Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 07:17 pm BST

PDB ID	:	8CQK
Title	:	pVHL:EloB:EloC in complex with (2S,4R)-1-((S)-2-(1-Fluorocyclopropane-1-carboxamido)-3,3-dimethylbutanoyl)-4-hydroxy-N-((S)-1-(2-methyl-4-(4-methylthiazol-5-yl)phenyl)ethyl)pyrrolidine-2-carboxamide (Compound 30)
Authors	:	Casement, R.; Phuong Vu, L.; Ciulli, A.; Gutschow, M.
Deposited on	:	2023-03-06
Resolution	:	2.62 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:

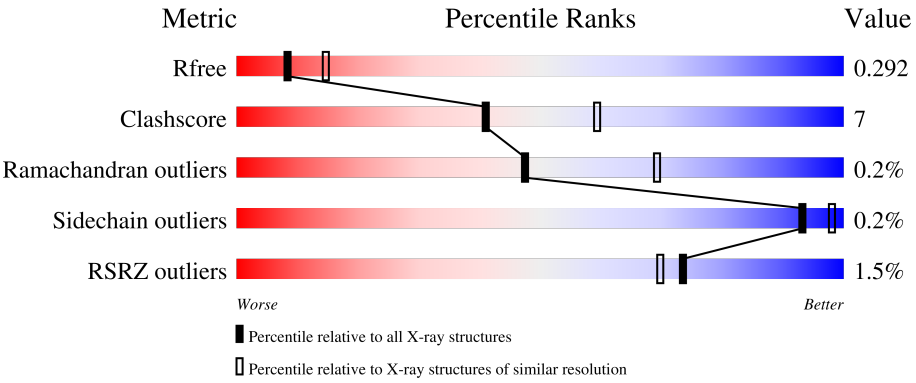
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 <=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	104	90% 10%
1	D	104	4% 78% 22%
1	G	104	80% 20%
1	J	104	79% 21%

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Mol	Chain	Length	Quality of chain
2	B	97	3% 74% 16% 9%
2	E	97	% 72% 16% 10%
2	H	97	80% 10% 9%
2	K	97	2% 69% 21% 10%
3	C	162	% 77% 11% 12%
3	F	162	2% 74% 14% 12%
3	I	162	% 69% 19% 12%
3	L	162	% 71% 16% 13%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10567 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 Elongin-B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	104	Total	As	C	N	O	S	0	0	0
			801	2	508	135	152	4			
1	D	104	Total	As	C	N	O	S	0	0	0
			783	2	499	126	152	4			
1	G	104	Total	As	C	N	O	S	0	0	0
			815	2	517	137	154	5			
1	J	104	Total	As	C	N	O	S	0	0	0
			807	2	512	136	152	5			

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			685	443	107	129	6			
2	E	87	Total	C	N	O	S	0	0	0
			674	436	107	126	5			
2	H	88	Total	C	N	O	S	0	0	0
			689	443	112	127	7			
2	K	87	Total	C	N	O	S	0	0	0
			680	441	108	124	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	16	MET	-	initiating methionine	UNP Q15369
E	16	MET	-	initiating methionine	UNP Q15369
H	16	MET	-	initiating methionine	UNP Q15369
K	16	MET	-	initiating methionine	UNP Q15369

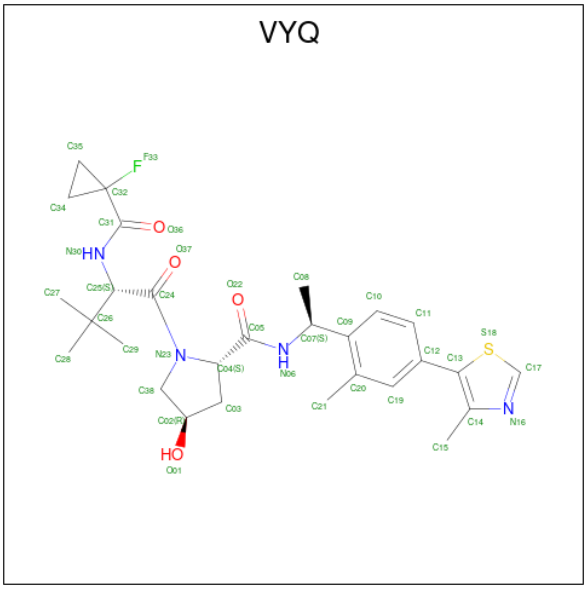
- Molecule 3 is a protein called von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	143	Total	As	C	N	O	S	0	0	0
			1094	1	696	195	200	2			
3	F	142	Total	As	C	N	O	S	0	0	0
			1092	1	697	193	199	2			
3	I	142	Total	As	C	N	O	S	0	0	0
			1098	1	701	195	199	2			
3	L	141	Total	As	C	N	O	S	0	0	0
			1101	1	704	195	199	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	52	GLY	-	expression tag	UNP P40337
C	53	SER	-	expression tag	UNP P40337
F	52	GLY	-	expression tag	UNP P40337
F	53	SER	-	expression tag	UNP P40337
I	52	GLY	-	expression tag	UNP P40337
I	53	SER	-	expression tag	UNP P40337
L	52	GLY	-	expression tag	UNP P40337
L	53	SER	-	expression tag	UNP P40337

- Molecule 4 is (2 {S},4 {R})-1-[(2 {S})-2-[(1-fluoranylcyclopropyl)carbonylamino]-3,3-dimethyl-butanoyl]- {N}-[(1 {S})-1-[2-methyl-4-(4-methyl-1,3-thiazol-5-yl)phenyl]ethyl]-4-oxidanyl-pyrrolidine-2-carboxamide (three-letter code: VYQ) (formula: $C_{28}H_{37}FN_4O_4S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	C	1	Total	C	F	N	O	S	0	0
			38	28	1	4	4	1		
4	F	1	Total	C	F	N	O	S	0	0
			38	28	1	4	4	1		
4	I	1	Total	C	F	N	O	S	0	0
			38	28	1	4	4	1		
4	L	1	Total	C	F	N	O	S	0	0
			38	28	1	4	4	1		

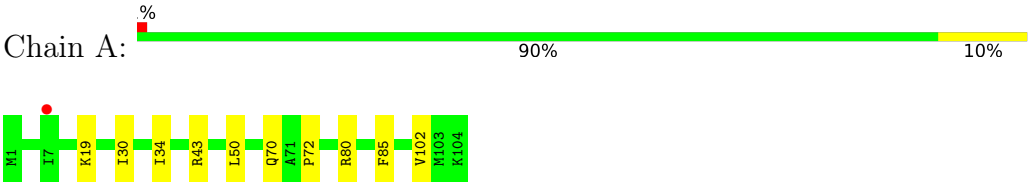
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	0
			10	10		
5	B	4	Total	O	0	0
			4	4		
5	C	10	Total	O	0	0
			10	10		
5	D	4	Total	O	0	0
			4	4		
5	E	7	Total	O	0	0
			7	7		
5	F	14	Total	O	0	0
			14	14		
5	G	4	Total	O	0	0
			4	4		
5	H	8	Total	O	0	0
			8	8		
5	I	13	Total	O	0	0
			13	13		
5	J	2	Total	O	0	0
			2	2		
5	K	7	Total	O	0	0
			7	7		
5	L	13	Total	O	0	0
			13	13		

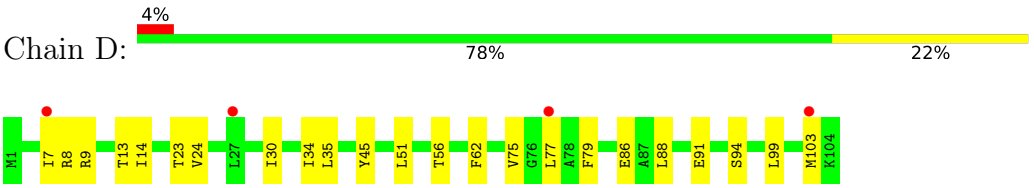
3 Residue-property plots (i)

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.

