Full wwPDB X-ray Structure Validation Report (i)

Oct 15, 2023 – 08:14 PM EDT

PDB ID	:	8DUS
Title	:	Estrogen Receptor Alpha Ligand Binding Domain in Complex with (1'-(4-(2-(ethylamino)ethoxy)phenyl)-6'-hydroxy-1',4'-dihydro-2'H-spiro[cyclopropane-1,3'-isoquinolin]-2'-yl)(phenyl)methanone
Authors	:	Hancock, G.R.; Young, K.S.; Hosfield, D.J.; Joiner, C.; Sullivan, E.A.; Yildz, Y.; Laine, M.; Greene, G.L.; Fanning, S.W.
Deposited on	:	2022-07-27
Resolution	:	1.90 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 (i) 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 (1)) were used in the production of this report:

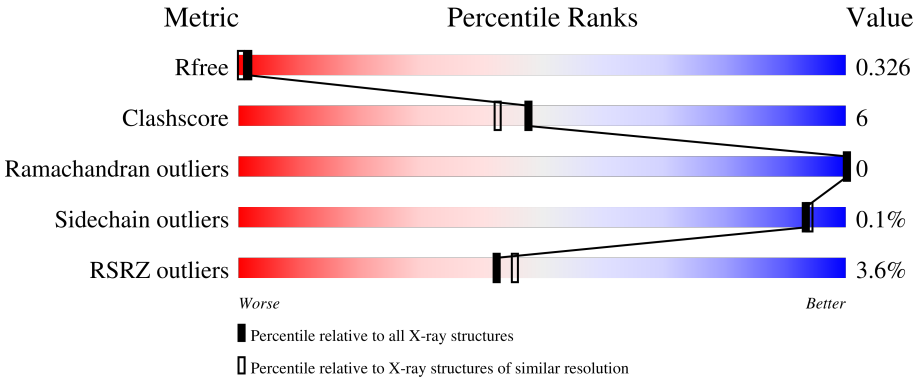
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	255	4% 81% 11% 8%
1	B	255	% 74% 13% 13%
1	E	255	3% 78% 13% 9%
1	F	255	4% 76% 11% 14%
1	G	255	3% 80% 12% 8%

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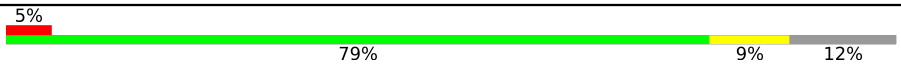
Mol	Chain	Length	Quality of chain
1	H	255	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11334 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	3	2	0
			1821	1159	311	336	15			
1	B	221	Total	C	N	O	S	0	0	0
			1721	1108	294	305	14			
1	E	232	Total	C	N	O	S	1	4	0
			1808	1155	310	329	14			
1	F	220	Total	C	N	O	S	0	0	0
			1732	1115	295	307	15			
1	G	234	Total	C	N	O	S	0	2	0
			1817	1161	309	332	15			
1	H	224	Total	C	N	O	S	1	1	0
			1748	1120	300	313	15			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	300	MET	-	initiating methionine	UNP P03372
A	381	SER	CYS	engineered mutation	UNP P03372
A	417	SER	CYS	engineered mutation	UNP P03372
A	530	SER	CYS	engineered mutation	UNP P03372
A	536	SER	LEU	engineered mutation	UNP P03372
B	300	MET	-	initiating methionine	UNP P03372
B	381	SER	CYS	engineered mutation	UNP P03372
B	417	SER	CYS	engineered mutation	UNP P03372
B	530	SER	CYS	engineered mutation	UNP P03372
B	536	SER	LEU	engineered mutation	UNP P03372
E	300	MET	-	initiating methionine	UNP P03372
E	381	SER	CYS	engineered mutation	UNP P03372
E	417	SER	CYS	engineered mutation	UNP P03372
E	530	SER	CYS	engineered mutation	UNP P03372
E	536	SER	LEU	engineered mutation	UNP P03372
F	300	MET	-	initiating methionine	UNP P03372
F	381	SER	CYS	engineered mutation	UNP P03372

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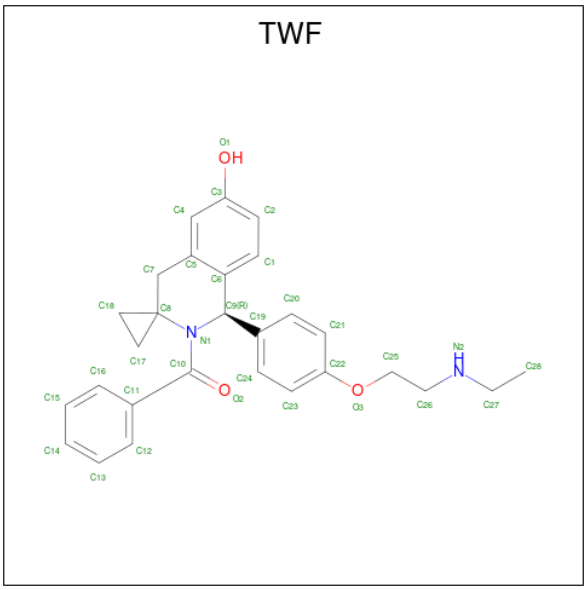
Chain	Residue	Modelled	Actual	Comment	Reference
F	417	SER	CYS	engineered mutation	UNP P03372
F	530	SER	CYS	engineered mutation	UNP P03372
F	536	SER	LEU	engineered mutation	UNP P03372
G	300	MET	-	initiating methionine	UNP P03372
G	381	SER	CYS	engineered mutation	UNP P03372
G	417	SER	CYS	engineered mutation	UNP P03372
G	530	SER	CYS	engineered mutation	UNP P03372
G	536	SER	LEU	engineered mutation	UNP P03372
H	300	MET	-	initiating methionine	UNP P03372
H	381	SER	CYS	engineered mutation	UNP P03372
H	417	SER	CYS	engineered mutation	UNP P03372
H	530	SER	CYS	engineered mutation	UNP P03372
H	536	SER	LEU	engineered mutation	UNP P03372

- Molecule 2 is [(1'R)-1'-{4-[2-(ethylamino)ethoxy]phenyl}-6'-hydroxy-1',4'-dihydro-2'H-spiro [cyclopropane-1,3'-isoquinolin]-2'-yl](phenyl)methanone (three-letter code: TWF) (formula: $C_{28}H_{30}N_2O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			33	28	2	3		
2	B	1	Total	C	N	O	0	0
			33	28	2	3		
2	E	1	Total	C	N	O	0	0
			33	28	2	3		
2	F	1	Total	C	N	O	0	0
			33	28	2	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	G	1	Total	C	N	O	0	0
			33	28	2	3		
2	H	1	Total	C	N	O	0	0
			33	28	2	3		

- Molecule 3 is water.

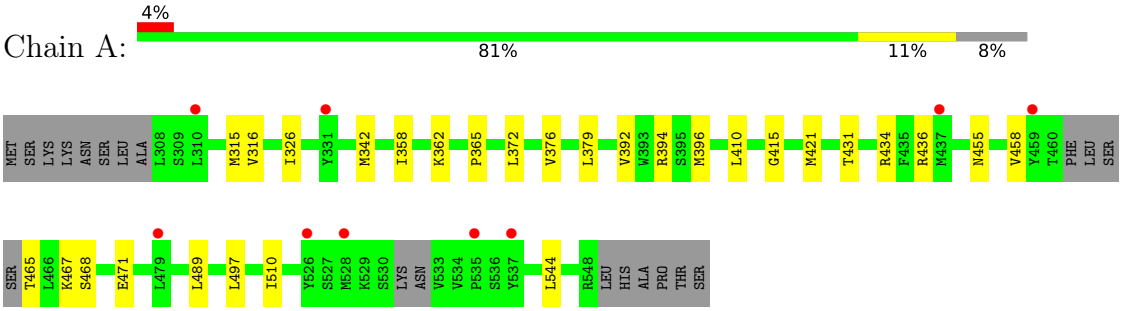
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	81	Total	O	0	0
			81	81		
3	B	80	Total	O	0	0
			80	80		
3	E	79	Total	O	0	0
			79	79		
3	F	88	Total	O	0	0
			88	88		
3	G	78	Total	O	0	0
			78	78		
3	H	83	Total	O	0	0
			83	83		

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.

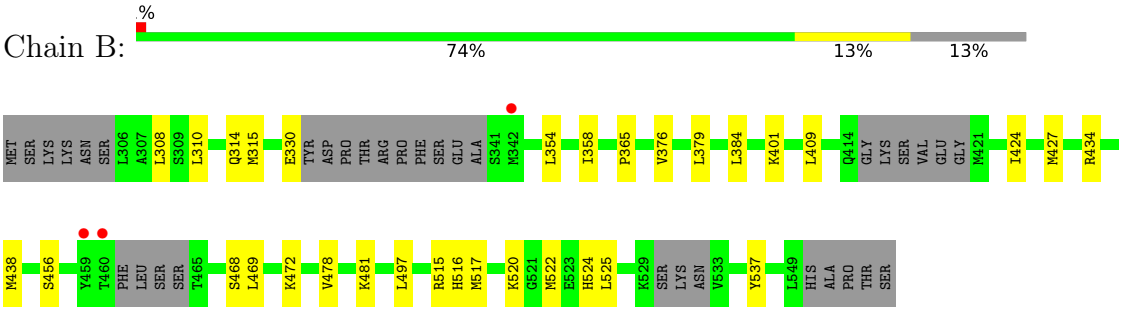
• Molecule 1: Estrogen receptor

Chain A:



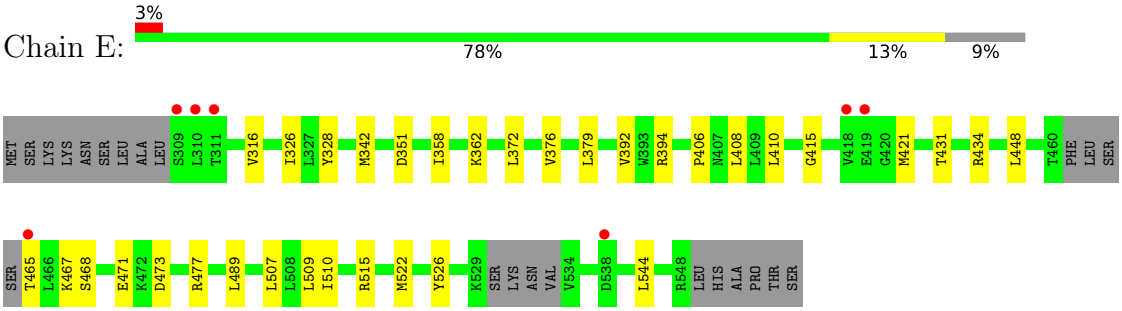
• Molecule 1: Estrogen receptor

Chain B:



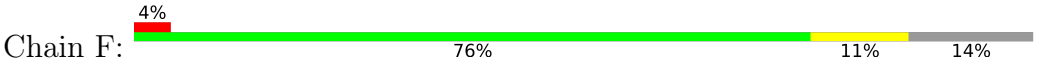
• Molecule 1: Estrogen receptor

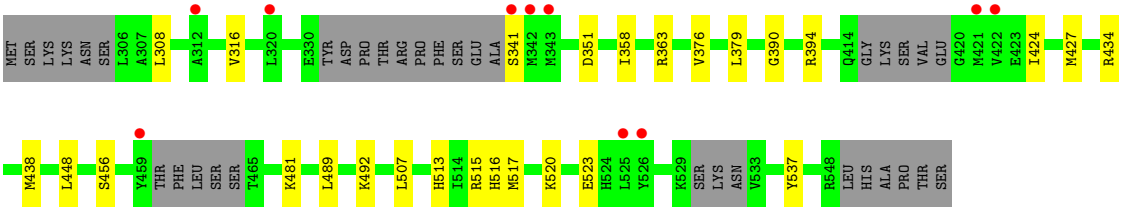
Chain E:



