-PBD-OAF
2	A	401	BH5	CAZ-CBC-PBD-OAF
2	A	401	BH5	PBE-CBC-PBD-OAB
2	A	401	BH5	OAD-CBC-PBD-OAB
2	A	401	BH5	CAZ-CBC-PBD-OAB
2	A	401	BH5	CBC-CAZ-NBB-CAK
2	A	401	BH5	CBC-CAZ-NBB-CAJ
2	B	401	BH5	NBB-CAZ-CBC-PBD
2	B	401	BH5	NBB-CAZ-CBC-PBE
2	B	401	BH5	NBB-CAZ-CBC-OAD
2	C	401	BH5	PBE-CBC-PBD-OAE
2	C	401	BH5	OAD-CBC-PBD-OAE
2	C	401	BH5	CAZ-CBC-PBD-OAE
2	C	401	BH5	PBE-CBC-PBD-OAF
2	C	401	BH5	OAD-CBC-PBD-OAF
2	C	401	BH5	CAZ-CBC-PBD-OAF
2	C	401	BH5	PBE-CBC-PBD-OAB
2	C	401	BH5	OAD-CBC-PBD-OAB
2	C	401	BH5	CAZ-CBC-PBD-OAB
2	C	401	BH5	NBB-CAZ-CBC-PBE
2	D	401	BH5	PBE-CBC-PBD-OAE
2	D	401	BH5	OAD-CBC-PBD-OAE
2	D	401	BH5	CAZ-CBC-PBD-OAE
2	D	401	BH5	PBE-CBC-PBD-OAF
2	D	401	BH5	OAD-CBC-PBD-OAF
2	D	401	BH5	CAZ-CBC-PBD-OAF
2	D	401	BH5	PBE-CBC-PBD-OAB
2	D	401	BH5	OAD-CBC-PBD-OAB
2	D	401	BH5	CAZ-CBC-PBD-OAB
2	D	401	BH5	NBB-CAZ-CBC-PBD
2	D	401	BH5	NBB-CAZ-CBC-PBE
2	D	401	BH5	NBB-CAZ-CBC-OAD

Continued on next page...

Continued from previous page...