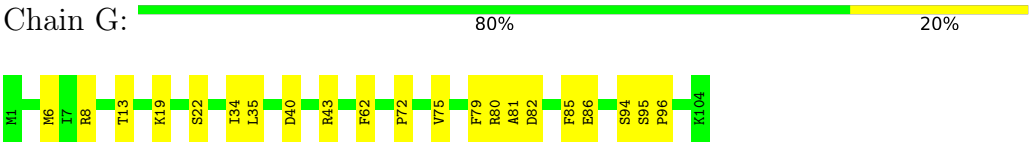
• Molecule 1: Elongin-B



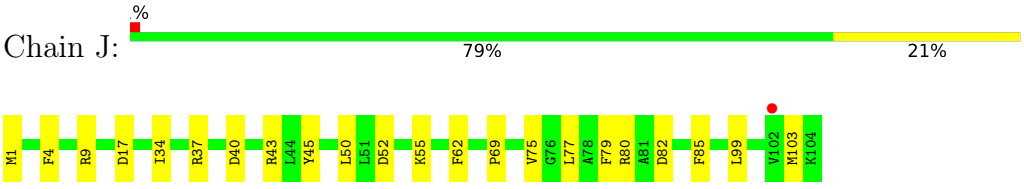
• Molecule 1: Elongin-B



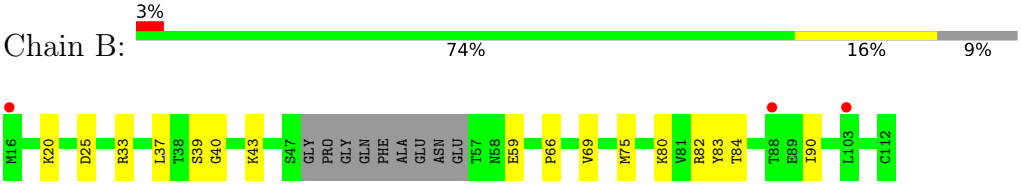
• Molecule 1: Elongin-B



• Molecule 1: Elongin-B

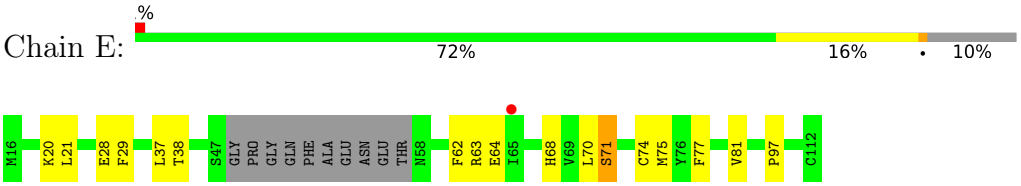


• Molecule 2: Elongin-C



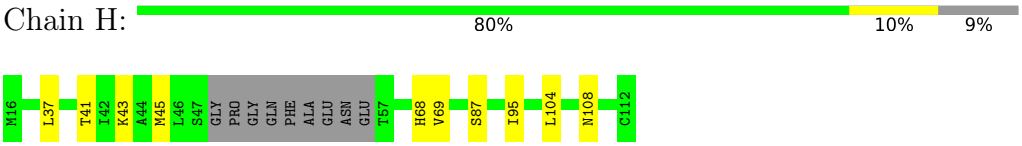
• Molecule 2: Elongin-C

Chain E:



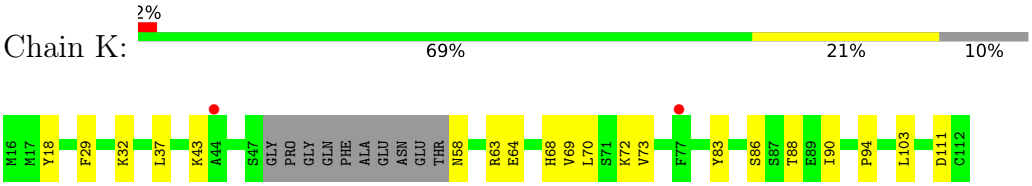
• Molecule 2: Elongin-C

Chain H:



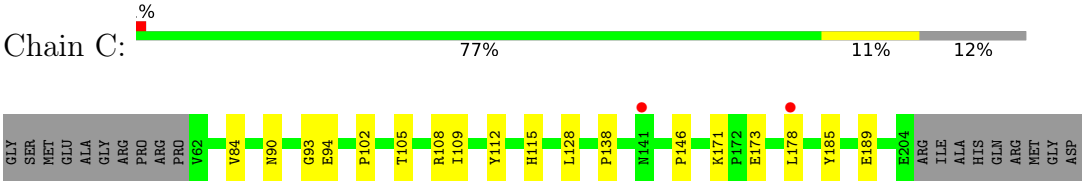
• Molecule 2: Elongin-C

Chain K:



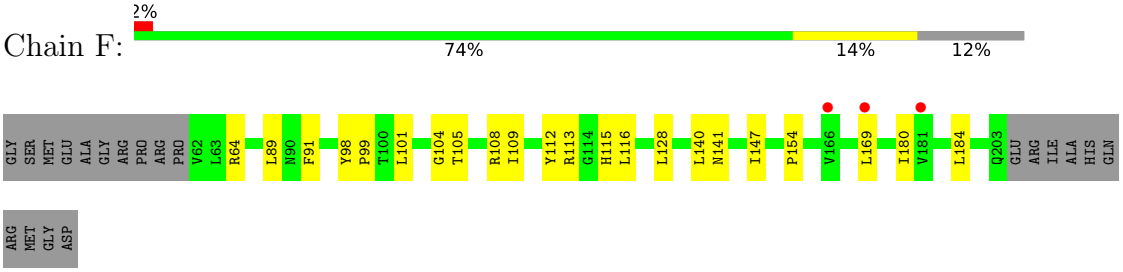
• Molecule 3: von Hippel-Lindau disease tumor suppressor

Chain C:



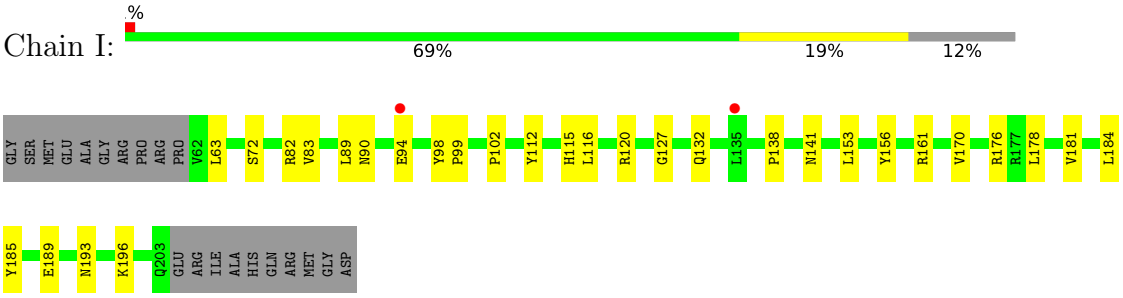
• Molecule 3: von Hippel-Lindau disease tumor suppressor

Chain F:



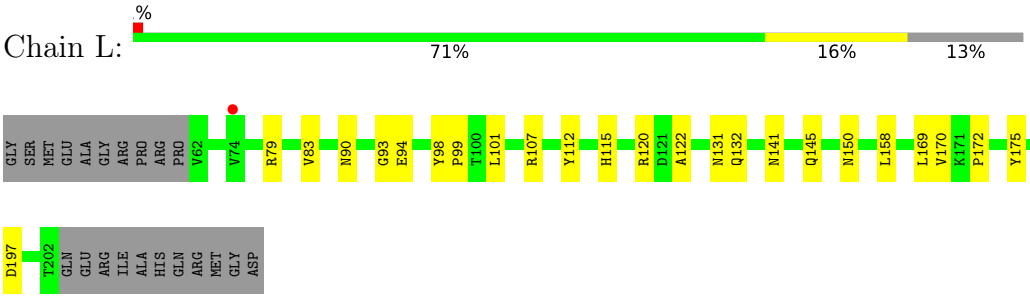
• Molecule 3: von Hippel-Lindau disease tumor suppressor

Chain I:



• Molecule 3: von Hippel-Lindau disease tumor suppressor

Chain L:


%
71%
16%
13%
GLY SER MET GLU ALA GLY ARG PRO ARG PRO V62 V74 R79 V83 N90 G93 E94 Y98 P99 T100 L101 R107 Y112 H115 R120 D121 A122 N131 Q132 N141 Q145 N150 L158 L169 V170 K171 P172 Y175 Y185 E189
D197 T202 GLN GLU ARG ILE ALA HIS GLN ARG MET GLY ASP

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	93.28Å 93.28Å 363.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.07 – 2.62 90.82 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.8 (65.07-2.62) 100.0 (90.82-2.62)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.54 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.18.2	Depositor
R, R_{free}	0.246 , 0.290 0.250 , 0.292	Depositor DCC
R_{free} test set	2437 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	56.8	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	10567	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.54 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0882e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CAS, VYQ