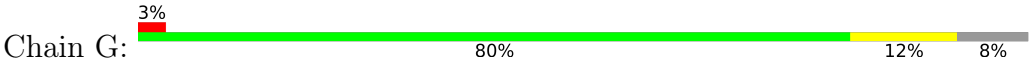
• Molecule 1: Estrogen receptor

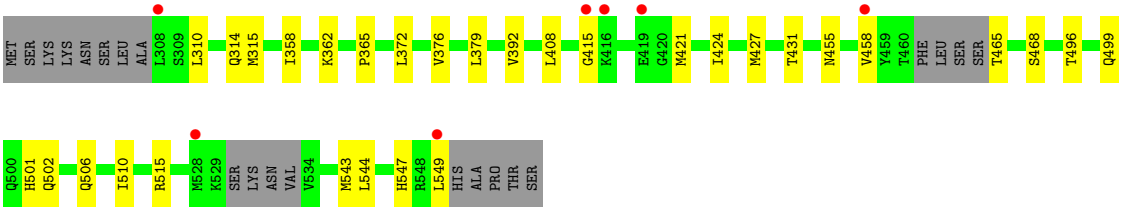
Chain F:



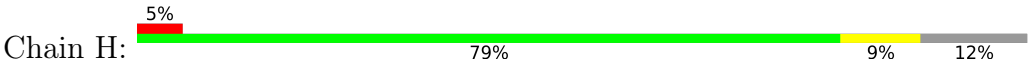


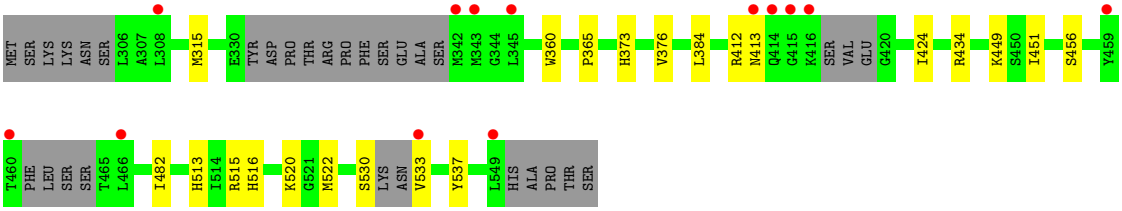
• Molecule 1: Estrogen receptor





• Molecule 1: Estrogen receptor





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	102.04Å 57.67Å 259.87Å 90.00° 100.08° 90.00°	Depositor
Resolution (Å)	49.91 – 1.90 49.91 – 1.90	Depositor EDS
% Data completeness (in resolution range)	84.5 (49.91-1.90) 85.0 (49.91-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.285 , 0.327 0.285 , 0.326	Depositor DCC
R_{free} test set	5082 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	18.7	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 60.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11334	wwPDB-VP
Average B, all atoms (Å^2)	25.0	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 85.01 % 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 1.4204e-07. 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: TWF

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	0.50	0/1853	0.67	0/2511
1	B	0.47	0/1747	0.69	0/2361
1	E	0.45	0/1843	0.64	0/2498
1	F	0.45	0/1759	0.63	0/2374
1	G	0.52	0/1852	0.72	0/2510
1	H	0.51	0/1774	0.71	0/2396
All	All	0.48	0/10828	0.68	0/14650

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	1821	0	1795	21	0
1	B	1721	0	1744	23	0
1	E	1808	0	1791	27	0
1	F	1732	0	1764	19	0
1	G	1817	0	1806	30	0
1	H	1748	0	1764	17	0
2	A	33	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	33	0	0	0	0
2	E	33	0	0	2	0
2	F	33	0	0	1	0
2	G	33	0	0	1	0
2	H	33	0	0	0	0
3	A	81	0	0	0	0
3	B	80	0	0	3	0
3	E	79	0	0	0	0
3	F	88	0	0	3	0
3	G	78	0	0	0	0
3	H	83	0	0	4	0
All	All	11334	0	10664	131	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 6.

All (131) 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:E:372:LEU:HD23	1:G:372:LEU:HD23	1.58	0.84
1:B:522:MET:HE1	1:B:525:LEU:HD12	1.63	0.81
1:E:342:MET:HE3	1:E:410:LEU:HD13	1.63	0.79
1:G:358:ILE:HG13	1:G:543:MET:HE2	1.64	0.78
1:A:465:THR:HG23	1:A:468:SER:HB2	1.71	0.72
1:E:515:ARG:HH22	1:F:513:HIS:CE1	2.07	0.71
1:F:489:LEU:HD23	1:F:492:LYS:HE2	1.77	0.67
1:B:310:LEU:HD22	1:B:314:GLN:HB3	1.77	0.65
1:E:351:ASP:OD1	2:E:601:TWF:N2	2.30	0.64
1:H:384:LEU:HD23	1:H:522:MET:HG2	1.80	0.63
1:A:342:MET:HE3	1:A:410:LEU:HD13	1.81	0.62
1:E:415:GLY:HA2	1:E:421:MET:CE	2.28	0.62
1:B:434:ARG:NH2	3:B:702:HOH:O	2.32	0.62
1:B:524:HIS:HB2	3:B:729:HOH:O	2.00	0.62
1:F:424:ILE:HD11	1:F:520:LYS:HB2	1.81	0.61
1:F:358:ILE:HD12	1:F:379:LEU:HD13	1.83	0.60
1:F:516:HIS:CE1	1:F:520:LYS:HE2	2.35	0.60
1:A:342:MET:HE3	1:A:410:LEU:CD1	2.32	0.60
1:G:310:LEU:HD22	1:G:314:GLN:HB3	1.84	0.59
1:B:384:LEU:HD22	1:B:522:MET:CE	2.31	0.59
1:H:516:HIS:CE1	1:H:520:LYS:HE2	2.37	0.59
1:B:456:SER:HA	1:B:515:ARG:NH2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:LEU:HD22	1:B:522:MET:HE2	1.85	0.58
1:E:392:VAL:HG11	1:E:431:THR:HG22	1.85	0.58
1:G:455:ASN:O	1:G:458:VAL:HG12	2.04	0.58
1:H:360:TRP:CH2	1:H:449:LYS:HG2	2.39	0.58
1:G:465:THR:HG23	1:G:468:SER:OG	2.05	0.57
1:F:456:SER:HA	1:F:515:ARG:NH2	2.19	0.57
1:G:515:ARG:HH12	1:H:513:HIS:CD2	2.22	0.57
1:F:520:LYS:O	1:F:523:GLU:HG2	2.04	0.57
1:F:341:SER:N	3:F:704:HOH:O	2.38	0.56
1:H:373:HIS:NE2	3:H:702:HOH:O	2.33	0.56
1:B:434:ARG:NH1	1:B:438:MET:SD	2.79	0.56
1:G:379:LEU:HD12	1:G:544:LEU:HD11	1.87	0.56
1:A:465:THR:HG23	1:A:468:SER:CB	2.35	0.55
1:A:392:VAL:HG11	1:A:431:THR:HG22	1.87	0.55
1:E:342:MET:HE3	1:E:410:LEU:CD1	2.37	0.54
1:E:473:ASP:OD1	1:E:477[B]:ARG:NE	2.41	0.54
1:G:415:GLY:HA2	1:G:421:MET:CE	2.38	0.54
1:B:516:HIS:CE1	1:B:520:LYS:HE2	2.43	0.54
1:A:455:ASN:O	1:A:458:VAL:HG12	2.09	0.53
1:G:392:VAL:HG11	1:G:431:THR:HG22	1.91	0.53
1:B:308:LEU:HD21	1:B:478:VAL:HG22	1.89	0.53
1:H:424:ILE:HD11	1:H:520:LYS:HD2	1.91	0.52
1:B:354:LEU:O	1:B:358:ILE:HG12	2.09	0.52
1:E:326:ILE:HD12	1:E:394:ARG:HD3	1.92	0.52
1:B:358:ILE:HD12	1:B:379:LEU:HD13	1.90	0.52
1:G:358:ILE:HG13	1:G:543:MET:CE	2.38	0.52
1:E:465:THR:HA	1:E:468:SER:OG	2.09	0.52
1:G:496:THR:OG1	1:G:499:GLN:HG3	2.10	0.52
1:B:376:VAL:HG11	1:B:537:TYR:CD2	2.44	0.51
1:A:415:GLY:HA2	1:A:421:MET:CE	2.41	0.50
1:F:316:VAL:HG21	1:F:489:LEU:HD21	1.94	0.50
1:G:372:LEU:O	1:G:376:VAL:HG23	2.12	0.50
1:B:468:SER:O	1:B:472:LYS:HG3	2.11	0.50
1:A:434:ARG:HG2	1:A:510:ILE:HD11	1.92	0.50
1:A:421:MET:HG3	2:A:601:TWF:C15	2.42	0.50
1:A:326:ILE:HD12	1:A:394:ARG:HD3	1.94	0.49
1:F:363:ARG:NH2	3:F:701:HOH:O	2.32	0.49
1:G:421:MET:HG3	2:G:601:TWF:C15	2.43	0.49
1:E:379:LEU:HD12	1:E:544:LEU:HD11	1.93	0.49
1:E:434:ARG:HG2	1:E:510:ILE:HD11	1.95	0.49
1:E:467:LYS:O	1:E:471:GLU:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:376:VAL:HG11	1:H:537:TYR:CD2	2.48	0.48
1:A:372:LEU:O	1:A:376:VAL:HG23	2.13	0.47
1:H:451:ILE:HG13	1:H:482:ILE:HG21	1.96	0.47
1:B:330:GLU:HG3	3:B:774:HOH:O	2.13	0.47
1:F:427:MET:HB3	1:F:517:MET:SD	2.55	0.47
1:A:316:VAL:HG21	1:A:489:LEU:HD21	1.96	0.47
1:E:415:GLY:HA2	1:E:421:MET:HE2	1.95	0.47
1:G:415:GLY:HA2	1:G:421:MET:HE1	1.97	0.47
1:B:469:LEU:HD23	1:B:472:LYS:HE2	1.97	0.46
1:E:421:MET:HG3	2:E:601:TWF:C15	2.45	0.46
1:B:401:LYS:HB3	1:B:409:LEU:HD22	1.96	0.46
1:G:501:HIS:HD2	3:H:777:HOH:O	1.98	0.46
1:H:456:SER:HA	1:H:515:ARG:NH2	2.29	0.46
1:A:358:ILE:O	1:A:362:LYS:HG3	2.15	0.46
1:B:424:ILE:HD11	1:B:520:LYS:HB2	1.98	0.46
1:G:315:MET:SD	1:G:365:PRO:HG2	2.56	0.46
1:G:515:ARG:HH12	1:H:513:HIS:HD2	1.61	0.46
1:F:434:ARG:NH2	3:F:709:HOH:O	2.49	0.46
1:G:358:ILE:CG1	1:G:543:MET:HE2	2.41	0.45
1:E:328:TYR:CE2	1:E:406:PRO:HB2	2.51	0.45
1:A:379:LEU:HD12	1:A:544:LEU:HD11	1.98	0.45
1:E:415:GLY:HA2	1:E:421:MET:HE1	1.99	0.45
1:H:516:HIS:NE2	1:H:520:LYS:HE2	2.30	0.45
1:E:507:LEU:HD23	1:E:507:LEU:HA	1.77	0.45
1:E:522:MET:HE3	1:E:526:TYR:CE2	2.52	0.45
1:A:467:LYS:O	1:A:471:GLU:HG2	2.17	0.44
1:E:372:LEU:O	1:E:376:VAL:HG23	2.17	0.44
1:B:384:LEU:HD22	1:B:522:MET:HE3	2.00	0.44
1:E:448:LEU:HD21	1:E:507:LEU:HB3	2.00	0.44
1:A:497:LEU:HD11	1:B:497:LEU:HD11	2.00	0.44
1:G:415:GLY:HA2	1:G:421:MET:HE2	2.00	0.44
1:E:316:VAL:HG21	1:E:489:LEU:HD21	1.99	0.44
1:G:465:THR:HG23	1:G:468:SER:CB	2.48	0.44
1:H:412:ARG:HG2	1:H:412:ARG:HH11	1.84	0.43
1:F:390:GLY:O	1:F:394:ARG:HG3	2.19	0.43
1:A:415:GLY:HA2	1:A:421:MET:HE1	1.99	0.43
1:H:373:HIS:CE1	3:H:702:HOH:O	2.68	0.43
1:F:351:ASP:OD1	2:F:601:TWF:N2	2.51	0.43
1:G:358:ILE:O	1:G:362:LYS:HG3	2.19	0.43
1:G:502:GLN:O	1:G:506:GLN:HG3	2.18	0.43
1:G:310:LEU:HA	1:G:314:GLN:OE1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:506:GLN:O	1:G:510:ILE:HG12	2.18	0.42
1:F:434:ARG:NH1	1:F:438:MET:SD	2.91	0.42
1:H:315:MET:SD	1:H:365:PRO:HG2	2.59	0.42
1:H:530:SER:HB3	1:H:533:VAL:HG21	2.01	0.42
1:E:515:ARG:HH12	1:F:513:HIS:HD1	1.68	0.42
1:H:413:ASN:ND2	3:H:701:HOH:O	2.24	0.42
1:E:358:ILE:O	1:E:362:LYS:HG3	2.20	0.42
1:G:408:LEU:HA	1:G:408:LEU:HD12	1.76	0.42
1:B:308:LEU:HA	1:B:481:LYS:HE3	2.02	0.41
1:G:543:MET:HE3	1:G:543:MET:HB3	1.89	0.41
1:G:424:ILE:HA	1:G:427:MET:CE	2.50	0.41
1:G:424:ILE:HA	1:G:427:MET:HE2	2.02	0.41
1:A:376:VAL:HG22	1:A:544:LEU:HD12	2.01	0.41
1:A:510:ILE:HD13	1:A:510:ILE:HA	1.83	0.41
1:B:315:MET:SD	1:B:365:PRO:HG2	2.61	0.41
1:B:427:MET:HB3	1:B:517:MET:SD	2.60	0.41
1:E:434:ARG:HG2	1:E:510:ILE:CD1	2.51	0.41
1:E:509:LEU:HD23	1:E:509:LEU:HA	1.87	0.41
1:F:448:LEU:HD11	1:F:507:LEU:HD22	2.02	0.41
1:G:547:HIS:CE1	1:G:549:LEU:HB2	2.56	0.41
1:A:315:MET:SD	1:A:365:PRO:HG2	2.60	0.41
1:E:408:LEU:HD12	1:E:408:LEU:HA	1.86	0.41
1:F:308:LEU:O	1:F:481:LYS:HE2	2.20	0.41
1:H:360:TRP:CZ2	1:H:449:LYS:HG2	2.55	0.41
1:F:376:VAL:HG11	1:F:537:TYR:CD2	2.56	0.40
1:G:515:ARG:HE	1:G:515:ARG:HB2	1.76	0.40
1:A:396:MET:O	1:A:436:ARG:HD3	2.22	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	231/255 (91%)	227 (98%)	4 (2%)	0	100	100
1	B	211/255 (83%)	207 (98%)	4 (2%)	0	100	100
1	E	230/255 (90%)	227 (99%)	3 (1%)	0	100	100
1	F	210/255 (82%)	206 (98%)	4 (2%)	0	100	100
1	G	230/255 (90%)	227 (99%)	3 (1%)	0	100	100
1	H	215/255 (84%)	211 (98%)	4 (2%)	0	100	100
All	All	1327/1530 (87%)	1305 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	197/230 (86%)	197 (100%)	0	100	100
1	B	185/230 (80%)	185 (100%)	0	100	100
1	E	194/230 (84%)	194 (100%)	0	100	100
1	F	188/230 (82%)	188 (100%)	0	100	100
1	G	197/230 (86%)	197 (100%)	0	100	100
1	H	188/230 (82%)	187 (100%)	1 (0%)	88	89
All	All	1149/1380 (83%)	1148 (100%)	1 (0%)	93	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	434	ARG