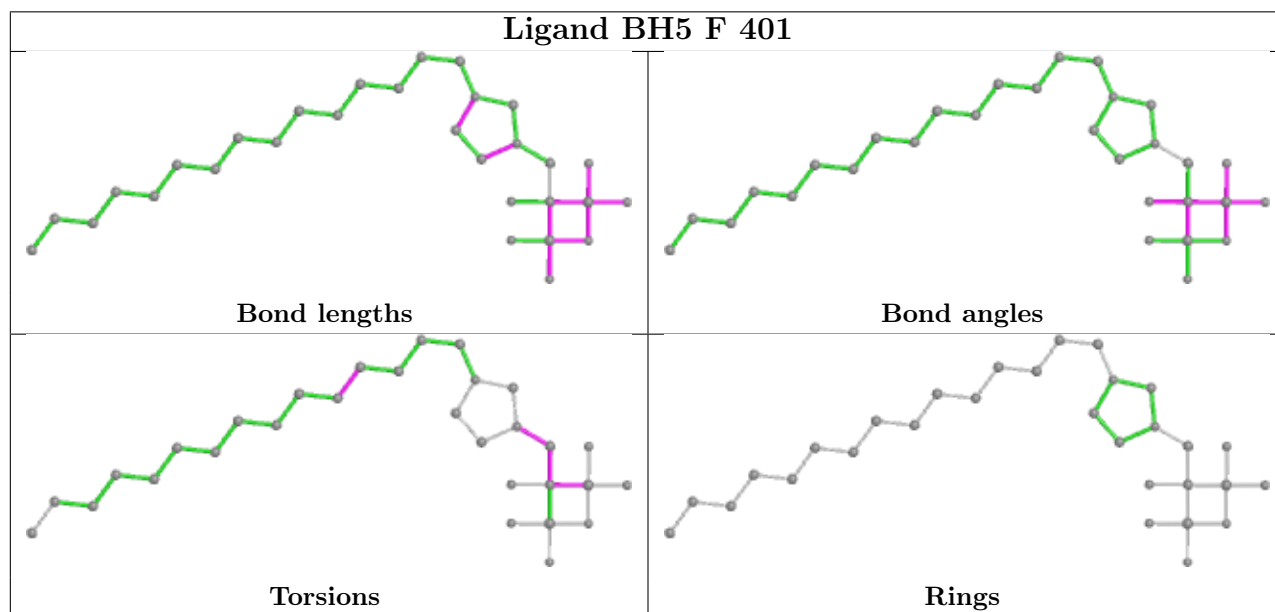
Mol	Chain	Res	Type	Atoms
2	F	401	BH5	PBE-CBC-PBD-OAE
2	F	401	BH5	OAD-CBC-PBD-OAE
2	F	401	BH5	CAZ-CBC-PBD-OAE
2	F	401	BH5	PBE-CBC-PBD-OAF
2	F	401	BH5	OAD-CBC-PBD-OAF
2	F	401	BH5	CAZ-CBC-PBD-OAF
2	F	401	BH5	PBE-CBC-PBD-OAB
2	F	401	BH5	OAD-CBC-PBD-OAB
2	F	401	BH5	CAZ-CBC-PBD-OAB
2	F	401	BH5	NBB-CAZ-CBC-PBD
2	F	401	BH5	CBC-CAZ-NBB-CAJ
2	C	401	BH5	CAR-CAS-CAT-CAU
2	B	401	BH5	PBE-CBC-PBD-OAF
2	B	401	BH5	OAD-CBC-PBE-OAH
2	D	401	BH5	PBD-CBC-PBE-OAG
2	D	401	BH5	PBD-CBC-PBE-OAC
2	E	401	BH5	CBC-CAZ-NBB-CAJ
2	A	401	BH5	NBB-CAZ-CBC-PBD
2	C	401	BH5	NBB-CAZ-CBC-PBD
2	E	401	BH5	CBC-CAZ-NBB-CAK
2	F	401	BH5	NBB-CAZ-CBC-PBE
2	F	401	BH5	CBC-CAZ-NBB-CAK
2	D	401	BH5	CAX-CAY-NBA-CAI
2	B	401	BH5	PBE-CBC-PBD-OAB
2	D	401	BH5	PBD-CBC-PBE-OAH
2	D	401	BH5	CAR-CAS-CAT-CAU
2	B	401	BH5	CAZ-CBC-PBD-OAF
2	B	401	BH5	CAZ-CBC-PBE-OAH
2	D	401	BH5	CAZ-CBC-PBE-OAG
2	E	401	BH5	CAR-CAS-CAT-CAU
2	B	401	BH5	CAX-CAY-NBA-CAI
2	C	401	BH5	NBB-CAZ-CBC-OAD
2	C	401	BH5	CAX-CAY-NBA-CAI
2	F	401	BH5	NBB-CAZ-CBC-OAD
2	F	401	BH5	CAT-CAU-CAV-CAW
2	D	401	BH5	CAT-CAU-CAV-CAW
2	B	401	BH5	OAD-CBC-PBD-OAF
2	D	401	BH5	OAD-CBC-PBE-OAG
2	A	401	BH5	CAZ-CBC-PBE-OAC
2	E	401	BH5	CAZ-CBC-PBD-OAE

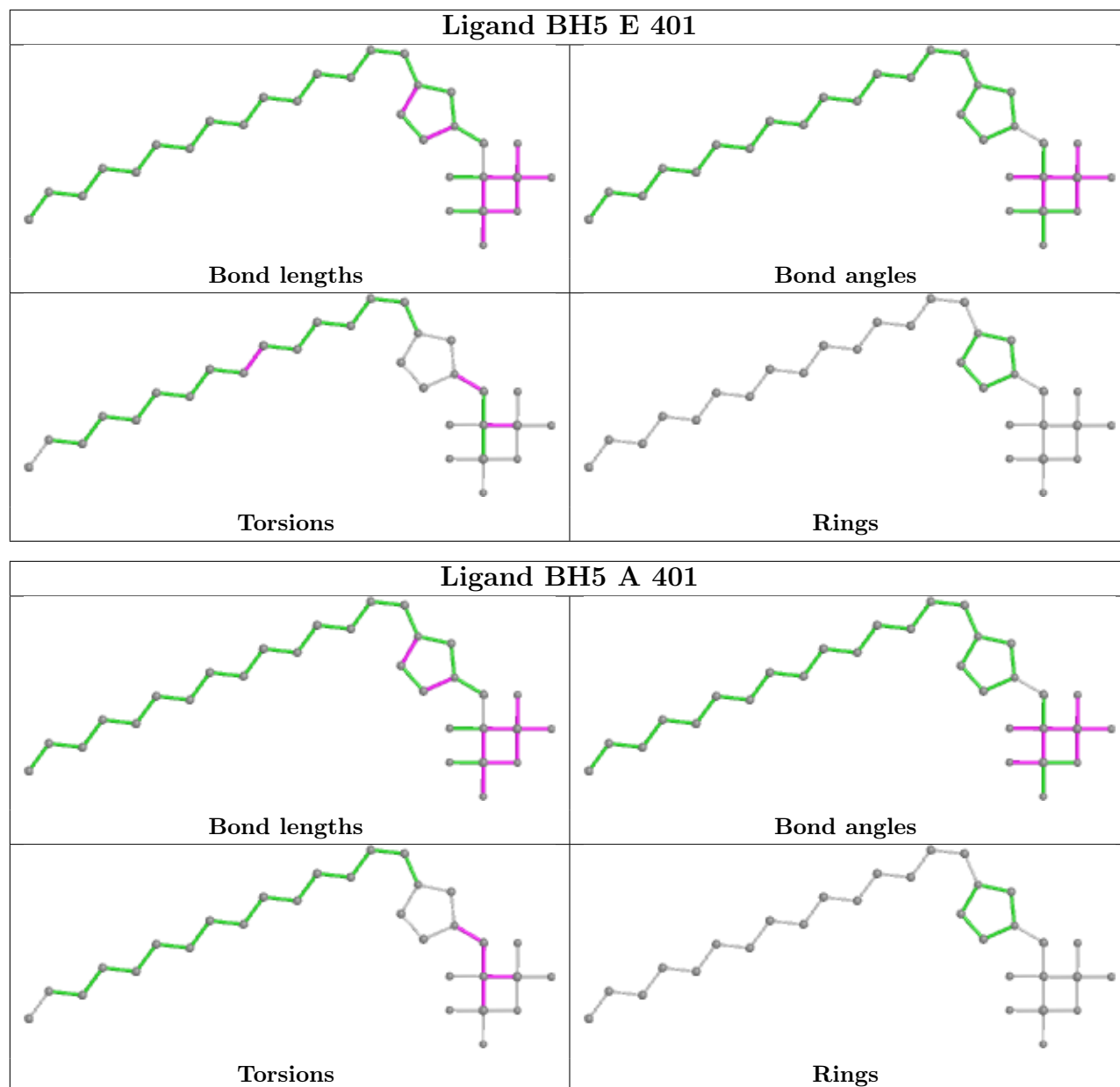
There are no ring outliers.