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	0.39	0/797	0.57	0/1078
1	D	0.37	0/779	0.60	0/1057
1	G	0.36	0/811	0.60	0/1093
1	J	0.32	0/803	0.57	0/1084
2	B	0.33	0/699	0.54	0/946
2	E	0.63	0/688	0.64	0/932
2	H	0.34	0/702	0.50	0/947
2	K	0.38	0/694	0.58	0/937
3	C	0.43	0/1113	0.52	0/1526
3	F	0.37	0/1111	0.60	0/1525
3	I	0.35	0/1117	0.59	0/1530
3	L	0.39	0/1120	0.52	0/1534
All	All	0.39	0/10434	0.57	0/14189

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	801	0	771	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	783	0	738	14	0
1	G	815	0	802	13	0
1	J	807	0	787	17	0
2	B	685	0	668	10	0
2	E	674	0	654	10	0
2	H	689	0	685	9	0
2	K	680	0	675	14	0
3	C	1094	0	1016	12	0
3	F	1092	0	1026	16	0
3	I	1098	0	1041	25	0
3	L	1101	0	1059	17	0
4	C	38	0	0	1	0
4	F	38	0	0	2	0
4	I	38	0	0	0	0
4	L	38	0	0	0	0
5	A	10	0	0	0	0
5	B	4	0	0	1	0
5	C	10	0	0	0	0
5	D	4	0	0	0	0
5	E	7	0	0	0	0
5	F	14	0	0	0	0
5	G	4	0	0	0	0
5	H	8	0	0	0	0
5	I	13	0	0	0	0
5	J	2	0	0	0	0
5	K	7	0	0	1	0
5	L	13	0	0	0	0
All	All	10567	0	9922	145	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 7.

All (145) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:37:LEU:HD22	2:H:43:LYS:HG3	1.52	0.90
2:B:40:GLY:HA2	2:B:43:LYS:HD3	1.55	0.89
2:K:37:LEU:HD22	2:K:43:LYS:HD2	1.62	0.82
1:J:52:ASP:HB2	1:J:55:LYS:HG2	1.66	0.77
1:A:43:ARG:HG2	1:A:50:LEU:HD11	1.67	0.77
1:G:40:ASP:OD1	1:G:80:ARG:NH2	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:LYS:HE3	1:G:81:ALA:HB1	1.74	0.70
2:B:83:TYR:HB3	2:B:90:ILE:HD12	1.75	0.68
1:J:1:MET:SD	1:J:1:MET:N	2.59	0.67
1:D:94:SER:HB3	2:E:68:HIS:ND1	2.11	0.64
2:K:58:ASN:N	5:K:201:HOH:O	2.31	0.62
3:L:90:ASN:ND2	3:L:94:GLU:HB3	2.15	0.62
1:D:45:TYR:CG	1:D:88:LEU:HD11	2.36	0.61
2:B:33:ARG:O	2:B:37:LEU:HD23	2.02	0.60
1:D:99:LEU:HD11	1:D:103:MET:SD	2.42	0.60
2:E:63:ARG:O	2:E:64:GLU:HB2	2.00	0.60
2:K:29:PHE:CD2	2:K:70:LEU:HD22	2.38	0.59
2:H:108:ASN:CG	3:I:184:LEU:HD11	2.23	0.58
2:K:83:TYR:HB3	2:K:90:ILE:HG12	1.85	0.58
1:D:9:ARG:HB2	1:D:77:LEU:HB3	1.85	0.58
1:G:94:SER:O	2:H:68:HIS:HB3	2.04	0.58
3:I:90:ASN:HD21	3:I:94:GLU:HB3	1.69	0.57
3:I:82:ARG:HH11	3:I:153:LEU:HD21	1.69	0.57
1:J:99:LEU:HD11	1:J:103:MET:HE2	1.85	0.57
3:I:89:LEU:HD12	3:I:116:LEU:HB3	1.85	0.57
3:I:185:TYR:O	3:I:189:GLU:HG3	2.05	0.57
1:J:43:ARG:HB3	1:J:50:LEU:HD11	1.84	0.57
3:C:90:ASN:OD1	3:C:93:GLY:N	2.37	0.57
3:F:104:GLY:HA3	2:K:63:ARG:HD2	1.88	0.56
1:J:9:ARG:HB2	1:J:77:LEU:HB3	1.86	0.56
3:C:102:PRO:O	3:C:105:THR:OG1	2.23	0.56
1:G:8:ARG:HG2	1:G:13:THR:HG23	1.87	0.55
1:A:30:ILE:O	1:A:34:ILE:HG12	2.06	0.55
2:E:97:PRO:HB3	3:F:169:LEU:HD21	1.89	0.55
3:F:64:ARG:HD3	3:F:91:PHE:O	2.07	0.55
1:J:40:ASP:N	1:J:40:ASP:OD1	2.40	0.55
1:J:80:ARG:HA	1:J:85:PHE:HA	1.90	0.54
2:E:70:LEU:HD23	2:E:74:CYS:SG	2.48	0.54
3:L:79:ARG:NH1	3:L:150:ASN:OD1	2.41	0.53
1:D:8:ARG:HD2	1:D:13:THR:HG23	1.89	0.53
3:C:171:LYS:HB3	3:C:173:GLU:OE1	2.08	0.53
3:I:90:ASN:ND2	3:I:94:GLU:HB3	2.24	0.53
1:D:30:ILE:O	1:D:34:ILE:HG13	2.09	0.53
3:I:181:VAL:HG22	3:I:184:LEU:HD13	1.90	0.53
2:H:95:ILE:HD11	3:I:161:ARG:HG3	1.91	0.53
1:J:103:MET:HE3	3:L:169:LEU:HD23	1.90	0.52
3:F:105:THR:HG22	2:K:64:GLU:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:185:TYR:O	3:L:189:GLU:HG3	2.10	0.52
3:F:108:ARG:HD3	2:K:111:ASP:HB2	1.91	0.52
2:E:20:LYS:NZ	2:E:28:GLU:OE1	2.36	0.51
3:L:90:ASN:HD21	3:L:94:GLU:HB3	1.74	0.51
3:C:90:ASN:OD1	3:C:94:GLU:N	2.36	0.50
3:C:109:ILE:HB	4:C:301:VYQ:C11	2.40	0.50
3:F:109:ILE:HB	4:F:301:VYQ:C11	2.41	0.50
1:G:34:ILE:HG22	1:G:35:LEU:HD23	1.94	0.50
1:A:70:GLN:N	1:A:70:GLN:OE1	2.42	0.50
2:B:39:SER:O	2:B:43:LYS:HG3	2.12	0.50
3:L:101:LEU:HD23	3:L:107:ARG:NH1	2.26	0.50
2:B:82:ARG:NH2	5:B:201:HOH:O	2.42	0.50
3:I:83:VAL:HG12	3:I:102:PRO:HA	1.94	0.50
2:H:87:SER:OG	3:I:132:GLN:NE2	2.44	0.50
3:I:120:ARG:HD2	3:I:127:GLY:HA2	1.94	0.49
2:H:41:THR:HG22	2:H:45:MET:SD	2.53	0.49
3:L:90:ASN:OD1	3:L:94:GLU:N	2.40	0.49
1:D:99:LEU:HG	1:D:103:MET:HB3	1.95	0.48
1:G:19:LYS:O	1:G:22:SER:OG	2.27	0.48
1:J:17:ASP:OD2	2:K:32:LYS:NZ	2.45	0.48
3:L:120:ARG:NH2	3:L:197:ASP:OD2	2.43	0.48