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

Mol	Chain	Res	Type
1	G	455	ASN

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Mol	Chain	Res	Type
1	G	501	HIS
1	H	356	HIS
1	H	513	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	TWF	E	601	-	35,37,37	4.95	23 (65%)	44,53,53	2.02	18 (40%)
2	TWF	A	601	-	35,37,37	5.02	27 (77%)	44,53,53	1.78	10 (22%)
2	TWF	G	601	-	35,37,37	5.02	26 (74%)	44,53,53	2.12	18 (40%)
2	TWF	B	601	-	35,37,37	5.12	22 (62%)	44,53,53	1.84	12 (27%)
2	TWF	H	601	-	35,37,37	5.14	24 (68%)	44,53,53	2.09	15 (34%)
2	TWF	F	601	-	35,37,37	5.23	23 (65%)	44,53,53	1.77	12 (27%)

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	TWF	E	601	-	-	6/18/41/41	0/5/5/5
2	TWF	A	601	-	-	7/18/41/41	0/5/5/5
2	TWF	G	601	-	-	6/18/41/41	0/5/5/5
2	TWF	B	601	-	-	6/18/41/41	0/5/5/5
2	TWF	H	601	-	-	5/18/41/41	0/5/5/5
2	TWF	F	601	-	-	6/18/41/41	0/5/5/5

All (145) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	601	TWF	C24-C19	10.61	1.56	1.39
2	G	601	TWF	C24-C19	10.59	1.56	1.39
2	F	601	TWF	C24-C19	10.40	1.55	1.39
2	E	601	TWF	C21-C20	10.40	1.57	1.38
2	F	601	TWF	C1-C6	10.33	1.53	1.39
2	G	601	TWF	C1-C6	10.17	1.53	1.39
2	B	601	TWF	C24-C19	10.09	1.55	1.39
2	B	601	TWF	C1-C6	10.04	1.52	1.39
2	H	601	TWF	C1-C6	9.95	1.52	1.39
2	A	601	TWF	C24-C19	9.86	1.55	1.39
2	F	601	TWF	C10-N1	9.56	1.57	1.36
2	B	601	TWF	C10-N1	9.45	1.57	1.36
2	B	601	TWF	C16-C11	9.44	1.55	1.39
2	E	601	TWF	C1-C6	9.40	1.52	1.39
2	H	601	TWF	C10-N1	9.39	1.57	1.36
2	F	601	TWF	C16-C11	9.36	1.55	1.39
2	H	601	TWF	C16-C11	9.27	1.55	1.39
2	F	601	TWF	C21-C20	9.26	1.55	1.38
2	E	601	TWF	C24-C19	9.07	1.53	1.39
2	G	601	TWF	C10-N1	8.98	1.56	1.36
2	A	601	TWF	C21-C20	8.89	1.54	1.38
2	A	601	TWF	C16-C11	8.84	1.54	1.39
2	E	601	TWF	C16-C11	8.74	1.54	1.39
2	B	601	TWF	C4-C5	8.65	1.54	1.39
2	B	601	TWF	C21-C20	8.44	1.54	1.38
2	F	601	TWF	C4-C5	8.44	1.53	1.39
2	E	601	TWF	C10-N1	8.44	1.54	1.36
2	G	601	TWF	C16-C11	8.43	1.53	1.39
2	H	601	TWF	C4-C5	8.42	1.53	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	601	TWF	C21-C20	8.37	1.54	1.38
2	A	601	TWF	C1-C6	8.28	1.50	1.39
2	B	601	TWF	C13-C12	8.12	1.56	1.38
2	F	601	TWF	C2-C3	7.88	1.54	1.38
2	G	601	TWF	C21-C20	7.88	1.53	1.38
2	G	601	TWF	C23-C22	7.79	1.54	1.38
2	H	601	TWF	C13-C12	7.78	1.55	1.38
2	A	601	TWF	C10-N1	7.78	1.53	1.36
2	F	601	TWF	C13-C12	7.75	1.55	1.38
2	H	601	TWF	C2-C3	7.74	1.53	1.38
2	B	601	TWF	C2-C3	7.69	1.53	1.38
2	A	601	TWF	C23-C22	7.63	1.53	1.38
2	G	601	TWF	C2-C3	7.63	1.53	1.38
2	H	601	TWF	C23-C22	7.60	1.53	1.38
2	B	601	TWF	C23-C22	7.56	1.53	1.38
2	E	601	TWF	C2-C3	7.55	1.53	1.38
2	F	601	TWF	C23-C22	7.48	1.53	1.38
2	E	601	TWF	C4-C5	7.32	1.52	1.39
2	G	601	TWF	C13-C12	7.32	1.54	1.38
2	E	601	TWF	C13-C12	7.28	1.54	1.38
2	A	601	TWF	C12-C11	-7.20	1.27	1.39
2	A	601	TWF	C4-C5	7.12	1.51	1.39
2	G	601	TWF	C4-C5	7.07	1.51	1.39
2	E	601	TWF	C23-C22	6.70	1.52	1.38
2	A	601	TWF	C2-C3	6.67	1.51	1.38
2	A	601	TWF	C13-C12	6.22	1.52	1.38
2	F	601	TWF	C12-C11	-6.12	1.28	1.39
2	G	601	TWF	C12-C11	-6.06	1.28	1.39
2	H	601	TWF	C12-C11	-5.97	1.29	1.39
2	E	601	TWF	C12-C11	-5.70	1.29	1.39
2	B	601	TWF	C14-C15	5.62	1.52	1.38
2	A	601	TWF	C4-C3	-5.61	1.30	1.39
2	B	601	TWF	C12-C11	-5.53	1.29	1.39
2	E	601	TWF	C14-C15	5.31	1.52	1.38
2	H	601	TWF	C14-C15	5.19	1.51	1.38
2	G	601	TWF	C14-C15	5.18	1.51	1.38
2	A	601	TWF	C5-C6	-5.15	1.31	1.40
2	F	601	TWF	C14-C15	5.08	1.51	1.38
2	A	601	TWF	C11-C10	4.87	1.58	1.50
2	F	601	TWF	C11-C10	4.80	1.57	1.50
2	B	601	TWF	C11-C10	4.71	1.57	1.50
2	H	601	TWF	C11-C10	4.50	1.57	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	TWF	O2-C10	-4.47	1.13	1.22
2	H	601	TWF	C5-C6	-4.46	1.32	1.40
2	G	601	TWF	C4-C3	-4.45	1.32	1.39
2	F	601	TWF	C7-C5	4.43	1.59	1.50
2	F	601	TWF	C5-C6	-4.35	1.32	1.40
2	A	601	TWF	C2-C1	-4.33	1.30	1.38
2	A	601	TWF	C15-C16	-4.29	1.29	1.38
2	B	601	TWF	C18-C8	4.29	1.57	1.50
2	E	601	TWF	C11-C10	4.29	1.57	1.50
2	B	601	TWF	C5-C6	-4.28	1.33	1.40
2	A	601	TWF	C20-C19	-4.28	1.32	1.39
2	F	601	TWF	C18-C8	4.27	1.57	1.50
2	E	601	TWF	C5-C6	-4.23	1.33	1.40
2	H	601	TWF	C18-C8	4.22	1.57	1.50
2	E	601	TWF	C4-C3	-4.21	1.32	1.39
2	E	601	TWF	C7-C5	4.18	1.59	1.50
2	G	601	TWF	C11-C10	4.16	1.56	1.50
2	G	601	TWF	C7-C5	3.96	1.58	1.50
2	H	601	TWF	C7-C5	3.92	1.58	1.50
2	B	601	TWF	C7-C5	3.82	1.58	1.50
2	E	601	TWF	C17-C8	3.79	1.56	1.50
2	E	601	TWF	C23-C24	-3.75	1.31	1.38
2	G	601	TWF	C5-C6	-3.71	1.33	1.40
2	A	601	TWF	C14-C15	3.71	1.47	1.38
2	B	601	TWF	C4-C3	-3.69	1.33	1.39
2	F	601	TWF	C2-C1	-3.68	1.32	1.38
2	H	601	TWF	C17-C8	3.67	1.56	1.50
2	G	601	TWF	C17-C8	3.63	1.56	1.50
2	E	601	TWF	C18-C8	3.55	1.56	1.50
2	F	601	TWF	C17-C8	3.50	1.55	1.50
2	A	601	TWF	C14-C13	-3.43	1.28	1.38
2	A	601	TWF	C18-C8	3.41	1.55	1.50
2	B	601	TWF	C17-C8	3.37	1.55	1.50
2	H	601	TWF	C2-C1	-3.35	1.32	1.38
2	G	601	TWF	C15-C16	-3.33	1.31	1.38
2	G	601	TWF	C19-C9	-3.29	1.48	1.52
2	A	601	TWF	C23-C24	-3.25	1.32	1.38
2	H	601	TWF	C4-C3	-3.24	1.34	1.39
2	A	601	TWF	C21-C22	-3.23	1.32	1.38
2	F	601	TWF	C4-C3	-3.23	1.34	1.39
2	F	601	TWF	C15-C16	-3.19	1.32	1.38
2	E	601	TWF	C15-C16	-3.12	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	601	TWF	C20-C19	-3.12	1.34	1.39
2	B	601	TWF	C2-C1	-3.11	1.33	1.38
2	H	601	TWF	C15-C16	-3.10	1.32	1.38
2	G	601	TWF	C20-C19	-3.08	1.34	1.39
2	G	601	TWF	O3-C22	3.00	1.44	1.37
2	G	601	TWF	C18-C8	3.00	1.55	1.50
2	B	601	TWF	C15-C16	-2.95	1.32	1.38
2	E	601	TWF	C2-C1	-2.93	1.33	1.38
2	A	601	TWF	C19-C9	-2.88	1.48	1.52
2	A	601	TWF	C7-C5	2.76	1.56	1.50
2	G	601	TWF	C2-C1	-2.66	1.33	1.38
2	B	601	TWF	C20-C19	-2.65	1.34	1.39
2	F	601	TWF	C23-C24	-2.65	1.33	1.38
2	F	601	TWF	C20-C19	-2.58	1.34	1.39
2	H	601	TWF	C23-C24	-2.45	1.34	1.38
2	A	601	TWF	C6-C9	-2.41	1.49	1.51
2	G	601	TWF	C14-C13	-2.37	1.31	1.38
2	E	601	TWF	O3-C22	2.35	1.43	1.37
2	E	601	TWF	C14-C13	-2.30	1.31	1.38
2	G	601	TWF	C6-C9	-2.29	1.49	1.51
2	H	601	TWF	O1-C3	2.24	1.42	1.37
2	H	601	TWF	C6-C9	-2.22	1.49	1.51
2	G	601	TWF	C21-C22	-2.21	1.34	1.38
2	E	601	TWF	O2-C10	-2.19	1.18	1.22
2	G	601	TWF	C23-C24	-2.18	1.34	1.38
2	F	601	TWF	C6-C9	-2.15	1.49	1.51
2	A	601	TWF	O3-C22	2.14	1.42	1.37
2	B	601	TWF	C14-C13	-2.12	1.32	1.38
2	H	601	TWF	C14-C13	-2.11	1.32	1.38
2	A	601	TWF	C17-C8	2.11	1.53	1.50
2	B	601	TWF	C23-C24	-2.10	1.34	1.38
2	F	601	TWF	C21-C22	-2.05	1.34	1.38

