Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:35 pm BST

PDB ID	:	3BEJ
Title	:	Structure of human FXR in complex with MFA-1 and co-activator peptide
Authors	:	Soisson, S.M.; Parthasarathy, G.; Becker, J.W.
Deposited on	:	2007-11-19
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 ⓘ symbol.

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

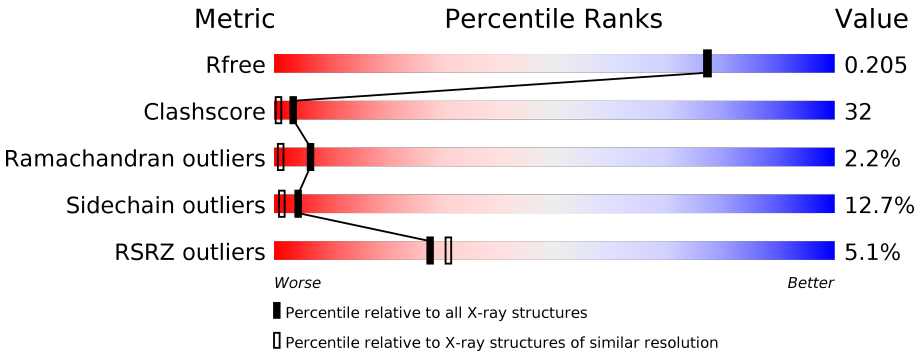
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 on 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	238	7%, 53%, 32%, 8%, 6%
1	B	238	2%, 66%, 24%, 5%
2	E	25	12%, 8%, 16%, 12%, 8%, 56%
2	F	25	8%, 16%, 24%, 52%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4349 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 Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1842	1178	310	343	11			
1	B	228	Total	C	N	O	S	0	0	0
			1872	1197	314	350	11			

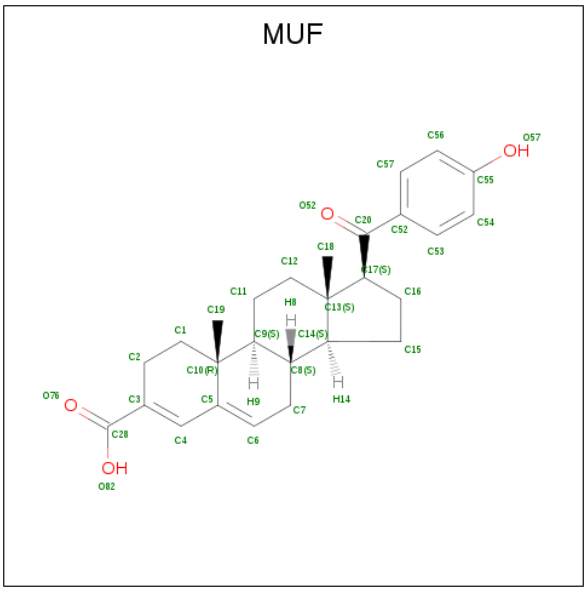
- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	0	0	0
			101	64	23	14			
2	F	12	Total	C	N	O	0	0	0
			108	68	24	16			

- Molecule 3 is YTTRIUM (III) ION (three-letter code: YT3) (formula: Y).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Y	0	0
			1	1		
3	A	1	Total	Y	0	0
			1	1		

- Molecule 4 is (8alpha,10alpha,13alpha,17beta)-17-[(4-hydroxyphenyl)carbonyl]androsta-3,5-diene-3-carboxylic acid (three-letter code: MUF) (formula: $C_{27}H_{32}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 31 27 4	0	0
4	B	1	Total C O 31 27 4	0	0

- Molecule 5 is water.