3:L:98:TYR:HB3	3:L:99:PRO:HD2	1.95	0.48
2:E:29:PHE:CD2	2:E:70:LEU:HD22	2.49	0.48
2:K:103:LEU:HD11	3:L:158:LEU:HD21	1.95	0.48
1:J:4:PHE:CE1	1:J:69:PRO:HG3	2.48	0.48
2:E:71:SER:O	2:E:75:MET:HG3	2.13	0.47
1:G:79:PHE:O	1:G:86:GLU:HG2	2.15	0.47
1:J:80:ARG:HD3	1:J:85:PHE:CE2	2.49	0.47
3:L:83:VAL:HG13	3:L:122:ALA:HB3	1.95	0.47
2:H:68:HIS:CD2	2:H:69:VAL:HG23	2.50	0.47
3:C:173:GLU:H	3:C:173:GLU:CD	2.18	0.47
1:D:24:VAL:HG21	1:D:51:LEU:HB3	1.95	0.47
3:F:113:ARG:CZ	3:F:140:LEU:HD23	2.44	0.47
3:I:170:VAL:HG21	3:I:178:LEU:HD11	1.96	0.47
1:J:103:MET:HG2	3:L:170:VAL:HG22	1.97	0.47
3:F:141:ASN:ND2	3:F:147:ILE:HG12	2.30	0.47
2:K:72:LYS:HE2	2:K:94:PRO:O	2.14	0.47
3:I:193:ASN:OD1	3:I:196:LYS:HB3	2.15	0.47
3:F:112:TYR:HB2	3:F:115:HIS:CD2	2.50	0.46
2:E:21:LEU:HB3	2:E:62:PHE:HE2	1.81	0.46
2:K:69:VAL:O	2:K:73:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:80:ARG:HA	1:G:85:PHE:HA	1.98	0.45
1:G:80:ARG:HD3	1:G:85:PHE:CE1	2.51	0.45
1:J:34:ILE:HD11	2:K:18:TYR:CZ	2.52	0.45
2:K:68:HIS:CD2	2:K:69:VAL:HG23	2.51	0.45
1:G:6:MET:HG3	1:G:72:PRO:HG2	1.99	0.45
3:F:101:LEU:HD11	4:F:301:VYQ:C17	2.46	0.45
1:D:79:PHE:O	1:D:86:GLU:HG2	2.16	0.45
2:B:20:LYS:HB3	2:B:59:GLU:HG2	1.99	0.44
2:B:66:PRO:HG2	2:B:69:VAL:HG23	1.99	0.44
1:J:37:ARG:NH1	1:J:79:PHE:HB3	2.32	0.44
3:L:112:TYR:HB2	3:L:115:HIS:NE2	2.33	0.44
1:G:95:SER:HA	1:G:96:PRO:HD3	1.82	0.44
1:J:45:TYR:CE2	1:J:50:LEU:HD13	2.53	0.44
3:C:84:VAL:HG22	3:C:128:LEU:HD13	2.00	0.44
1:J:80:ARG:HB2	1:J:85:PHE:CE1	2.53	0.44
3:L:131:ASN:O	3:L:132:GLN:HB2	2.18	0.44
3:F:89:LEU:HD12	3:F:116:LEU:HB3	2.00	0.43
3:C:185:TYR:O	3:C:189:GLU:HG3	2.18	0.43
1:A:102:VAL:HG21	3:C:178:LEU:HG	1.99	0.43
3:F:98:TYR:HB3	3:F:99:PRO:HD2	2.00	0.43
3:I:112:TYR:HB2	3:I:115:HIS:CD2	2.53	0.43
3:I:115:HIS:O	3:I:138:PRO:HD2	2.19	0.43
2:H:104:LEU:HG	3:I:184:LEU:HD23	1.99	0.43
3:I:181:VAL:CG2	3:I:184:LEU:HD13	2.49	0.43
2:B:80:LYS:O	2:B:84:THR:OG1	2.20	0.43
3:C:108:ARG:HH21	3:C:146:PRO:HG3	1.83	0.43
3:I:72:SER:HA	3:I:141:ASN:OD1	2.19	0.42
3:L:172:PRO:HA	3:L:175:TYR:CZ	2.54	0.42
1:A:80:ARG:HB2	1:A:85:PHE:CE1	2.54	0.42
1:D:7:ILE:HD12	1:D:75:VAL:HB	2.01	0.42
3:F:112:TYR:HB2	3:F:115:HIS:NE2	2.35	0.42
3:I:82:ARG:HH12	3:I:156:TYR:HE2	1.66	0.42
3:C:112:TYR:HB2	3:C:115:HIS:CD2	2.55	0.42
2:E:77:PHE:O	2:E:81:VAL:HG23	2.19	0.42
3:I:196:LYS:O	3:I:196:LYS:HG3	2.20	0.42
3:C:115:HIS:O	3:C:138:PRO:HD2	2.20	0.42
3:I:63:LEU:HD23	3:I:63:LEU:HA	1.82	0.42
2:B:40:GLY:HA2	2:B:43:LYS:CD	2.36	0.42
1:D:8:ARG:NH2	1:D:91:GLU:O	2.48	0.42
3:F:116:LEU:HD23	3:F:116:LEU:HA	1.93	0.41
1:G:43:ARG:HG3	1:G:85:PHE:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:95:ILE:CD1	3:I:161:ARG:HG3	2.50	0.41
3:I:196:LYS:HD2	3:I:196:LYS:HA	1.77	0.41
3:L:90:ASN:OD1	3:L:93:GLY:N	2.53	0.41
3:L:141:ASN:ND2	3:L:145:GLN:O	2.53	0.41
1:G:62:PHE:CZ	1:G:75:VAL:HG22	2.56	0.41
1:D:23:THR:HA	1:D:56:THR:HA	2.03	0.41
2:E:37:LEU:O	2:E:38:THR:C	2.59	0.41
1:J:62:PHE:CZ	1:J:75:VAL:HG22	2.56	0.41
3:F:128:LEU:HA	3:F:154:PRO:HD3	2.03	0.41
3:I:98:TYR:HB3	3:I:99:PRO:HD2	2.02	0.41
1:D:62:PHE:CZ	1:D:75:VAL:HG22	2.56	0.40
2:K:86:SER:OG	2:K:88:THR:HG22	2.21	0.40
3:F:180:ILE:HD12	3:F:184:LEU:HB2	2.03	0.40
3:I:176:ARG:NH2	3:I:189:GLU:OE1	2.54	0.40
1:A:72:PRO:HD2	2:B:75:MET:CE	2.51	0.40
1:D:14:ILE:HD11	1:D:35:LEU:HD11	2.02	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	100/104 (96%)	97 (97%)	3 (3%)	0	100	100
1	D	100/104 (96%)	97 (97%)	3 (3%)	0	100	100
1	G	100/104 (96%)	97 (97%)	2 (2%)	1 (1%)	15	30
1	J	100/104 (96%)	97 (97%)	2 (2%)	1 (1%)	15	30
2	B	84/97 (87%)	84 (100%)	0	0	100	100
2	E	83/97 (86%)	81 (98%)	2 (2%)	0	100	100
2	H	84/97 (87%)	83 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	83/97 (86%)	83 (100%)	0	0	100	100
3	C	140/162 (86%)	135 (96%)	5 (4%)	0	100	100
3	F	139/162 (86%)	134 (96%)	5 (4%)	0	100	100
3	I	139/162 (86%)	134 (96%)	5 (4%)	0	100	100
3	L	138/162 (85%)	133 (96%)	5 (4%)	0	100	100
All	All	1290/1452 (89%)	1255 (97%)	33 (3%)	2 (0%)	47	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	82	ASP
1	J	82	ASP