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	601	TWF	C7-C5-C4	-5.86	109.79	121.23
2	B	601	TWF	C7-C5-C4	-5.26	110.96	121.23
2	H	601	TWF	C7-C5-C4	-5.02	111.42	121.23
2	A	601	TWF	C7-C5-C4	-4.96	111.54	121.23
2	F	601	TWF	C7-C5-C4	-4.72	112.01	121.23
2	E	601	TWF	C7-C5-C4	-4.50	112.44	121.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	601	TWF	C7-C5-C6	4.13	127.08	120.75
2	A	601	TWF	C18-C17-C8	3.99	62.48	59.67
2	H	601	TWF	C3-C4-C5	-3.97	116.42	120.83
2	E	601	TWF	C24-C19-C9	-3.95	112.58	120.70
2	H	601	TWF	C21-C20-C19	-3.91	117.27	121.20
2	G	601	TWF	C24-C19-C20	3.68	122.88	118.29
2	E	601	TWF	C21-C20-C19	-3.65	117.52	121.20
2	A	601	TWF	O2-C10-N1	-3.50	116.82	121.82
2	F	601	TWF	C3-C4-C5	-3.48	116.97	120.83
2	G	601	TWF	C21-C20-C19	-3.42	117.76	121.20
2	H	601	TWF	C26-N2-C27	-3.40	106.19	113.43
2	H	601	TWF	C25-O3-C22	-3.38	109.09	117.93
2	E	601	TWF	C3-C4-C5	-3.34	117.12	120.83
2	B	601	TWF	C25-O3-C22	-3.33	109.23	117.93
2	H	601	TWF	C24-C19-C20	3.27	122.38	118.29
2	B	601	TWF	C18-C17-C8	3.26	61.97	59.67
2	B	601	TWF	C4-C5-C6	3.21	123.67	119.50
2	F	601	TWF	C7-C5-C6	3.19	125.64	120.75
2	E	601	TWF	C15-C16-C11	-3.16	116.60	120.34
2	F	601	TWF	C25-O3-C22	-3.15	109.69	117.93
2	F	601	TWF	C18-C17-C8	3.09	61.85	59.67
2	E	601	TWF	C12-C11-C10	-3.06	112.53	120.29
2	B	601	TWF	C7-C5-C6	3.02	125.37	120.75
2	B	601	TWF	O2-C10-N1	-2.99	117.55	121.82
2	H	601	TWF	C7-C5-C6	2.98	125.32	120.75
2	E	601	TWF	O2-C10-N1	-2.96	117.59	121.82
2	B	601	TWF	C3-C4-C5	-2.96	117.54	120.83
2	B	601	TWF	C19-C9-N1	2.93	115.82	112.83
2	A	601	TWF	C4-C5-C6	2.91	123.27	119.50
2	G	601	TWF	C25-O3-C22	-2.90	110.34	117.93
2	H	601	TWF	C16-C11-C10	-2.90	112.94	120.29
2	A	601	TWF	C7-C5-C6	2.89	125.18	120.75
2	H	601	TWF	C4-C5-C6	2.89	123.25	119.50
2	H	601	TWF	C18-C17-C8	2.82	61.66	59.67
2	G	601	TWF	C23-C24-C19	-2.81	118.37	121.20
2	G	601	TWF	C4-C5-C6	2.79	123.13	119.50
2	G	601	TWF	C12-C11-C10	-2.77	113.26	120.29
2	G	601	TWF	C11-C10-N1	2.75	122.76	117.86
2	G	601	TWF	C8-C7-C5	-2.73	108.01	113.41
2	G	601	TWF	C20-C19-C9	-2.71	115.12	120.70
2	E	601	TWF	C20-C19-C9	2.65	126.16	120.70
2	G	601	TWF	O2-C10-N1	-2.64	118.05	121.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	601	TWF	C19-C9-N1	-2.64	110.15	112.83
2	A	601	TWF	C12-C11-C10	-2.62	113.64	120.29
2	E	601	TWF	C7-C5-C6	2.60	124.74	120.75
2	F	601	TWF	C21-C20-C19	-2.59	118.59	121.20
2	G	601	TWF	C15-C16-C11	-2.58	117.28	120.34
2	E	601	TWF	C4-C5-C6	2.55	122.82	119.50
2	H	601	TWF	C16-C11-C12	2.54	122.20	118.59
2	E	601	TWF	C17-C18-C8	2.49	61.43	59.67
2	F	601	TWF	C26-N2-C27	-2.49	108.14	113.43
2	H	601	TWF	C24-C23-C22	-2.46	116.72	119.73
2	G	601	TWF	C3-C4-C5	-2.45	118.10	120.83
2	E	601	TWF	C25-C26-N2	-2.44	105.45	111.44
2	H	601	TWF	C1-C2-C3	2.44	122.56	119.88
2	A	601	TWF	C16-C11-C10	2.40	126.38	120.29
2	E	601	TWF	C11-C10-N1	2.39	122.12	117.86
2	G	601	TWF	C17-C18-C8	2.39	61.36	59.67
2	A	601	TWF	C11-C10-N1	2.36	122.06	117.86
2	B	601	TWF	C15-C16-C11	-2.35	117.56	120.34
2	F	601	TWF	O2-C10-N1	-2.35	118.46	121.82
2	B	601	TWF	C1-C2-C3	2.32	122.42	119.88
2	E	601	TWF	C24-C19-C20	2.30	121.16	118.29
2	F	601	TWF	C11-C10-N1	2.29	121.94	117.86
2	E	601	TWF	C16-C11-C12	2.28	121.83	118.59
2	G	601	TWF	C16-C11-C12	2.25	121.79	118.59
2	H	601	TWF	C1-C6-C9	-2.25	115.94	121.24
2	H	601	TWF	O2-C10-N1	-2.20	118.68	121.82
2	E	601	TWF	C19-C9-N1	-2.19	110.60	112.83
2	F	601	TWF	C4-C5-C6	2.17	122.32	119.50
2	F	601	TWF	C1-C6-C9	-2.14	116.19	121.24
2	E	601	TWF	C18-C17-C8	2.10	61.16	59.67
2	E	601	TWF	C16-C11-C10	2.07	125.54	120.29
2	B	601	TWF	C11-C10-N1	2.07	121.55	117.86
2	F	601	TWF	C16-C11-C12	2.05	121.51	118.59
2	B	601	TWF	C26-N2-C27	-2.05	109.07	113.43
2	A	601	TWF	C1-C2-C3	2.05	122.12	119.88
2	G	601	TWF	C26-N2-C27	-2.04	109.09	113.43
2	A	601	TWF	C23-C24-C19	-2.03	119.15	121.20