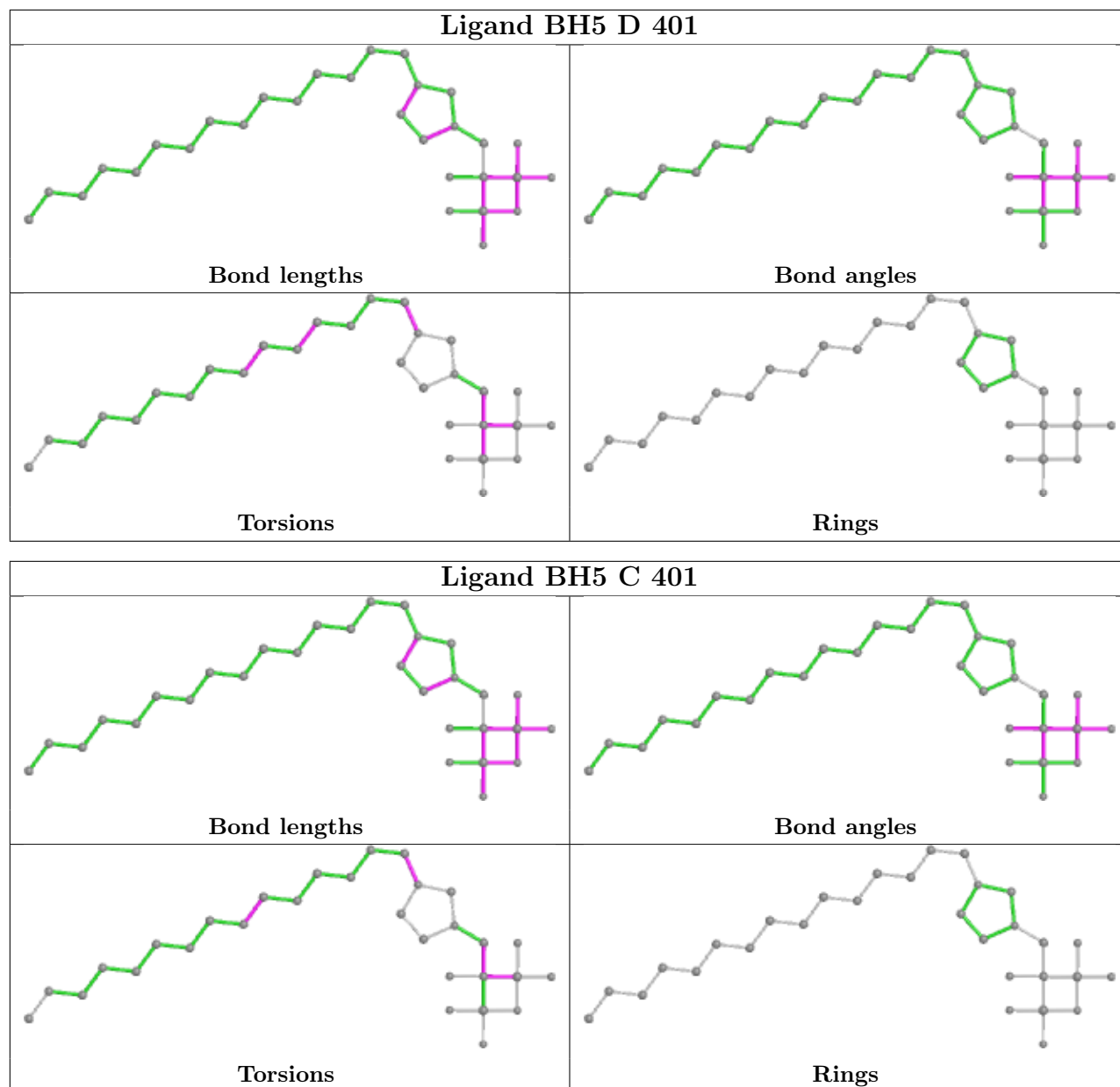
6 monomers are involved in 47 short contacts:

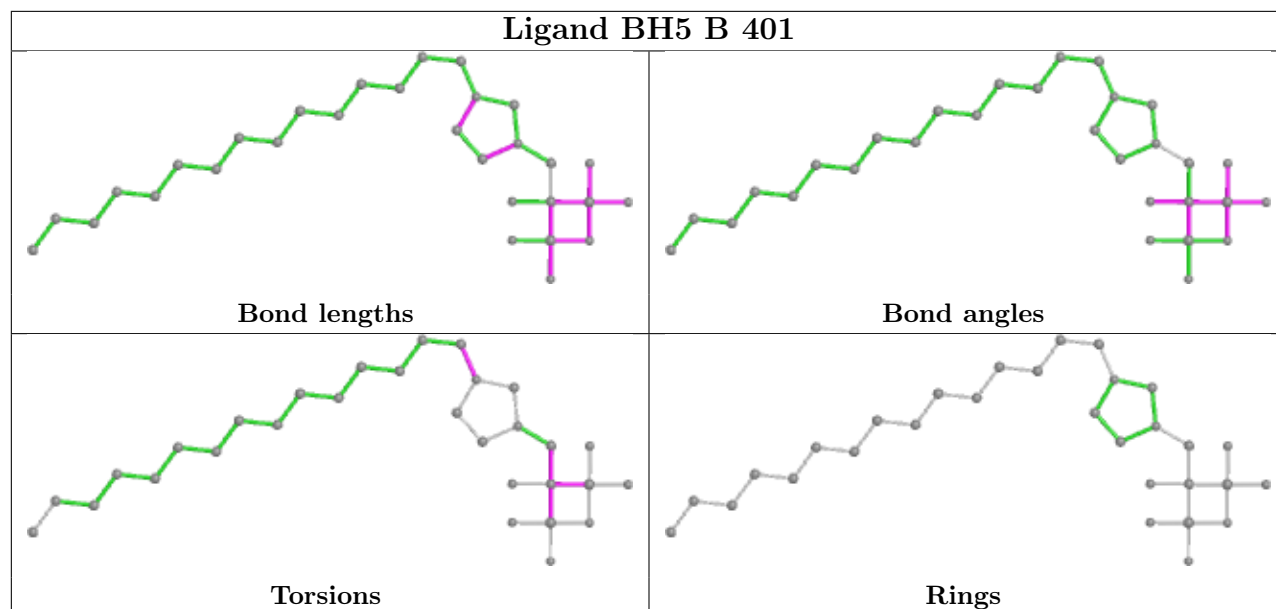
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	BH5	5	0
2	E	401	BH5	6	0
2	A	401	BH5	8	0
2	D	401	BH5	6	0
2	C	401	BH5	11	0
2	B	401	BH5	11	0