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	82/90 (91%)	82 (100%)	0	100	100
1	D	79/90 (88%)	79 (100%)	0	100	100
1	G	86/90 (96%)	86 (100%)	0	100	100
1	J	84/90 (93%)	84 (100%)	0	100	100
2	B	75/86 (87%)	74 (99%)	1 (1%)	69	85
2	E	73/86 (85%)	72 (99%)	1 (1%)	67	84
2	H	76/86 (88%)	76 (100%)	0	100	100
2	K	75/86 (87%)	75 (100%)	0	100	100
3	C	113/147 (77%)	113 (100%)	0	100	100
3	F	115/147 (78%)	115 (100%)	0	100	100
3	I	116/147 (79%)	116 (100%)	0	100	100
3	L	119/147 (81%)	119 (100%)	0	100	100
All	All	1093/1292 (85%)	1091 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	25	ASP
2	E	71	SER

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

Mol	Chain	Res	Type
1	A	10	HIS
2	B	27	HIS
3	I	96	GLN
3	I	132	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)

12 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CAS	A	89	1	5,8,9	0.81	0	1,9,11	0.51	0
1	CAS	G	60	1	5,8,9	1.03	0	1,9,11	1.26	0
1	CAS	J	60	1	5,8,9	1.04	0	1,9,11	1.09	0
3	CAS	F	77	3	5,8,9	1.10	0	1,9,11	1.69	0
1	CAS	D	60	1	5,8,9	1.10	0	1,9,11	0.57	0
3	CAS	C	77	3	5,8,9	1.05	0	1,9,11	1.60	0
1	CAS	G	89	1	5,8,9	1.14	0	1,9,11	0.79	0
3	CAS	L	77	3	5,8,9	1.15	0	1,9,11	0.97	0
3	CAS	I	77	3	5,8,9	1.10	0	1,9,11	0.07	0
1	CAS	D	89	1	5,8,9	1.21	0	1,9,11	0.40	0
1	CAS	J	89	1	5,8,9	1.13	0	1,9,11	0.73	0
1	CAS	A	60	1	5,8,9	1.02	0	1,9,11	1.43	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CAS	A	89	1	-	0/0/7/9	-
1	CAS	G	60	1	-	0/0/7/9	-
1	CAS	J	60	1	-	0/0/7/9	-
3	CAS	F	77	3	-	0/0/7/9	-
1	CAS	D	60	1	-	0/0/7/9	-
3	CAS	C	77	3	-	0/0/7/9	-
1	CAS	G	89	1	-	0/0/7/9	-
3	CAS	L	77	3	-	0/0/7/9	-
3	CAS	I	77	3	-	0/0/7/9	-
1	CAS	D	89	1	-	0/0/7/9	-
1	CAS	J	89	1	-	0/0/7/9	-
1	CAS	A	60	1	-	0/0/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	$\#\|Z\|>2$
4	VYQ	C	301	-	34,41,41	4.04	17 (50%)	45,63,63	1.39	6 (13%)
4	VYQ	F	301	-	34,41,41	4.06	16 (47%)	45,63,63	1.37	7 (15%)
4	VYQ	L	301	-	34,41,41	4.06	16 (47%)	45,63,63	1.41	6 (13%)
4	VYQ	I	301	-	34,41,41	4.06	16 (47%)	45,63,63	1.37	6 (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
4	VYQ	C	301	-	-	2/38/56/56	0/4/4/4
4	VYQ	F	301	-	-	2/38/56/56	0/4/4/4
4	VYQ	L	301	-	-	2/38/56/56	0/4/4/4
4	VYQ	I	301	-	-	7/38/56/56	0/4/4/4

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	301	VYQ	C10-C09	10.81	1.53	1.39
4	C	301	VYQ	C10-C09	10.75	1.53	1.39
4	I	301	VYQ	C10-C09	10.72	1.53	1.39
4	F	301	VYQ	C10-C09	10.66	1.53	1.39
4	F	301	VYQ	C19-C20	9.98	1.54	1.39
4	L	301	VYQ	C19-C20	9.88	1.54	1.39
4	I	301	VYQ	C19-C20	9.80	1.53	1.39
4	C	301	VYQ	C19-C20	9.79	1.53	1.39
4	L	301	VYQ	C11-C12	6.87	1.54	1.39
4	I	301	VYQ	C11-C12	6.84	1.53	1.39
4	C	301	VYQ	C11-C12	6.81	1.53	1.39
4	L	301	VYQ	C31-N30	6.79	1.47	1.34
4	F	301	VYQ	C11-C12	6.78	1.53	1.39
4	I	301	VYQ	C31-N30	6.68	1.47	1.34
4	C	301	VYQ	C31-N30	6.67	1.47	1.34
4	F	301	VYQ	C31-N30	6.61	1.47	1.34
4	I	301	VYQ	C05-N06	6.54	1.48	1.34
4	F	301	VYQ	C05-N06	6.51	1.48	1.34
4	L	301	VYQ	C05-N06	6.48	1.48	1.34
4	C	301	VYQ	C05-N06	6.47	1.48	1.34
4	I	301	VYQ	C24-N23	6.28	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	301	VYQ	C12-C13	6.27	1.54	1.48
4	F	301	VYQ	C20-C09	-6.24	1.33	1.40
4	C	301	VYQ	C24-N23	6.20	1.48	1.34
4	C	301	VYQ	C20-C09	-6.13	1.33	1.40
4	L	301	VYQ	C20-C09	-6.12	1.33	1.40
4	F	301	VYQ	C24-N23	6.11	1.48	1.34
4	F	301	VYQ	C12-C13	6.11	1.54	1.48
4	L	301	VYQ	C24-N23	6.10	1.48	1.34
4	I	301	VYQ	C20-C09	-6.06	1.33	1.40
4	L	301	VYQ	C12-C13	6.03	1.54	1.48
4	C	301	VYQ	C12-C13	5.94	1.54	1.48
4	F	301	VYQ	C34-C32	4.14	1.53	1.47
4	L	301	VYQ	C35-C32	4.11	1.53	1.47
4	I	301	VYQ	C35-C32	4.08	1.53	1.47
4	F	301	VYQ	C35-C32	4.07	1.53	1.47
4	C	301	VYQ	C34-C32	4.06	1.53	1.47
4	L	301	VYQ	C34-C32	4.03	1.53	1.47
4	C	301	VYQ	C35-C32	4.00	1.53	1.47
4	I	301	VYQ	C34-C32	4.00	1.53	1.47
4	I	301	VYQ	C19-C12	-3.88	1.33	1.39
4	L	301	VYQ	C19-C12	-3.84	1.33	1.39
4	F	301	VYQ	C19-C12	-3.81	1.33	1.39
4	C	301	VYQ	C19-C12	-3.81	1.33	1.39
4	C	301	VYQ	C11-C10	-3.29	1.32	1.38
4	F	301	VYQ	C11-C10	-3.28	1.32	1.38
4	L	301	VYQ	C11-C10	-3.19	1.32	1.38
4	I	301	VYQ	C11-C10	-3.15	1.33	1.38
4	I	301	VYQ	O22-C05	-2.41	1.18	1.23
4	L	301	VYQ	O22-C05	-2.36	1.18	1.23
4	F	301	VYQ	C15-C14	2.29	1.54	1.50
4	C	301	VYQ	O22-C05	-2.27	1.18	1.23
4	C	301	VYQ	O36-C31	-2.27	1.18	1.22
4	F	301	VYQ	O36-C31	-2.26	1.18	1.22
4	F	301	VYQ	O22-C05	-2.26	1.18	1.23
4	L	301	VYQ	O36-C31	-2.26	1.18	1.22
4	C	301	VYQ	C15-C14	2.22	1.54	1.50
4	I	301	VYQ	C15-C14	2.22	1.54	1.50
4	I	301	VYQ	C38-N23	2.22	1.50	1.47
4	I	301	VYQ	O36-C31	-2.20	1.19	1.22
4	L	301	VYQ	C15-C14	2.20	1.54	1.50
4	L	301	VYQ	C38-N23	2.20	1.50	1.47
4	C	301	VYQ	C38-N23	2.18	1.50	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	301	VYQ	C38-N23	2.17	1.50	1.47
4	C	301	VYQ	O37-C24	-2.01	1.18	1.22

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	I	301	VYQ	C03-C04-N23	4.41	108.92	103.10
4	L	301	VYQ	C03-C04-N23	4.36	108.86	103.10
4	C	301	VYQ	C03-C04-N23	4.31	108.79	103.10
4	F	301	VYQ	C03-C04-N23	4.17	108.61	103.10
4	L	301	VYQ	C03-C02-C38	3.57	107.70	103.31
4	C	301	VYQ	C38-N23-C04	-3.10	107.22	111.70
4	I	301	VYQ	C38-N23-C04	-3.07	107.27	111.70
4	I	301	VYQ	C03-C02-C38	3.05	107.05	103.31
4	F	301	VYQ	C38-N23-C04	-2.85	107.58	111.70
4	F	301	VYQ	C03-C02-C38	2.76	106.70	103.31
4	L	301	VYQ	C38-N23-C04	-2.73	107.75	111.70
4	I	301	VYQ	C26-C25-N30	-2.70	108.46	111.84
4	L	301	VYQ	C26-C25-N30	-2.68	108.48	111.84
4	C	301	VYQ	C03-C02-C38	2.53	106.42	103.31
4	C	301	VYQ	C12-C19-C20	-2.41	119.48	122.33
4	F	301	VYQ	C12-C19-C20	-2.33	119.57	122.33
4	L	301	VYQ	C12-C19-C20	-2.31	119.61	122.33
4	F	301	VYQ	C07-N06-C05	-2.26	119.76	122.93
4	F	301	VYQ	C08-C07-C09	-2.23	108.39	111.60
4	C	301	VYQ	C26-C25-N30	-2.21	109.07	111.84
4	L	301	VYQ	C08-C07-C09	-2.18	108.47	111.60
4	C	301	VYQ	C08-C07-C09	-2.18	108.47	111.60
4	F	301	VYQ	C26-C25-N30	-2.13	109.17	111.84
4	I	301	VYQ	C08-C07-C09	-2.10	108.57	111.60
4	I	301	VYQ	C12-C19-C20	-2.10	119.85	122.33

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	301	VYQ	N30-C25-C26-C27
4	I	301	VYQ	N30-C25-C26-C28
4	I	301	VYQ	N30-C25-C26-C29
4	I	301	VYQ	C24-C25-C26-C27
4	C	301	VYQ	C11-C12-C13-S18
4	C	301	VYQ	C19-C12-C13-S18