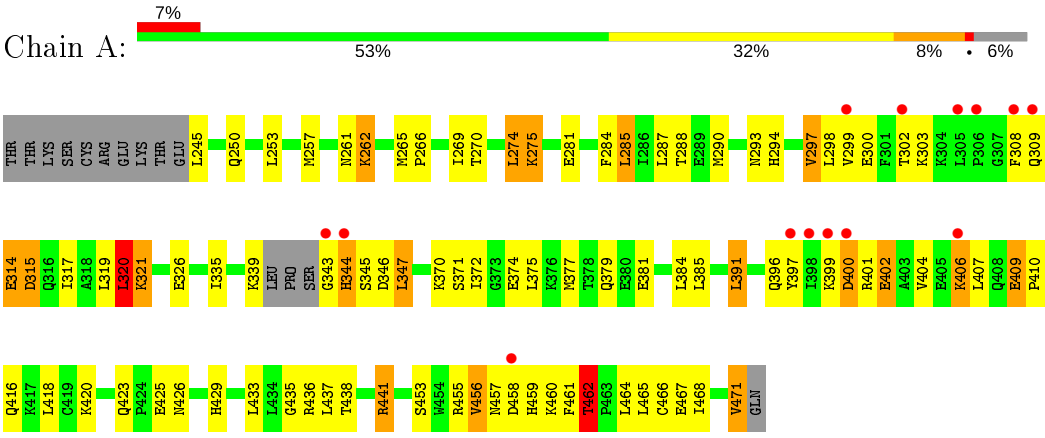
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	141	Total O 141 141	0	0
5	B	213	Total O 213 213	0	0
5	E	4	Total O 4 4	0	0
5	F	4	Total O 4 4	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

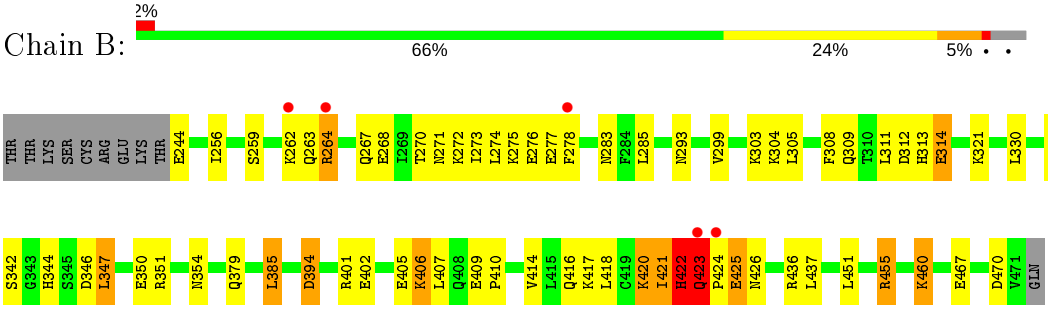
- Molecule 1: Bile acid receptor

Chain A:



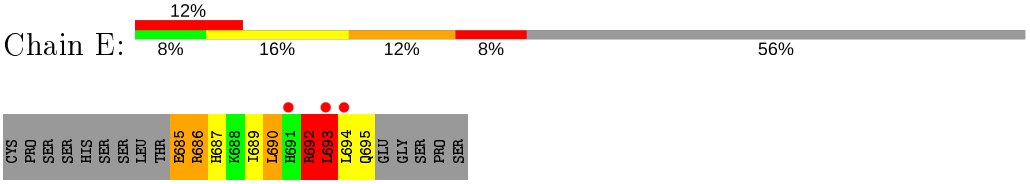
- Molecule 1: Bile acid receptor

Chain B:



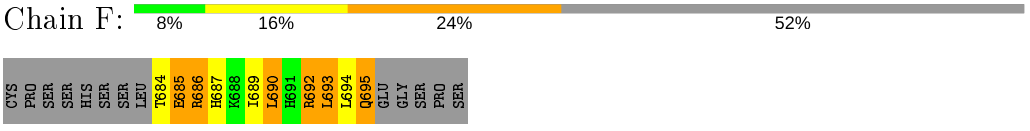
- Molecule 2: Nuclear receptor coactivator 1

Chain E:



- Molecule 2: Nuclear receptor coactivator 1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	41.64Å 90.89Å 129.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.65 – 1.90 39.65 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.65-1.90) 99.5 (39.65-1.89)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.35 (at 1.89Å)	Xtriage
Refinement program	TNT, BUSTER-TNT 2.1.1	Depositor
R, R_{free}	0.200 , 0.254 0.207 , 0.205	Depositor DCC
R_{free} test set	3998 reflections (10.05%)	wwPDB-VP
Wilson B-factor (Å^2)	25.2	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 63.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4349	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: MUF, YT3