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	334/360 (92%)	-0.18	12 (3%) 42 49	16, 29, 65, 116	0
1	B	334/360 (92%)	-0.04	15 (4%) 33 40	18, 32, 68, 100	0
1	C	334/360 (92%)	-0.10	14 (4%) 36 43	18, 34, 62, 101	0
1	D	334/360 (92%)	0.30	31 (9%) 8 11	21, 45, 84, 129	0
1	E	334/360 (92%)	0.12	16 (4%) 30 37	25, 42, 72, 116	0
1	F	334/360 (92%)	0.52	39 (11%) 4 6	25, 52, 89, 119	0
All	All	2004/2160 (92%)	0.10	127 (6%) 20 25	16, 38, 82, 129	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	318	LEU	12.5
1	F	315	LEU	9.8
1	D	319	GLY	9.6
1	F	318	LEU	8.8
1	B	318	LEU	7.7
1	D	315	LEU	7.5
1	A	315	LEU	7.1
1	E	319	GLY	6.8
1	F	313	ALA	6.6
1	F	319	GLY	6.4
1	B	315	LEU	6.2
1	E	36	LEU	6.1
1	F	320	GLN	6.1
1	E	321	ALA	6.1
1	A	320	GLN	6.1
1	F	321	ALA	6.0
1	D	316	ILE	6.0
1	E	323	THR	5.9
1	B	319	GLY	5.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	318	LEU	5.1
1	C	318	LEU	5.1
1	E	322	VAL	5.0
1	E	318	LEU	5.0
1	B	313	ALA	4.9
1	F	316	ILE	4.9
1	D	317	ARG	4.9
1	C	36	LEU	4.8
1	C	313	ALA	4.8
1	F	241	LYS	4.6
1	E	320	GLN	4.6
1	A	321	ALA	4.6
1	D	36	LEU	4.6
1	F	317	ARG	4.5
1	F	324	LEU	4.5
1	B	321	ALA	4.4
1	F	36	LEU	4.4
1	D	320	GLN	4.3
1	E	315	LEU	4.2
1	D	321	ALA	4.2
1	C	320	GLN	4.1
1	A	324	LEU	4.0
1	F	221	LEU	3.9
1	B	320	GLN	3.8
1	C	321	ALA	3.7
1	F	86	MET	3.6
1	D	221	LEU	3.5
1	D	52	ARG	3.4
1	C	317	ARG	3.4
1	F	351	ASP	3.4
1	F	312	GLY	3.3
1	C	315	LEU	3.3
1	F	217	ILE	3.3
1	F	231	TRP	3.3
1	C	159	ASP	3.3
1	D	117	LYS	3.2
1	F	347	HIS	3.2
1	D	313	ALA	3.2
1	B	259	LEU	3.1
1	A	313	ALA	3.1
1	E	52	ARG	3.1
1	E	317	ARG	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	312	GLY	3.1
1	F	159	ASP	3.1
1	D	322	VAL	3.0
1	F	89	SER	3.0
1	B	36	LEU	3.0
1	D	241	LYS	3.0
1	B	351	ASP	2.9
1	B	322	VAL	2.8
1	C	53	SER	2.8
1	B	317	ARG	2.8
1	F	161	HIS	2.8
1	D	91	GLU	2.8
1	F	225	GLN	2.7
1	D	115	LYS	2.7
1	D	347	HIS	2.7
1	D	159	ASP	2.7
1	F	53	SER	2.6
1	F	314	VAL	2.6
1	F	300	LEU	2.6
1	F	250	GLU	2.6
1	B	316	ILE	2.6
1	D	263	ILE	2.6
1	D	323	THR	2.5
1	F	108	ASP	2.5
1	F	323	THR	2.5
1	C	259	LEU	2.5
1	F	72	PHE	2.5
1	F	92	LYS	2.5
1	E	313	ALA	2.5
1	C	316	ILE	2.5
1	D	224	GLN	2.5
1	A	322	VAL	2.4
1	C	52	ARG	2.4
1	D	228	ARG	2.4
1	D	310	PHE	2.4
1	D	217	ILE	2.4
1	F	310	PHE	2.3
1	E	324	LEU	2.3
1	A	52	ARG	2.3
1	F	369	GLN	2.3
1	A	316	ILE	2.3
1	D	233	GLN	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	248	LEU	2.3
1	D	262	LEU	2.3
1	E	137	GLU	2.3
1	D	352	SER	2.2
1	E	38	SER	2.2
1	B	225	GLN	2.2
1	A	69	VAL	2.2
1	C	319	GLY	2.2
1	D	242	LYS	2.2
1	F	259	LEU	2.2
1	F	357	SER	2.2
1	E	325	MET	2.2
1	E	37	SER	2.1
1	F	73	TYR	2.1
1	F	322	VAL	2.1
1	F	166	GLN	2.1
1	A	36	LEU	2.1
1	F	76	LEU	2.1
1	B	323	THR	2.1
1	C	323	THR	2.1
1	F	224	GLN	2.1
1	D	75	VAL	2.1
1	D	231	TRP	2.1
1	D	90	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](#)