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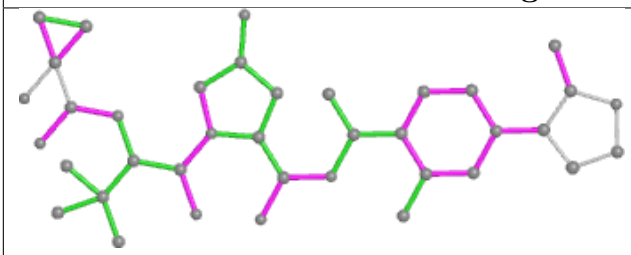
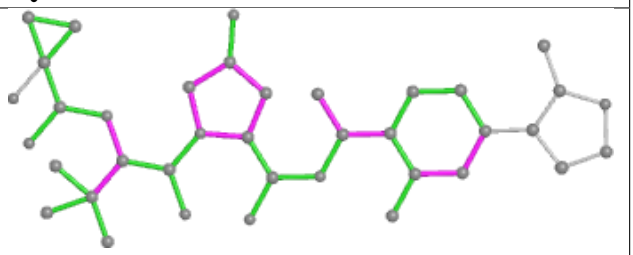
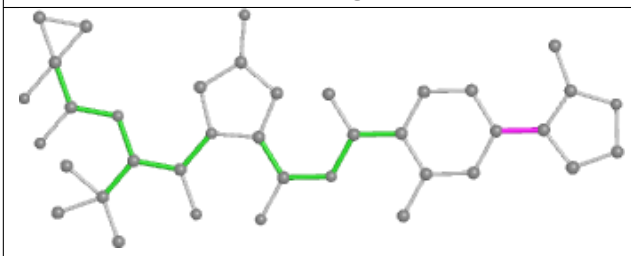
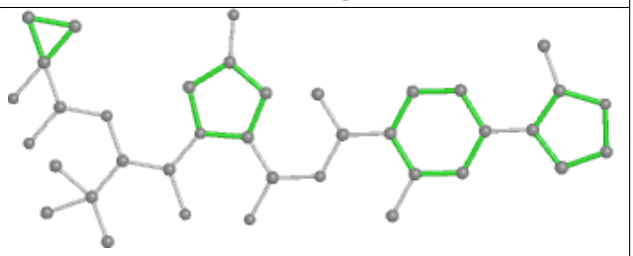
Mol	Chain	Res	Type	Atoms
4	F	301	VYQ	C11-C12-C13-S18
4	F	301	VYQ	C19-C12-C13-S18
4	I	301	VYQ	C19-C12-C13-S18
4	L	301	VYQ	C11-C12-C13-S18
4	L	301	VYQ	C19-C12-C13-S18
4	I	301	VYQ	C24-C25-C26-C28
4	I	301	VYQ	C24-C25-C26-C29

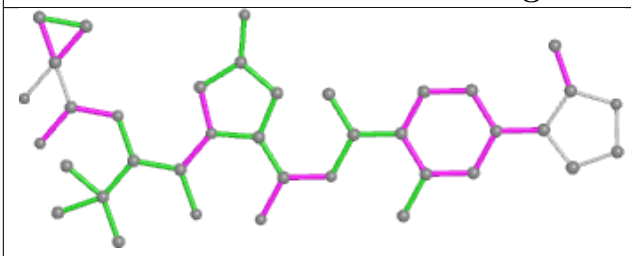
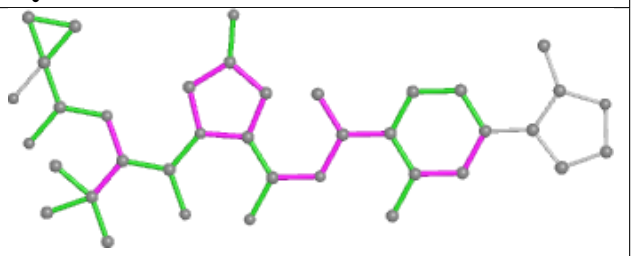
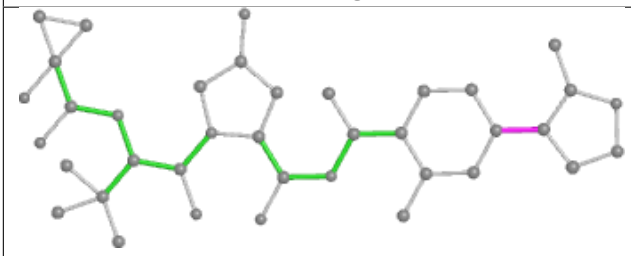
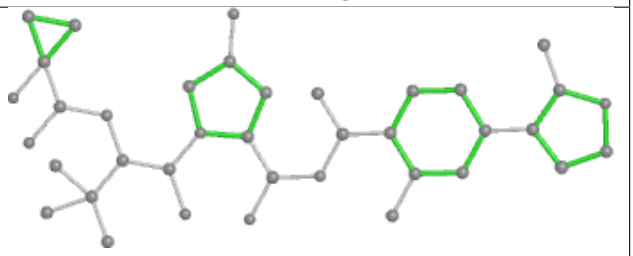
There are no ring outliers.

2 monomers are involved in 3 short contacts:

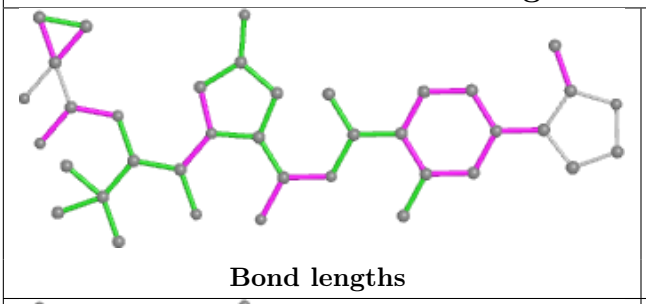
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	301	VYQ	1	0
4	F	301	VYQ	2	0

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 then 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.

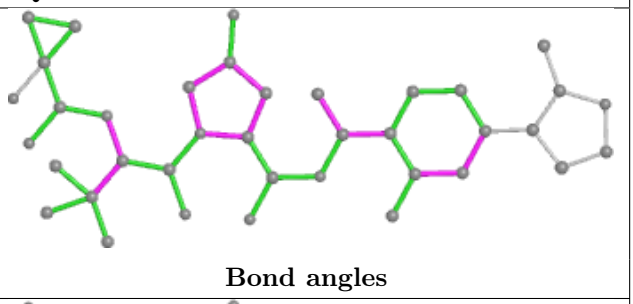
Ligand VYQ C 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand VYQ F 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