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	TWF	C11-C10-N1-C8
2	A	601	TWF	O2-C10-N1-C8
2	B	601	TWF	C11-C10-N1-C8
2	B	601	TWF	O2-C10-N1-C8
2	E	601	TWF	C11-C10-N1-C8
2	E	601	TWF	O2-C10-N1-C8
2	E	601	TWF	C25-C26-N2-C27
2	F	601	TWF	C11-C10-N1-C8
2	F	601	TWF	O2-C10-N1-C8
2	G	601	TWF	C11-C10-N1-C8
2	G	601	TWF	O2-C10-N1-C8
2	H	601	TWF	C11-C10-N1-C8
2	H	601	TWF	O2-C10-N1-C8
2	A	601	TWF	O3-C25-C26-N2
2	E	601	TWF	O3-C25-C26-N2
2	G	601	TWF	C25-C26-N2-C27
2	H	601	TWF	O3-C25-C26-N2
2	H	601	TWF	C21-C22-O3-C25
2	F	601	TWF	C21-C22-O3-C25
2	B	601	TWF	C23-C22-O3-C25
2	A	601	TWF	C23-C22-O3-C25
2	A	601	TWF	C21-C22-O3-C25
2	F	601	TWF	C23-C22-O3-C25
2	H	601	TWF	C23-C22-O3-C25
2	B	601	TWF	C21-C22-O3-C25
2	E	601	TWF	C28-C27-N2-C26
2	E	601	TWF	C26-C25-O3-C22
2	A	601	TWF	C25-C26-N2-C27
2	G	601	TWF	C21-C22-O3-C25
2	F	601	TWF	O3-C25-C26-N2
2	G	601	TWF	C23-C22-O3-C25
2	A	601	TWF	C26-C25-O3-C22
2	B	601	TWF	O3-C25-C26-N2
2	G	601	TWF	C28-C27-N2-C26
2	B	601	TWF	C25-C26-N2-C27
2	F	601	TWF	C25-C26-N2-C27

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	601	TWF	2	0
2	A	601	TWF	1	0

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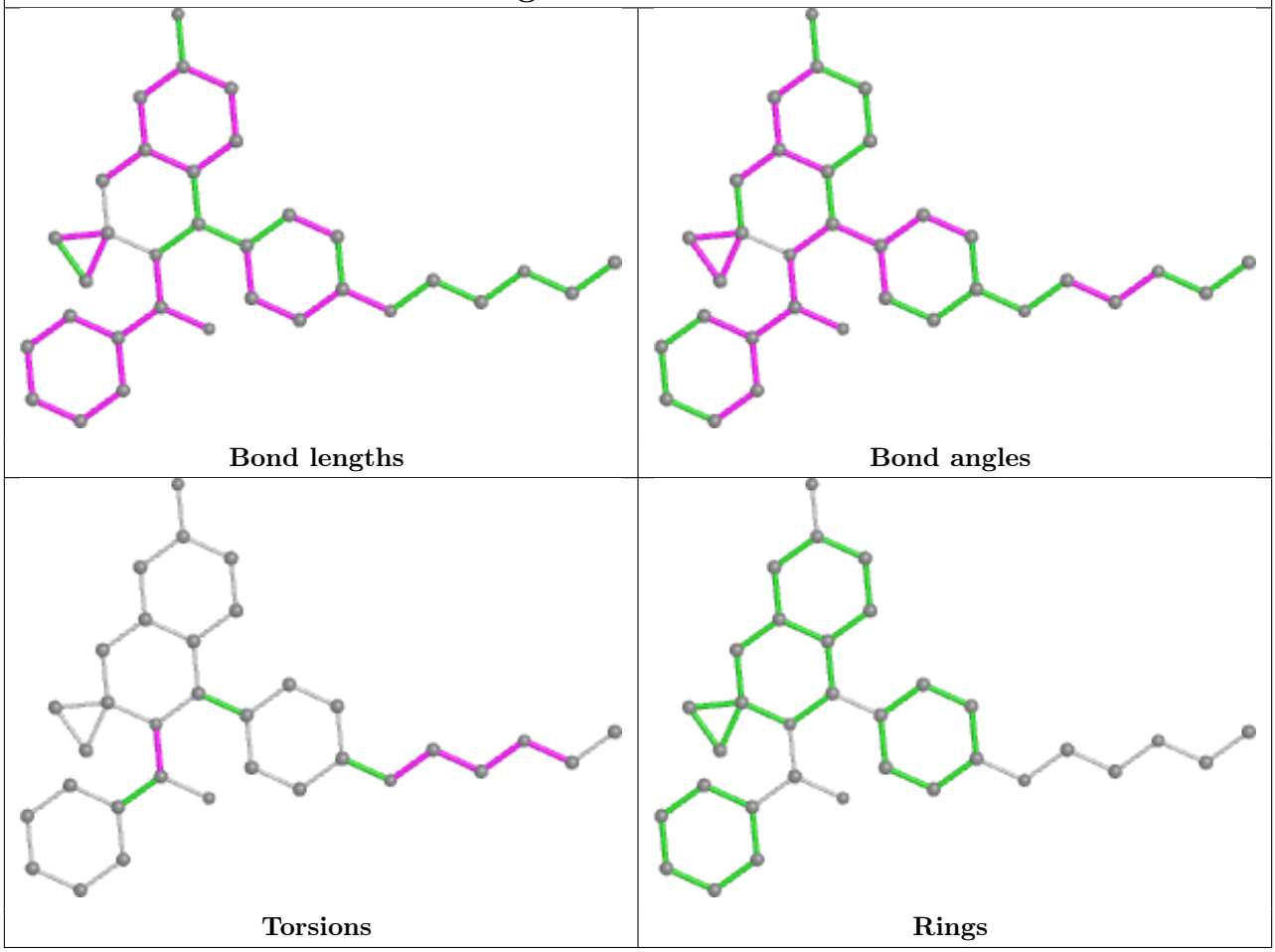
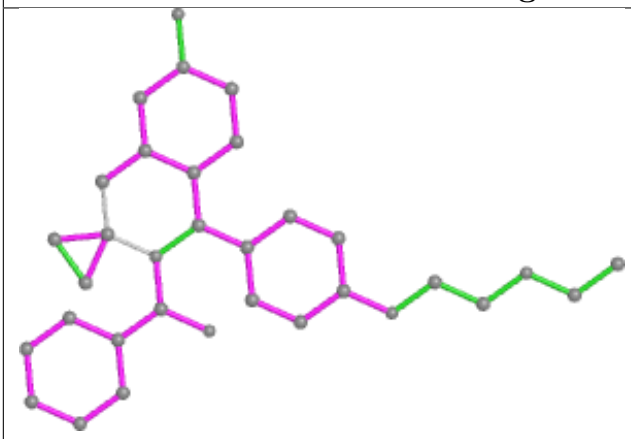
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	601	TWF	1	0
2	F	601	TWF	1	0