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	0.55	0/1880	0.73	1/2537 (0.0%)
1	B	0.67	0/1912	0.78	1/2583 (0.0%)
2	E	0.37	0/102	0.89	0/134
2	F	0.47	0/109	1.01	0/144
All	All	0.61	0/4003	0.76	2/5398 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	320	LEU	CA-CB-CG	5.54	128.05	115.30
1	B	422	HIS	N-CA-C	5.25	125.19	111.00

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	1842	0	1838	132	0
1	B	1872	0	1868	96	0
2	E	101	0	110	30	0
2	F	108	0	117	19	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	31	0	30	1	0
4	B	31	0	31	0	0
5	A	141	0	0	17	0
5	B	213	0	0	9	0
5	E	4	0	0	1	0
5	F	4	0	0	2	0
All	All	4349	0	3994	259	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 32.

All (259) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:LEU:HD12	1:A:437:LEU:HD21	1.22	1.14
2:E:685:GLU:HB3	2:E:687:HIS:HD1	1.05	1.12
1:A:266:PRO:HB2	1:A:269:ILE:HD13	1.25	1.10
1:B:385:LEU:HD11	1:B:437:LEU:HD21	1.32	1.06
1:B:423:GLN:HB2	1:B:424:PRO:HD3	1.39	1.05
1:A:317:ILE:HG21	2:E:685:GLU:HG3	1.37	1.03
2:E:685:GLU:HA	2:E:686:ARG:HB3	1.05	1.03
1:B:423:GLN:HB2	1:B:424:PRO:CD	1.92	0.97
1:B:455:ARG:HG3	1:B:455:ARG:HH11	1.31	0.95
2:E:685:GLU:HA	2:E:686:ARG:CB	1.96	0.95
2:E:685:GLU:CA	2:E:686:ARG:HB3	1.96	0.95
1:B:264:ARG:HH11	1:B:264:ARG:HG3	1.34	0.92
1:B:321:LYS:HZ3	2:F:687:HIS:CE1	1.87	0.91
1:B:321:LYS:HZ3	2:F:687:HIS:HE1	0.94	0.89
1:A:455:ARG:HG3	1:A:455:ARG:HH11	1.36	0.89
2:E:685:GLU:HB3	2:E:687:HIS:ND1	1.88	0.87
1:A:294:HIS:O	1:A:298:LEU:HD23	1.76	0.85
1:A:315:ASP:OD1	1:A:399:LYS:HG2	1.78	0.84
1:A:370:LYS:O	1:A:374:GLU:HG2	1.79	0.82
2:E:692:ARG:HE	2:E:693:LEU:N	1.77	0.82
1:B:385:LEU:HD11	1:B:437:LEU:CD2	2.11	0.81
1:A:414:VAL:O	1:A:418:LEU:HD13	1.80	0.81
1:A:467:GLU:OE1	2:E:689:ILE:HG22	1.80	0.81
1:B:385:LEU:CD1	1:B:437:LEU:HD21	2.10	0.80
1:A:294:HIS:NE2	1:A:298:LEU:HD21	1.96	0.80
1:A:315:ASP:OD2	1:A:400:ASP:HB2	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:ASP:OD2	1:A:347:LEU:HD13	1.81	0.80
1:A:344:HIS:HB2	5:A:547:HOH:O	1.82	0.78
1:A:423:GLN:HE22	1:A:426:ASN:HD22	1.30	0.78
1:A:423:GLN:HE21	1:A:426:ASN:HB3	1.48	0.78
1:A:429:HIS:O	1:A:433:LEU:HD23	1.82	0.78
1:A:402:GLU:O	1:A:406:LYS:HD3	1.84	0.78