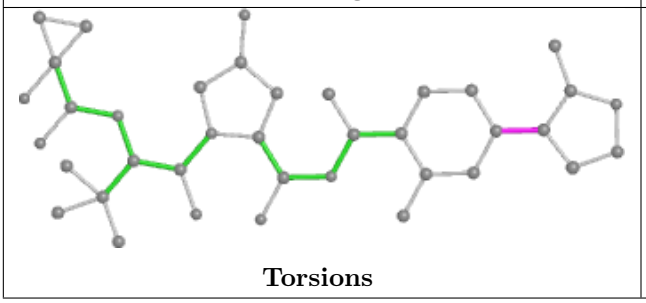
Ligand VYQ L 301



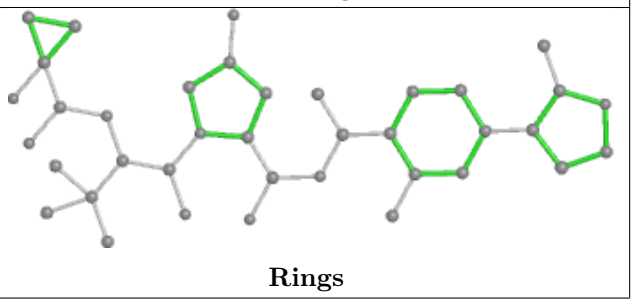
Bond lengths



Bond angles

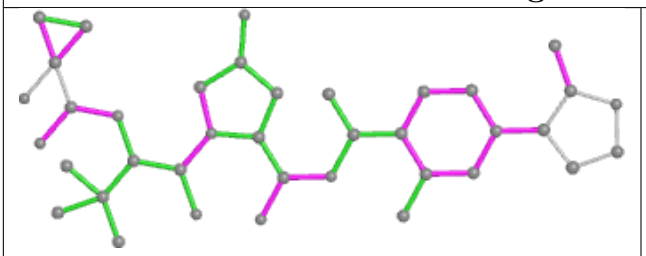


Torsions

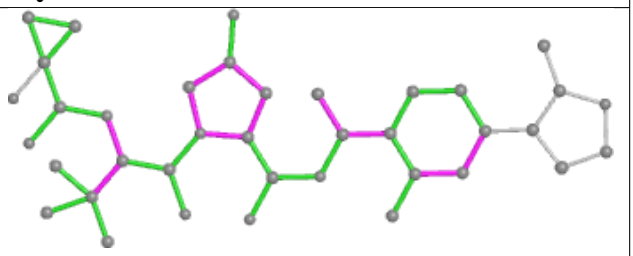


Rings

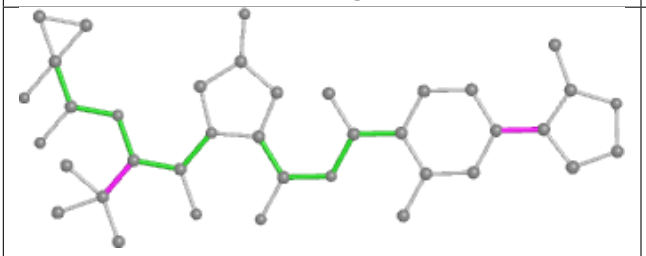
Ligand VYQ I 301



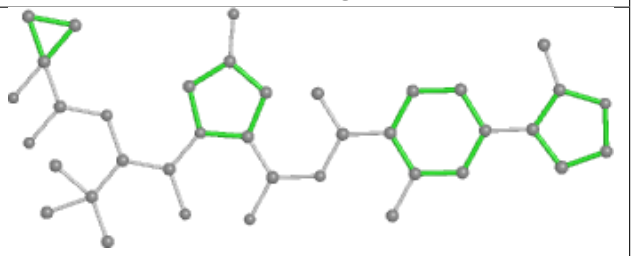
Bond lengths



Bond angles



Torsions



Rings

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^{th} 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	102/104 (98%)	-0.07	1 (0%) 82 80	39, 52, 84, 91	0
1	D	102/104 (98%)	0.10	4 (3%) 39 33	43, 66, 94, 102	0
1	G	102/104 (98%)	-0.16	0 100 100	32, 48, 77, 99	0
1	J	102/104 (98%)	-0.00	1 (0%) 82 80	41, 58, 77, 93	0
2	B	88/97 (90%)	0.10	3 (3%) 45 38	35, 52, 71, 78	0
2	E	87/97 (89%)	0.02	1 (1%) 80 78	44, 56, 69, 77	0
2	H	88/97 (90%)	0.02	0 100 100	35, 50, 63, 75	0
2	K	87/97 (89%)	0.15	2 (2%) 60 55	39, 52, 72, 84	0
3	C	142/162 (87%)	-0.03	2 (1%) 75 71	34, 50, 75, 84	0
3	F	141/162 (87%)	0.04	3 (2%) 63 58	37, 51, 78, 94	0
3	I	141/162 (87%)	-0.04	2 (1%) 75 71	33, 50, 74, 90	0
3	L	140/162 (86%)	-0.08	1 (0%) 87 85	35, 49, 71, 77	0
All	All	1322/1452 (91%)	-0.00	20 (1%) 73 70	32, 53, 78, 102	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	16	MET	4.4
1	D	103	MET	3.7
3	F	169	LEU	3.1
3	F	181	VAL	2.8
1	A	7	ILE	2.8
3	I	135	LEU	2.7
3	F	166	VAL	2.6
3	I	94	GLU	2.6
3	C	178	LEU	2.6
1	D	27	LEU	2.5
2	B	103	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	7	ILE	2.4
2	K	44	ALA	2.3
2	K	77	PHE	2.2
2	E	65	ILE	2.2
3	C	141	ASN	2.1
2	B	88	THR	2.1
3	L	74	VAL	2.1
1	D	77	LEU	2.0
1	J	102	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CAS	A	60	9/10	0.85	0.18	48,51,83,138	0
1	CAS	D	89	9/10	0.86	0.13	70,78,112,152	0
1	CAS	G	60	9/10	0.88	0.21	52,54,70,107	0
1	CAS	J	89	9/10	0.91	0.18	58,64,109,147	0
1	CAS	J	60	9/10	0.92	0.16	49,57,80,110	0
1	CAS	D	60	9/10	0.92	0.14	39,44,79,104	0
1	CAS	A	89	9/10	0.94	0.10	49,55,85,109	0
3	CAS	F	77	9/10	0.95	0.11	41,47,70,89	0
3	CAS	C	77	9/10	0.95	0.11	39,49,76,99	0
1	CAS	G	89	9/10	0.96	0.13	42,50,86,100	0
3	CAS	I	77	9/10	0.97	0.12	40,46,52,82	0
3	CAS	L	77	9/10	0.97	0.12	41,45,62,69	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

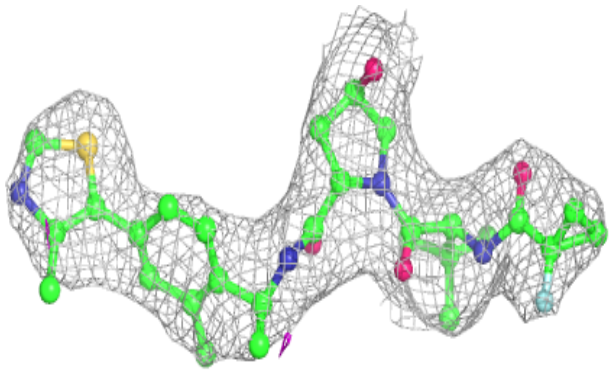
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

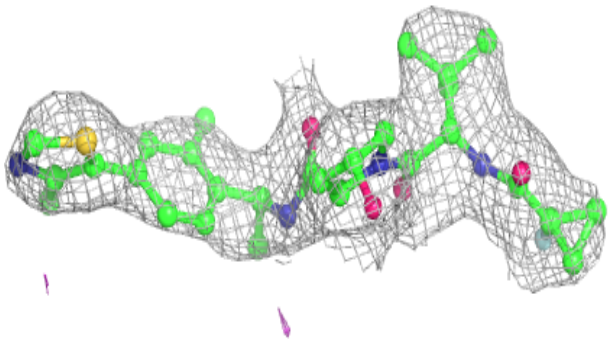
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	VYQ	F	301	38/38	0.93	0.19	36,51,61,65	0
4	VYQ	C	301	38/38	0.94	0.21	41,51,56,57	0
4	VYQ	I	301	38/38	0.94	0.22	30,43,57,60	0
4	VYQ	L	301	38/38	0.95	0.21	41,48,55,65	0

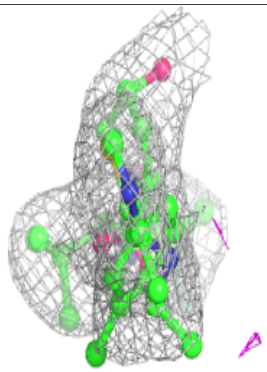
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around VYQ F 301:

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

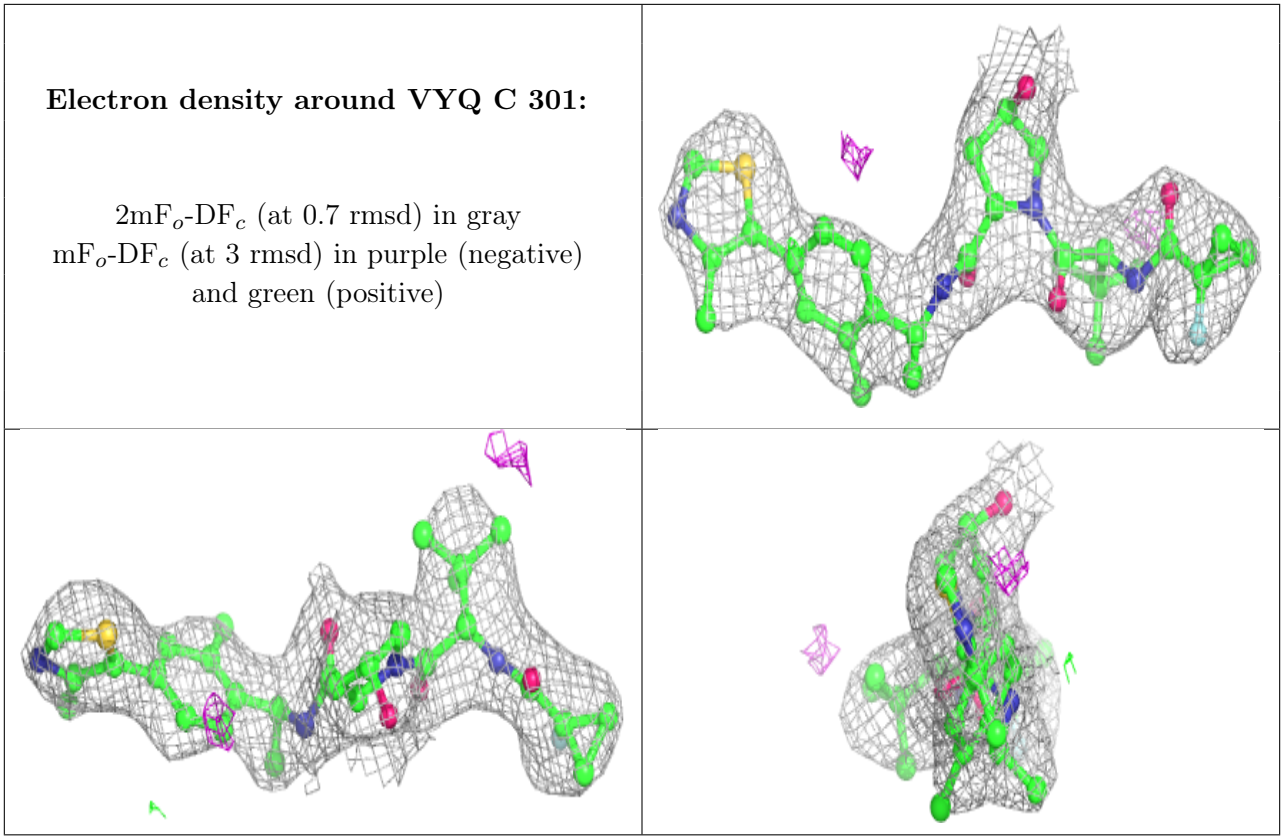






Electron density around VYQ C 301:

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



Electron density around VYQ I 301:

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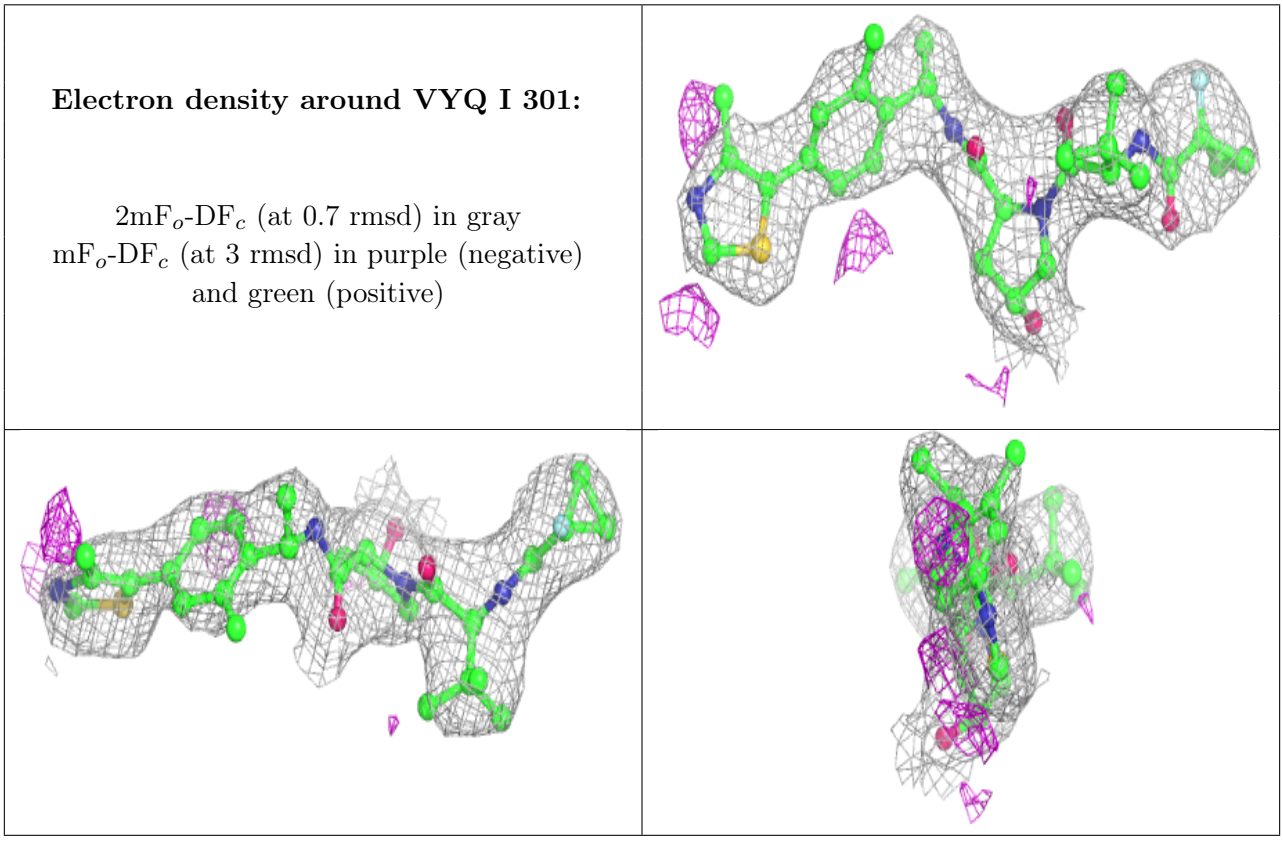
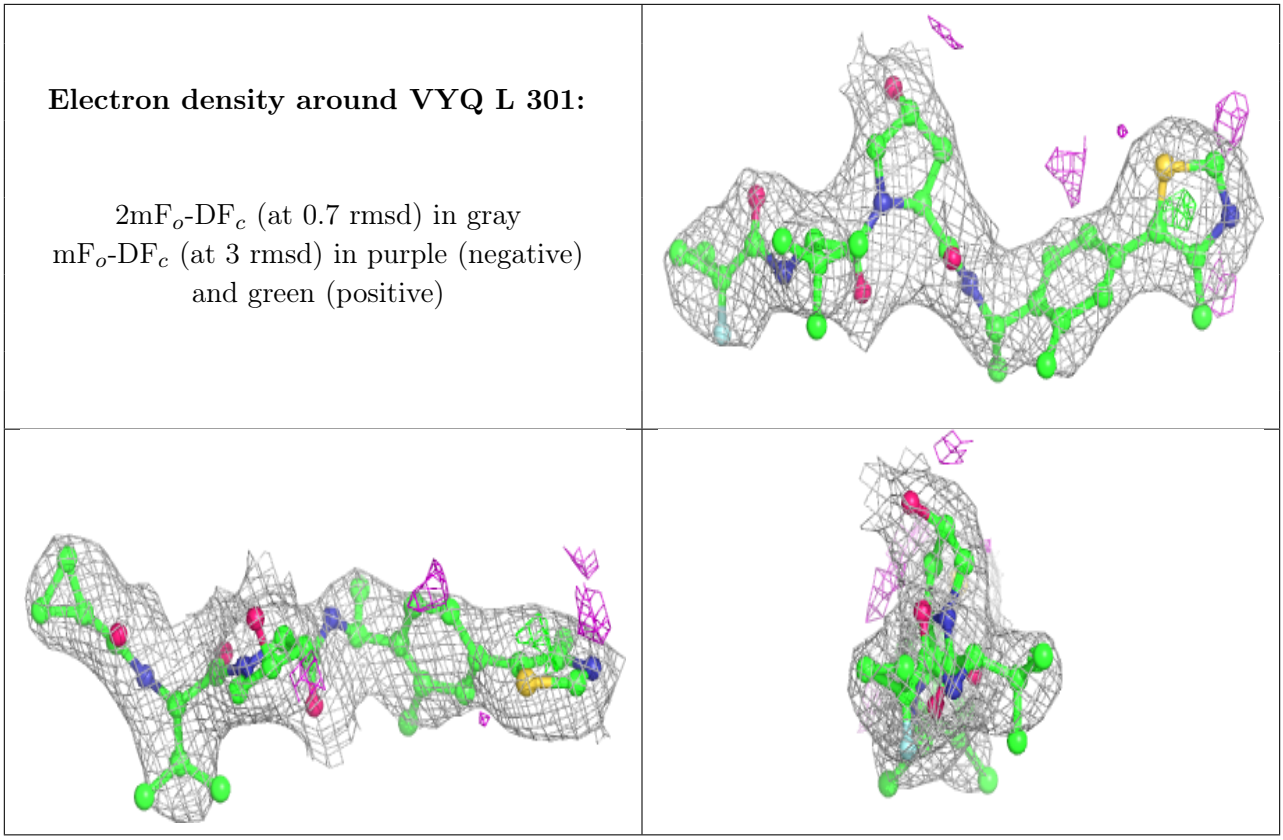
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around VYQ L 301:

$2mF_o$-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.