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

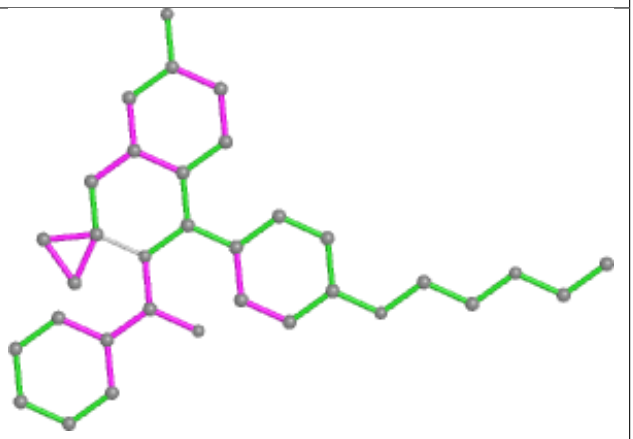
Ligand TWF E 601



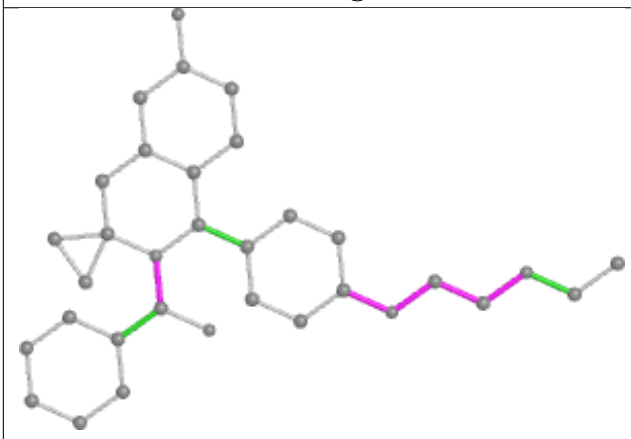
Ligand TWF A 601



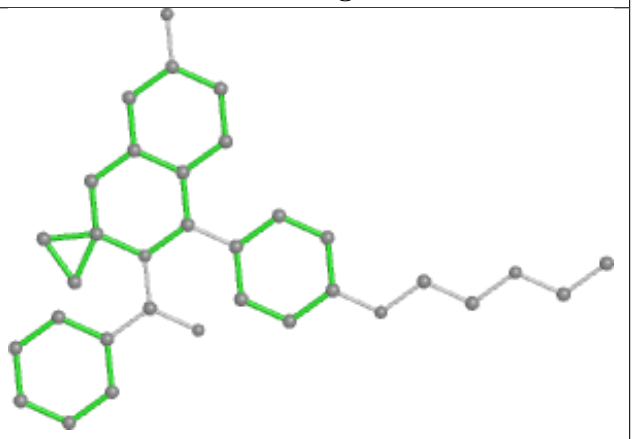
Bond lengths



Bond angles

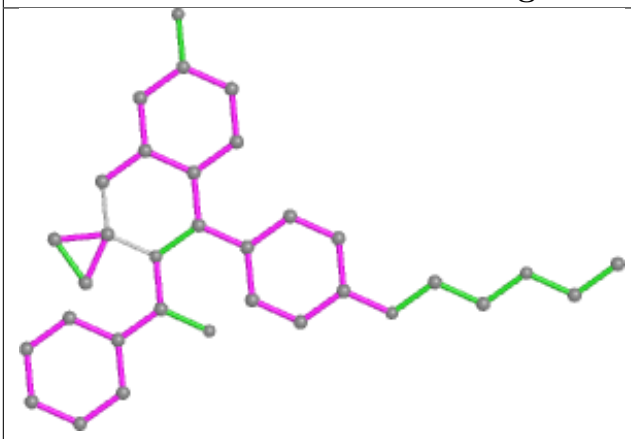


Torsions

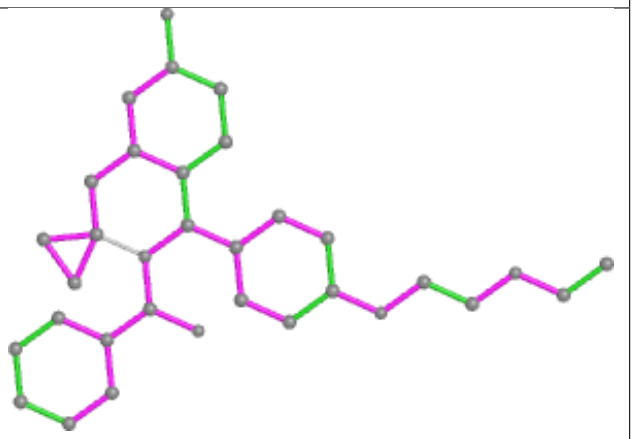


Rings

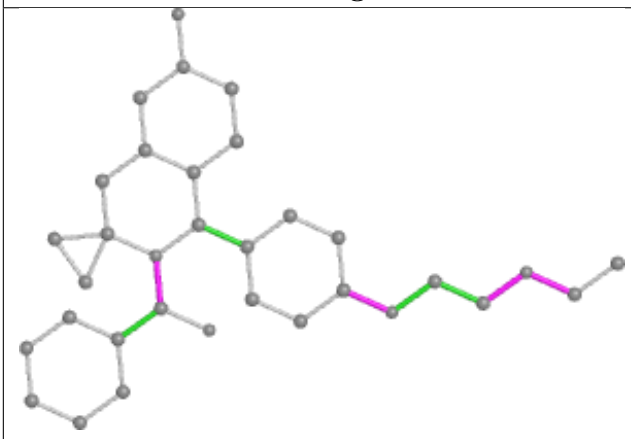
Ligand TWF G 601



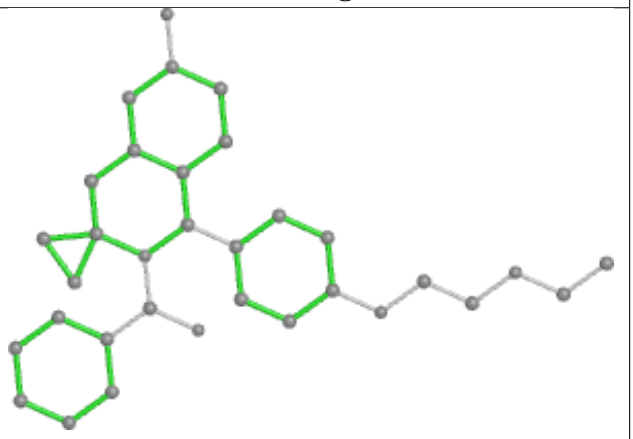
Bond lengths



Bond angles

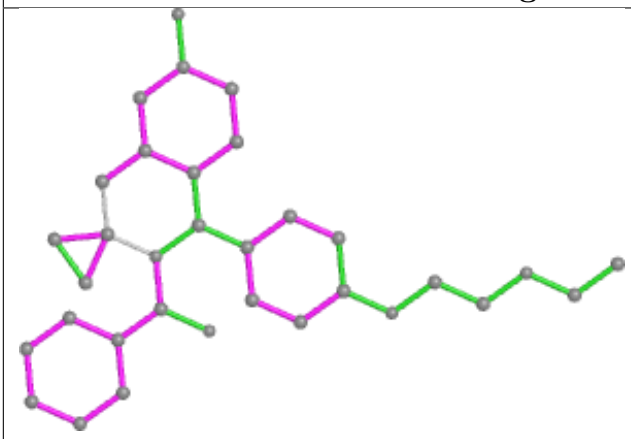


Torsions

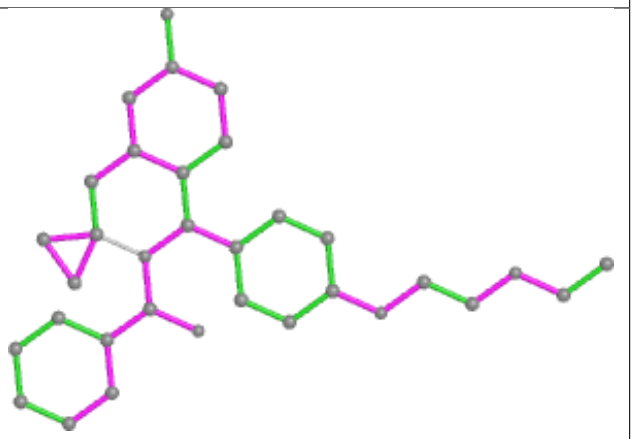


Rings

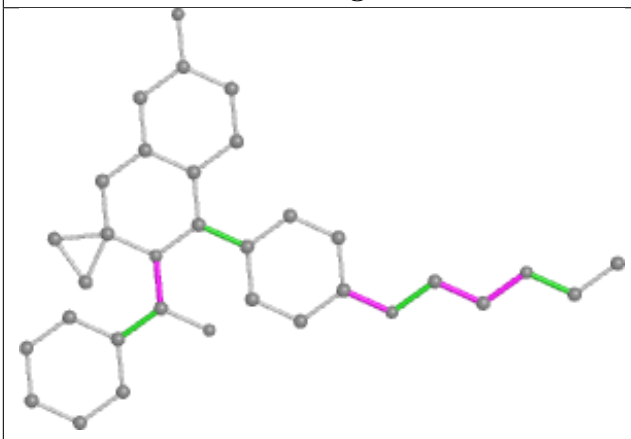
Ligand TWF B 601



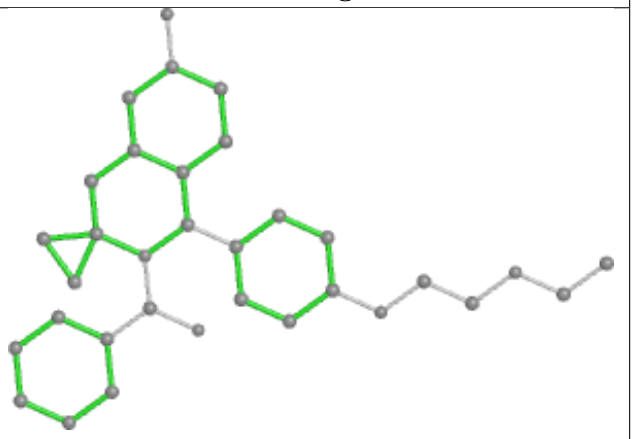
Bond lengths



Bond angles

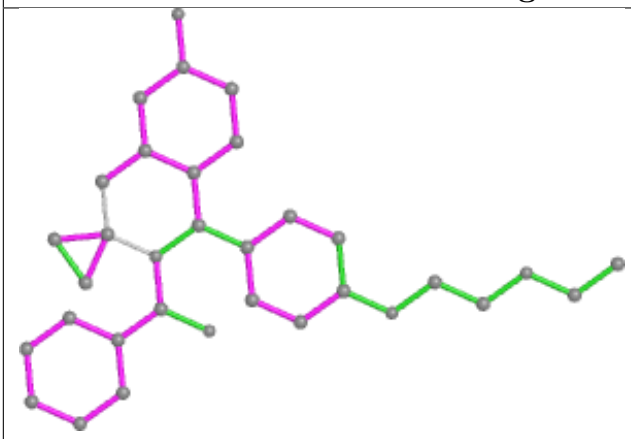


Torsions

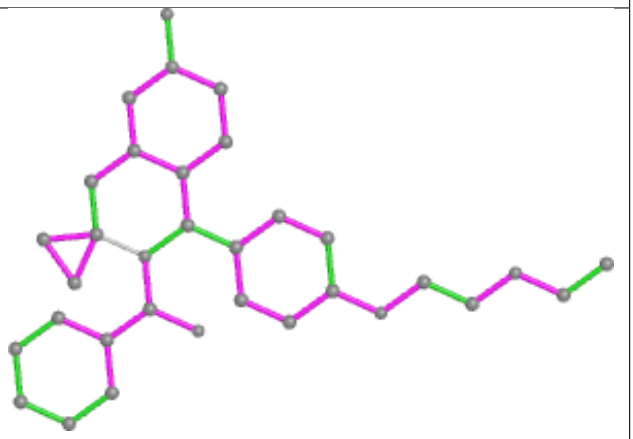


Rings

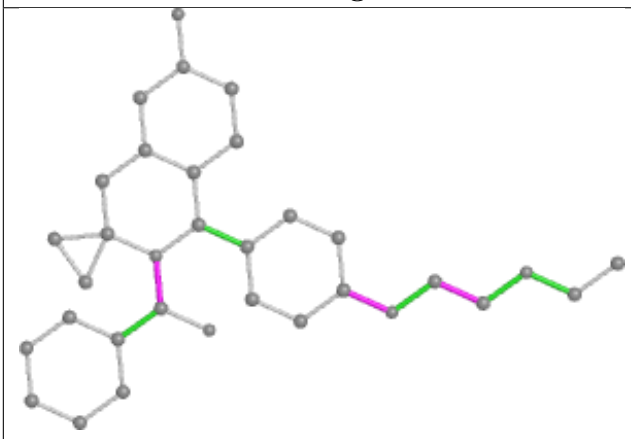
Ligand TWF H 601



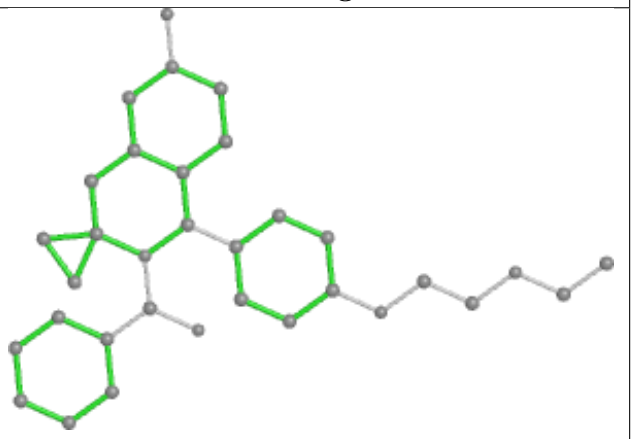
Bond lengths



Bond angles

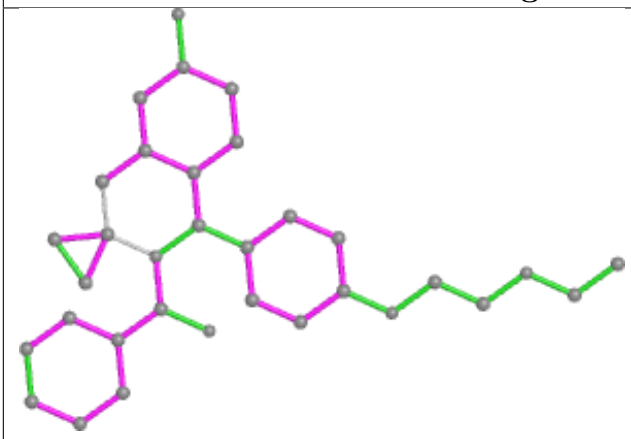


Torsions

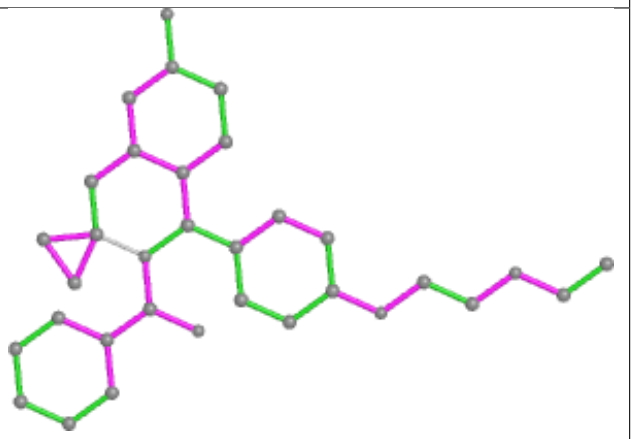


Rings

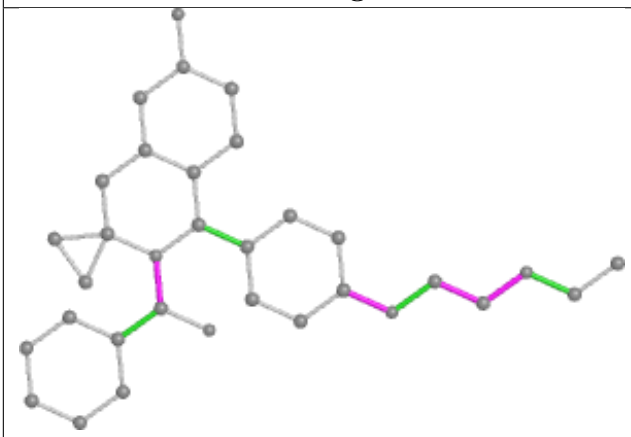
Ligand TWF F 601



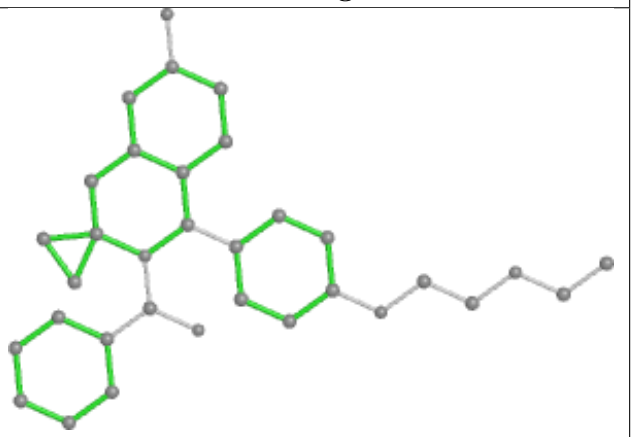
Bond lengths



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	235/255 (92%)	0.56	9 (3%)	40	43	19, 29, 47, 61	1 (0%)
1	B	221/255 (86%)	0.35	3 (1%)	75	77	20, 25, 39, 51	0
1	E	232/255 (90%)	0.52	7 (3%)	50	53	20, 25, 45, 56	1 (0%)
1	F	220/255 (86%)	0.52	10 (4%)	33	36	19, 27, 42, 52	1 (0%)
1	G	234/255 (91%)	0.06	7 (2%)	50	53	7, 18, 42, 52	0
1	H	224/255 (87%)	0.16	13 (5%)	23	25	9, 20, 43, 61	1 (0%)
All	All	1366/1530 (89%)	0.36	49 (3%)	42	45	7, 25, 43, 61	4 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	460	THR	4.5