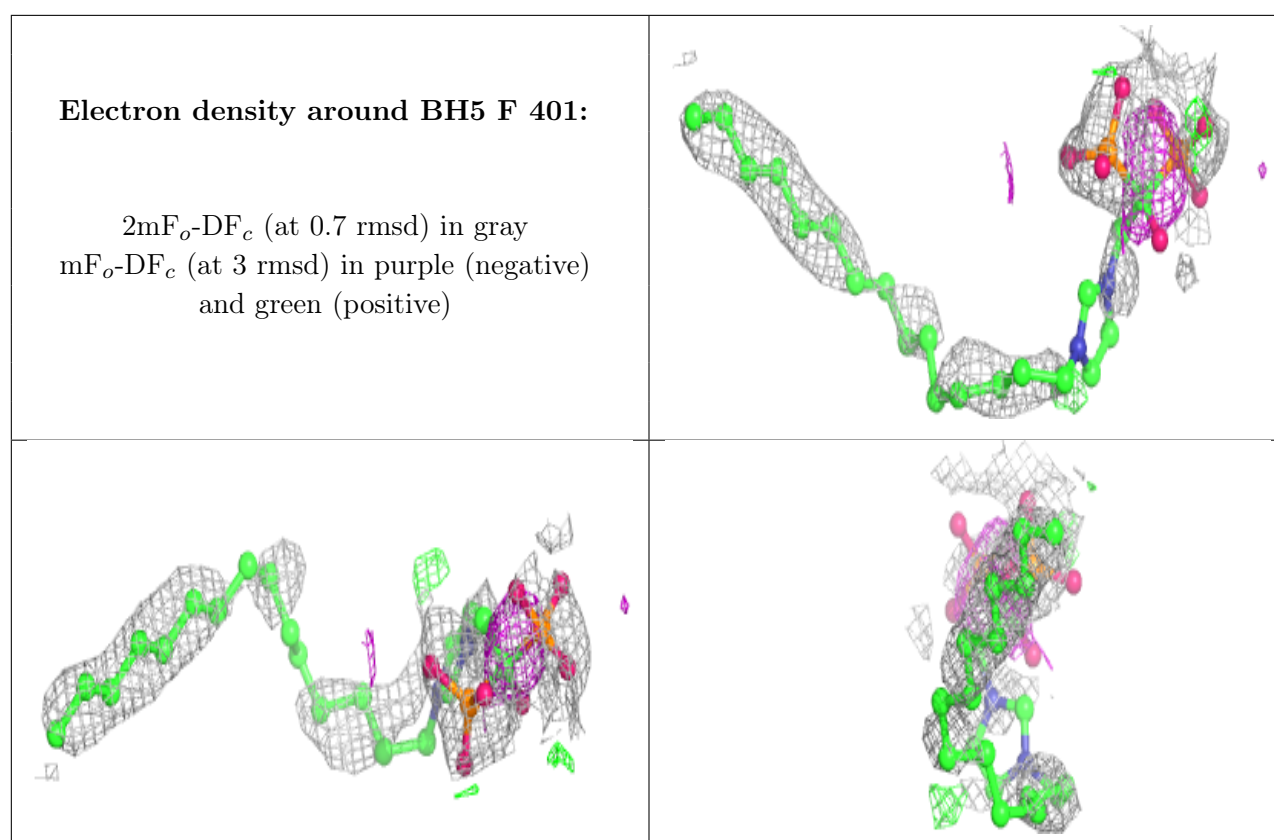
There are no monosaccharides in this entry.

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, 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.

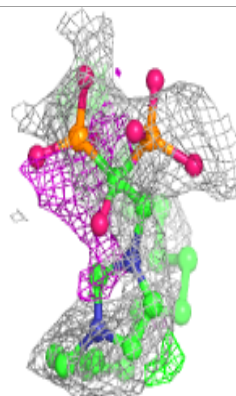
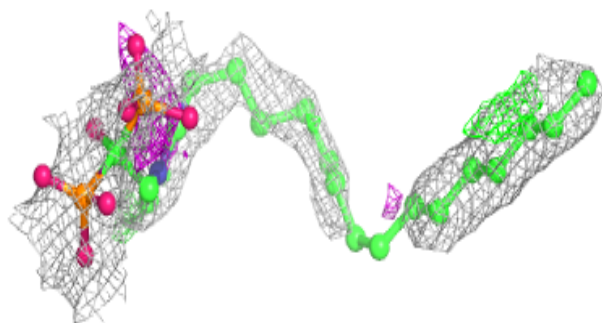
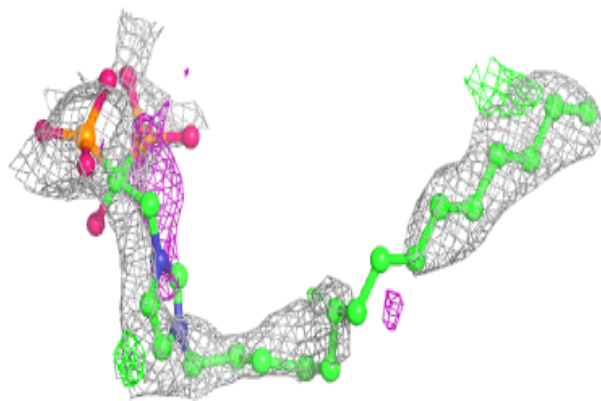
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BH5	F	401	31/31	0.38	0.46	63,115,130,130	0
2	BH5	D	401	31/31	0.43	0.42	53,104,125,125	0
2	BH5	C	401	31/31	0.50	0.41	35,111,128,129	0
2	BH5	E	401	31/31	0.58	0.43	59,109,123,123	0
2	BH5	B	401	31/31	0.59	0.34	37,102,120,121	0
2	BH5	A	401	31/31	0.61	0.35	37,107,128,128	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.

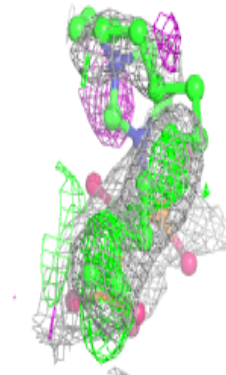
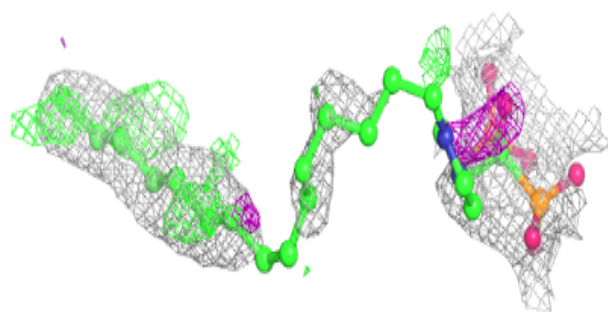
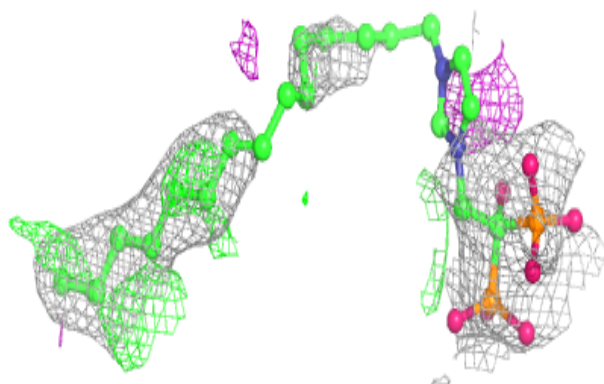


Electron density around BH5 D 401:

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

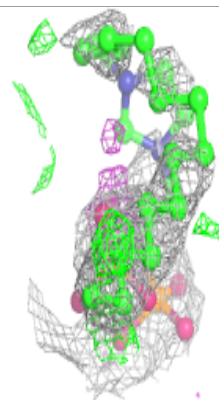
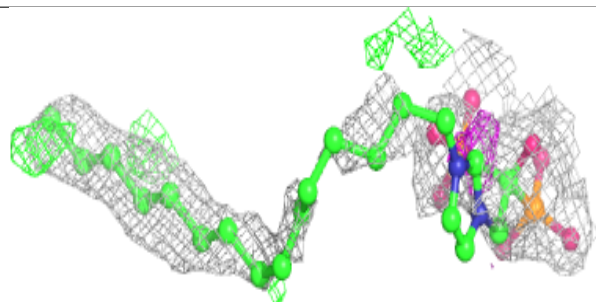
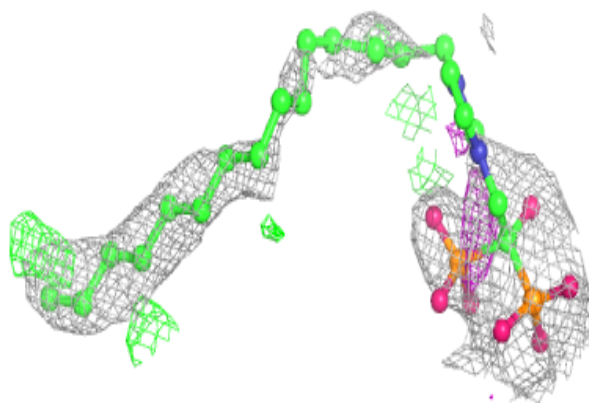
**Electron density around BH5 C 401:**