1	B	342	MET	4.3
1	G	415	GLY	3.9
1	E	310	LEU	3.8
1	H	308	LEU	3.8
1	H	415	GLY	3.7
1	H	342	MET	3.6
1	G	528	MET	3.5
1	H	460	THR	3.4
1	G	549	LEU	3.4
1	E	418	VAL	3.3
1	F	459	TYR	3.3
1	F	341	SER	3.2
1	G	308	LEU	3.0
1	B	459	TYR	3.0
1	F	342	MET	2.8
1	H	459	TYR	2.8
1	A	459	TYR	2.7
1	A	537	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	H	345	LEU	2.7
1	H	413	ASN	2.7
1	H	533	VAL	2.6
1	F	312	ALA	2.4
1	F	343	MET	2.4
1	H	414	GLN	2.4
1	A	479	LEU	2.3
1	F	320	LEU	2.3
1	A	526	TYR	2.3
1	E	311	THR	2.3
1	H	416	LYS	2.2
1	E	309	SER	2.2
1	F	421	MET	2.2
1	A	437	MET	2.2
1	A	331	TYR	2.2
1	F	526	TYR	2.2
1	F	422	VAL	2.2
1	A	535	PRO	2.1
1	A	310	LEU	2.1
1	F	525	LEU	2.1
1	H	343	MET	2.1
1	E	538	ASP	2.1
1	E	465	THR	2.1
1	E	419	GLU	2.1
1	H	466	LEU	2.1
1	G	416	LYS	2.1
1	G	419	GLU	2.0
1	G	458	VAL	2.0
1	A	528	MET	2.0
1	H	549	LEU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

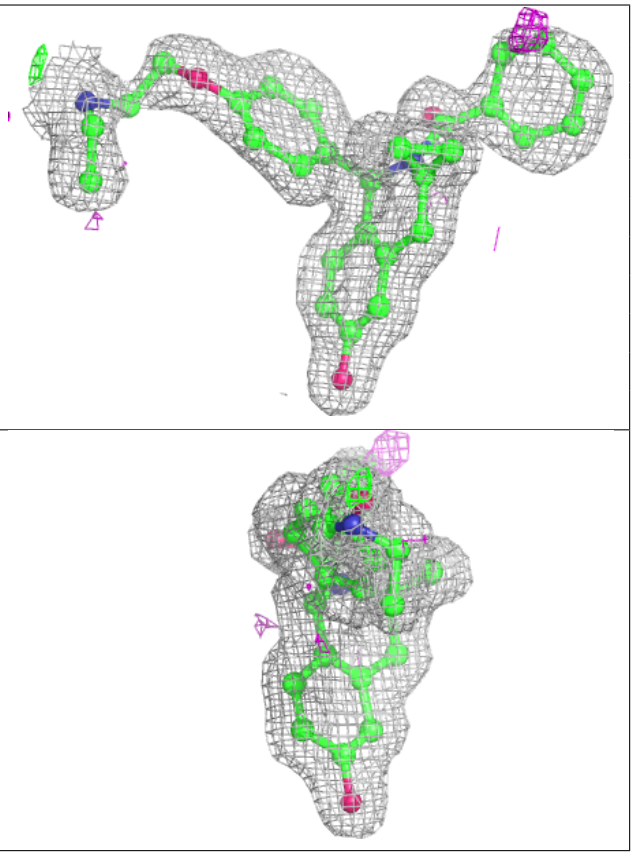
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	TWF	A	601	33/33	0.89	0.13	11,17,27,30	0
2	TWF	B	601	33/33	0.89	0.16	11,19,32,37	0
2	TWF	E	601	33/33	0.90	0.14	11,17,26,29	0
2	TWF	F	601	33/33	0.91	0.13	12,21,31,33	0
2	TWF	H	601	33/33	0.91	0.16	10,17,33,39	0
2	TWF	G	601	33/33	0.93	0.13	8,16,25,34	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.

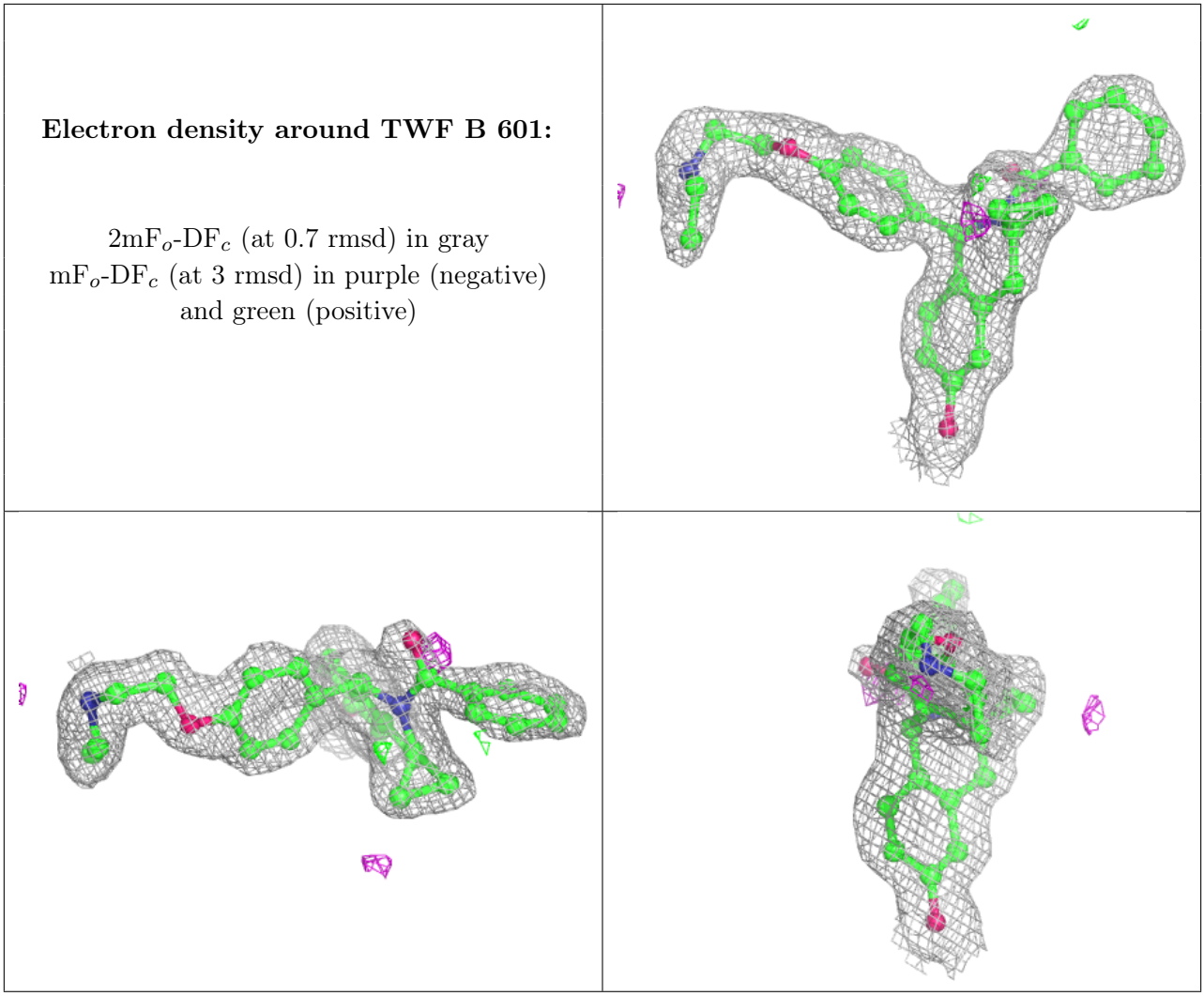
Electron density around TWF A 601:

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



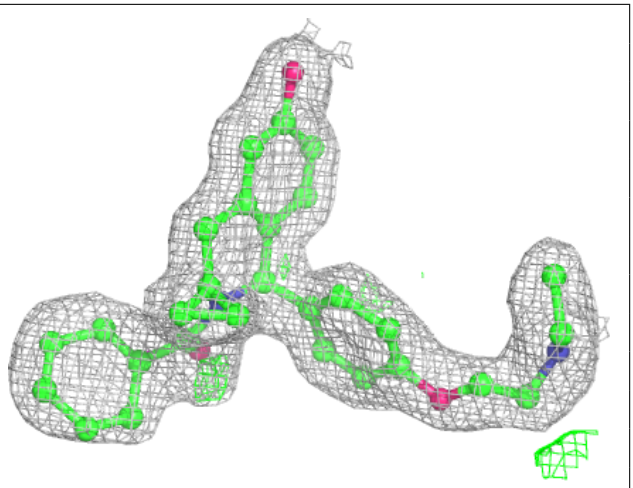
Electron density around TWF B 601:

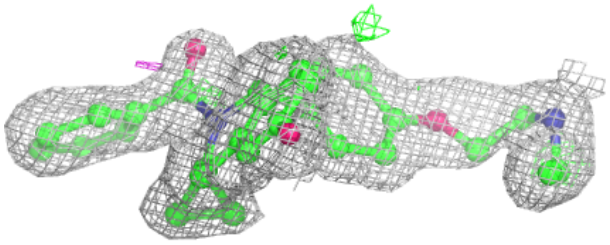
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

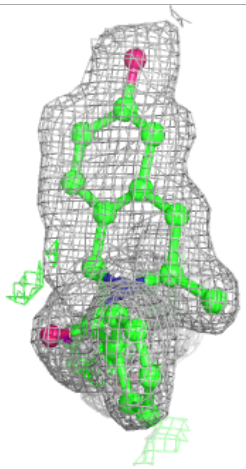


Electron density around TWF E 601:

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

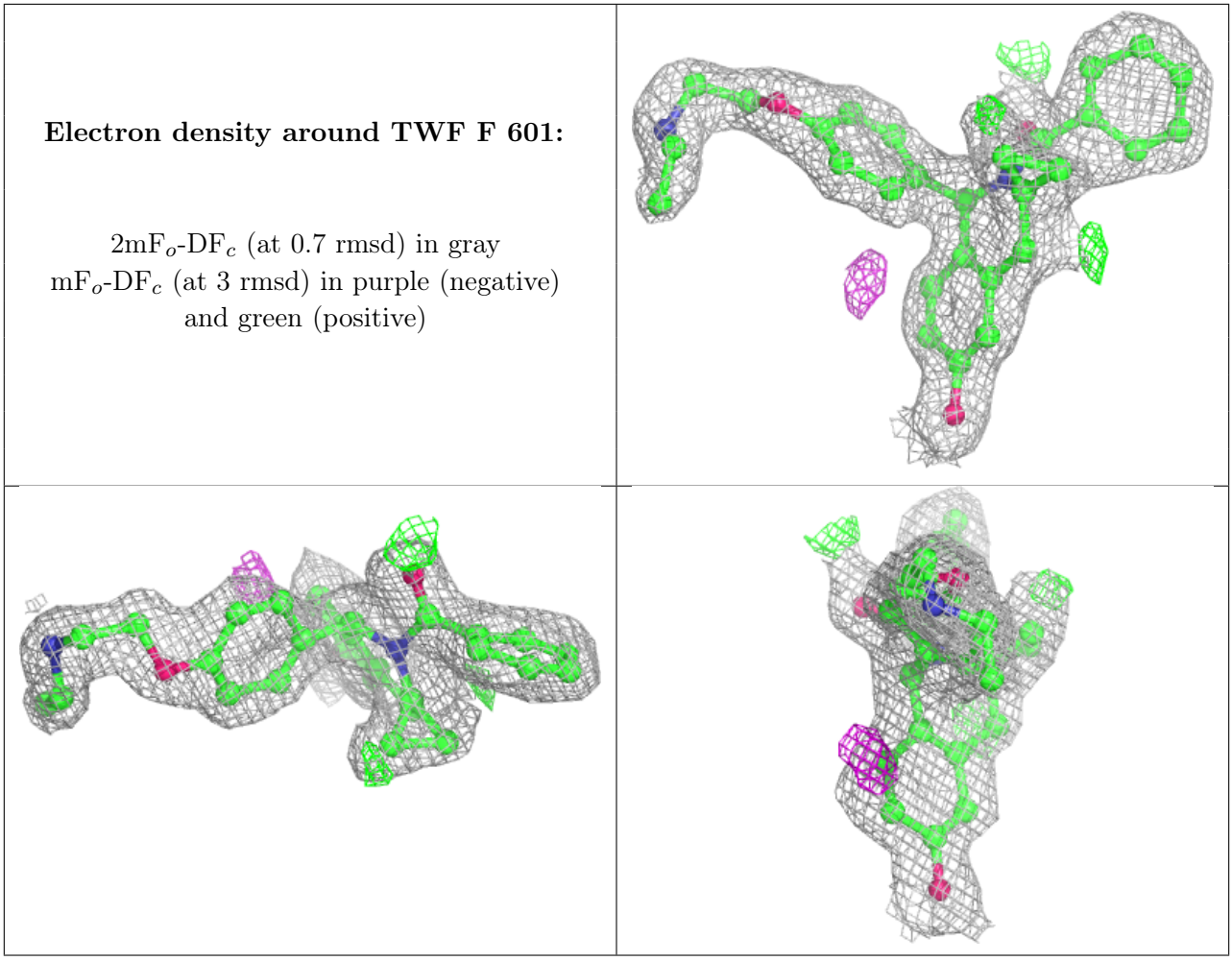






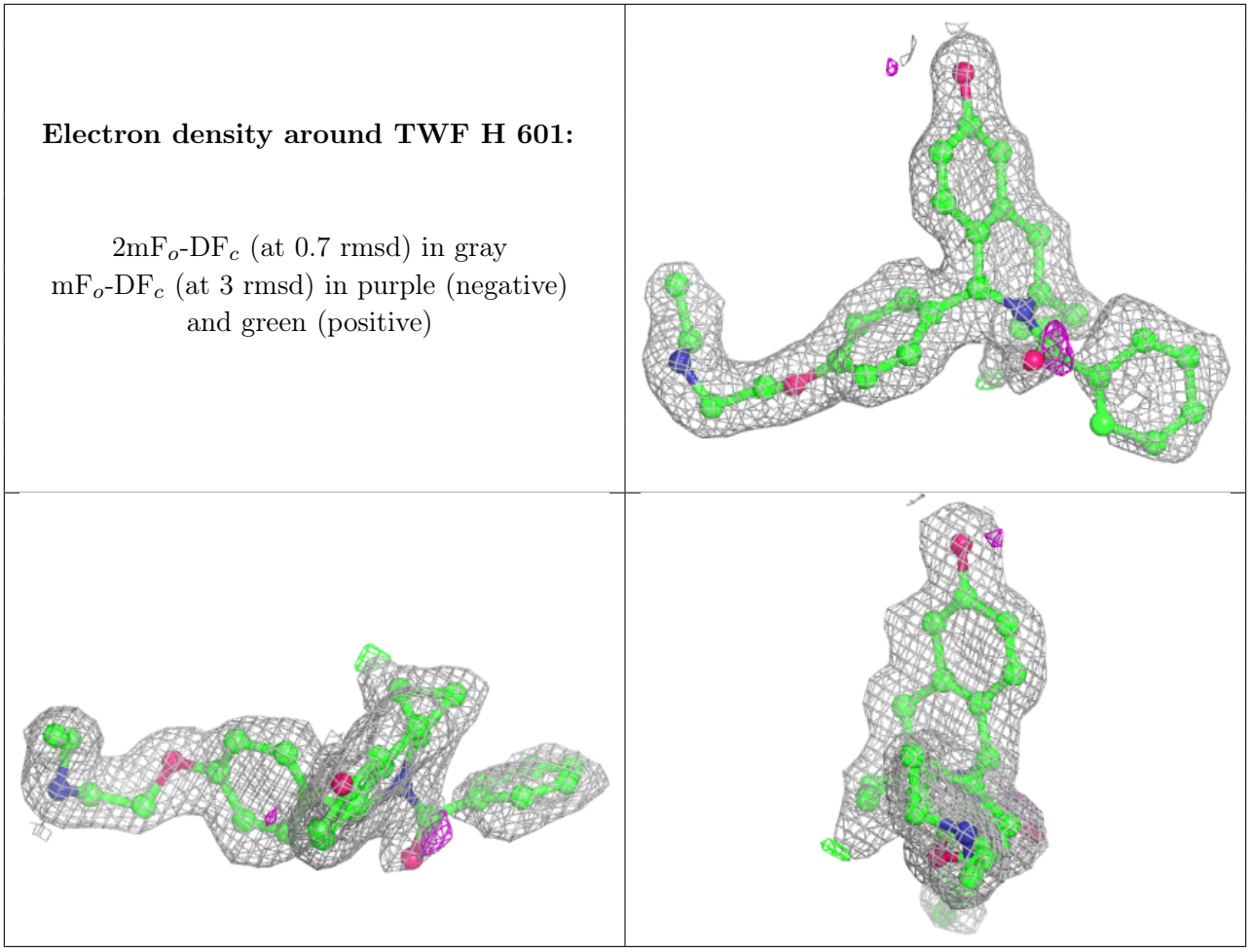
Electron density around TWF F 601:

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



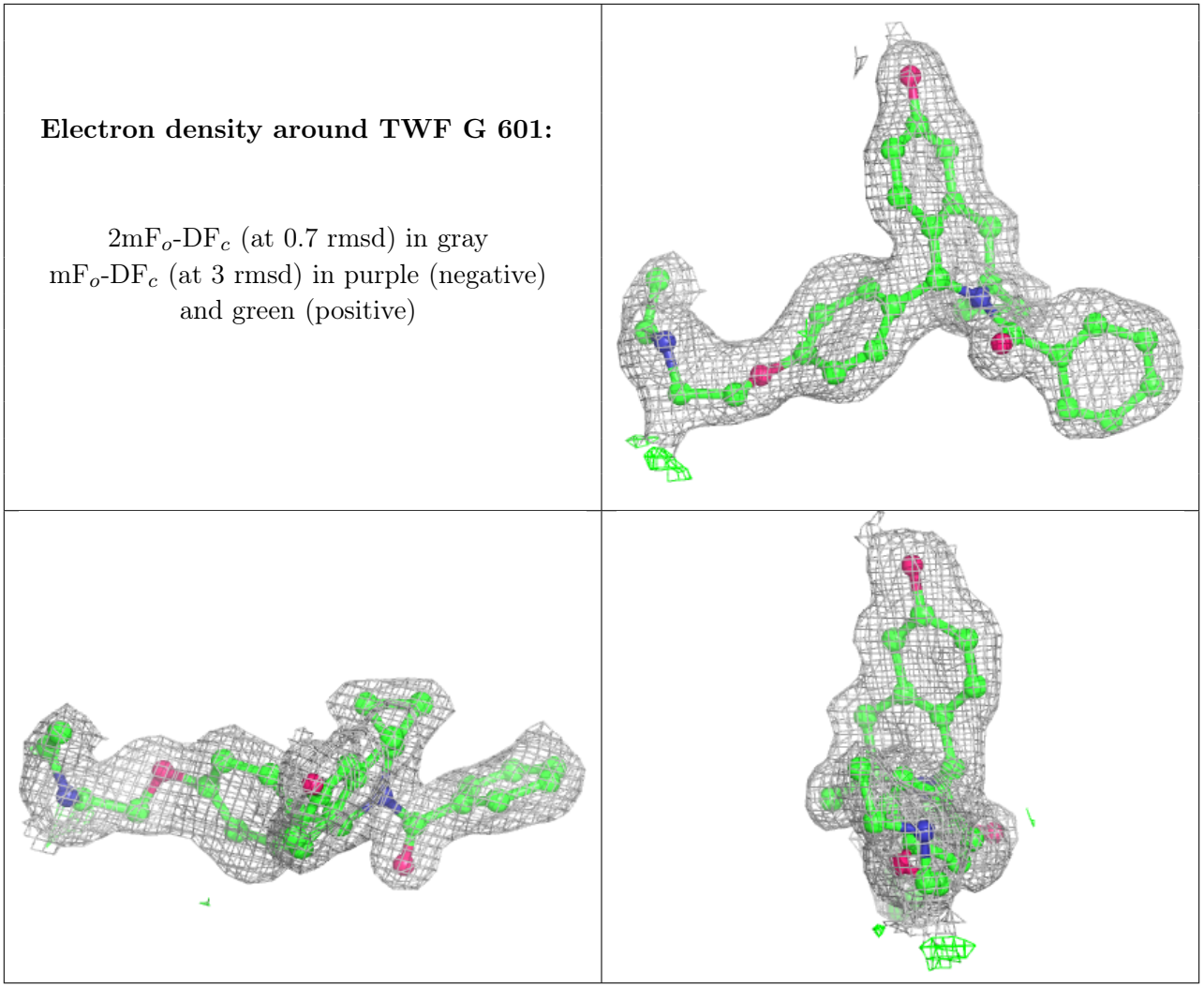
Electron density around TWF H 601:

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



Electron density around TWF G 601:

$2mF_o$-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

There are no such residues in this entry.