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

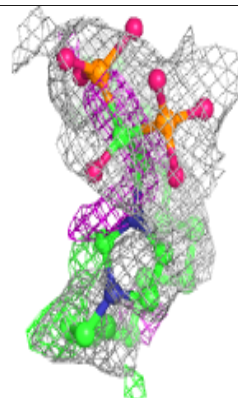
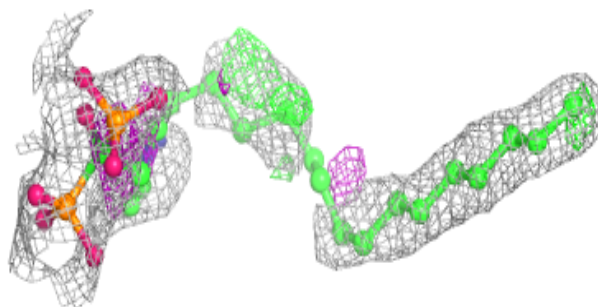
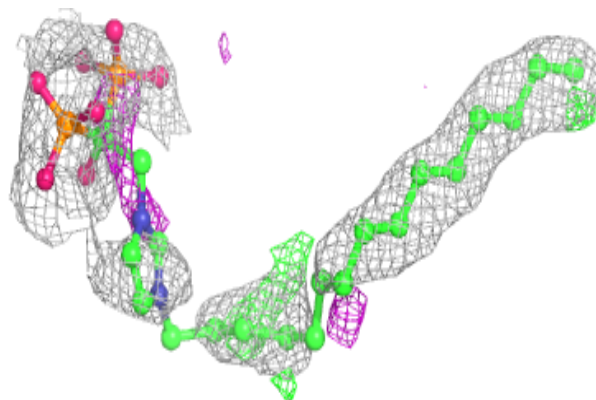


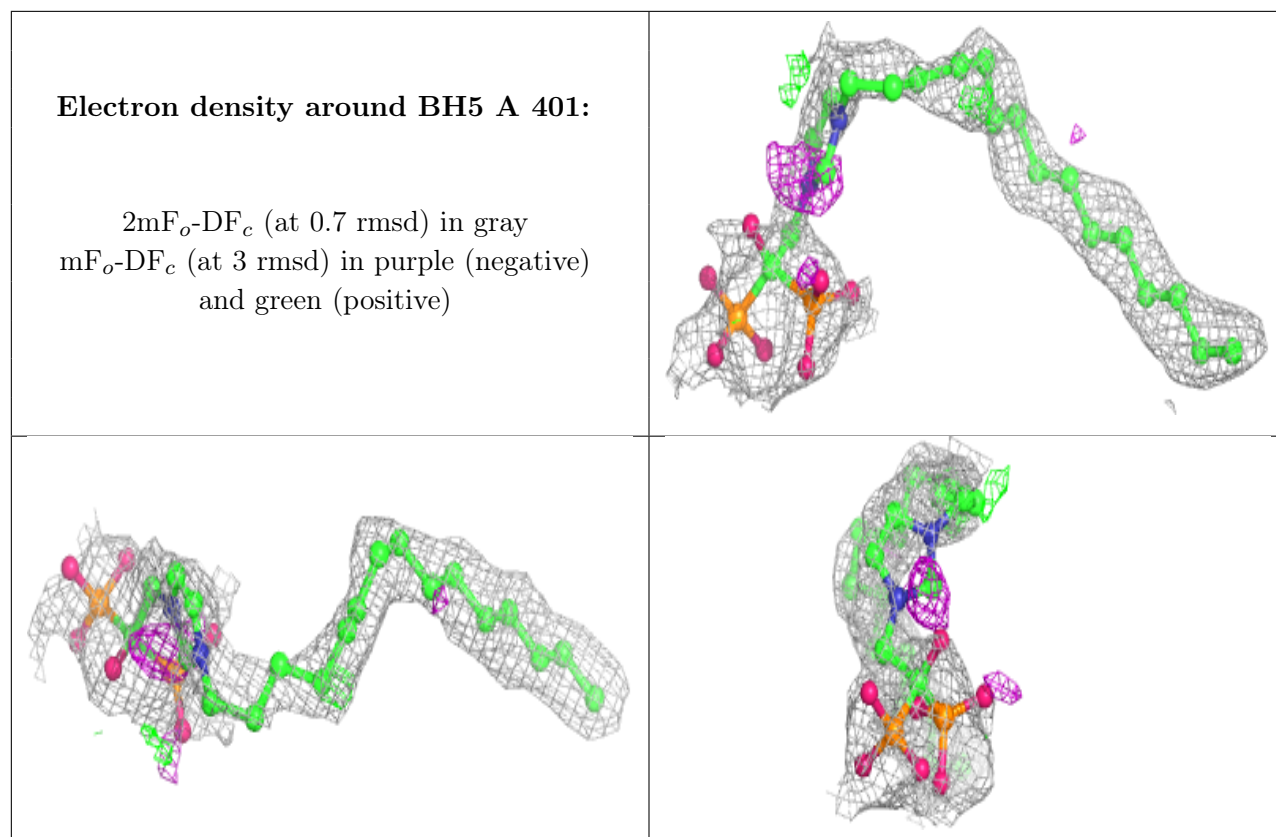
Electron density around BH5 E 401:

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

**Electron density around BH5 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.