1:B:270:THR:O	1:B:274:LEU:HD13	1.83	0.78
1:B:330:LEU:HD22	1:B:385:LEU:HD12	1.67	0.77
1:A:385:LEU:HD12	1:A:437:LEU:CD2	2.10	0.77
1:A:266:PRO:HB2	1:A:269:ILE:CD1	2.12	0.76
1:A:266:PRO:CB	1:A:269:ILE:HD13	2.09	0.76
1:B:385:LEU:HD13	1:B:385:LEU:O	1.87	0.75
1:A:294:HIS:CD2	1:A:298:LEU:HD21	2.24	0.73
1:A:310:THR:HB	5:A:560:HOH:O	1.88	0.72
1:A:321:LYS:HE3	2:E:687:HIS:NE2	2.03	0.72
1:B:421:ILE:N	1:B:421:ILE:HD13	2.04	0.72
1:A:344:HIS:NE2	5:A:536:HOH:O	2.21	0.71
1:A:455:ARG:NH1	1:A:455:ARG:HG3	2.03	0.71
1:B:455:ARG:HG3	1:B:455:ARG:NH1	2.06	0.70
1:A:300:GLU:HG2	5:A:569:HOH:O	1.91	0.70
1:A:312:ASP:O	1:A:314:GLU:N	2.24	0.70
1:B:259:SER:OG	1:B:304:LYS:HD3	1.92	0.69
1:A:245:LEU:N	5:A:581:HOH:O	2.24	0.69
1:A:344:HIS:N	1:A:346:ASP:OD1	2.26	0.69
1:B:308:PHE:O	1:B:311:LEU:HD23	1.94	0.68
1:B:414:VAL:O	1:B:418:LEU:HD13	1.92	0.68
1:B:422:HIS:ND1	1:B:423:GLN:HG3	2.09	0.68
1:B:311:LEU:HD21	1:B:407:LEU:HD11	1.74	0.68
1:B:405:GLU:O	1:B:409:GLU:HG3	1.94	0.68
1:B:264:ARG:NH1	1:B:264:ARG:HG3	2.07	0.67
2:E:685:GLU:OE2	2:E:685:GLU:N	2.27	0.67
1:A:467:GLU:CD	2:E:689:ILE:HG22	2.14	0.67
1:B:421:ILE:O	1:B:422:HIS:HB2	1.94	0.67
1:B:405:GLU:HB3	1:B:406:LYS:HE2	1.76	0.67
1:A:455:ARG:HD3	1:A:461:PHE:HE1	1.60	0.66
1:B:299:VAL:HG12	1:B:303:LYS:HD2	1.77	0.66
1:A:311:LEU:HD23	5:A:607:HOH:O	1.95	0.66
1:A:320:LEU:HD12	2:E:690:LEU:HD11	1.77	0.66
1:B:321:LYS:NZ	2:F:687:HIS:HE1	1.82	0.66
1:A:321:LYS:HA	1:A:468:ILE:HD11	1.78	0.66
1:B:424:PRO:O	1:B:425:GLU:HB2	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:GLU:HG2	5:B:750:HOH:O	1.96	0.65
1:A:265:MET:HE1	1:A:290:MET:HE2	1.78	0.64
1:B:460:LYS:NZ	5:B:641:HOH:O	2.30	0.64
1:A:315:ASP:CG	1:A:399:LYS:HG2	2.18	0.64
1:B:330:LEU:CD2	1:B:385:LEU:HD12	2.27	0.64
1:A:429:HIS:CE1	1:A:433:LEU:HD21	2.32	0.64
1:A:385:LEU:HD21	1:A:415:LEU:HD21	1.80	0.63
2:F:693:LEU:HD12	2:F:694:LEU:N	2.12	0.63
1:A:379:GLN:HG2	5:A:548:HOH:O	1.99	0.63
1:A:453:SER:O	1:A:456:VAL:HG12	1.99	0.63
2:E:692:ARG:HH21	2:E:693:LEU:HA	1.64	0.63
1:B:338:LYS:O	1:B:344:HIS:HE1	1.82	0.62
1:B:311:LEU:N	1:B:311:LEU:HD22	2.15	0.62
1:A:399:LYS:HG3	1:A:400:ASP:N	2.16	0.61
2:F:690:LEU:HD23	2:F:693:LEU:HD11	1.81	0.61
1:A:399:LYS:HG3	1:A:400:ASP:H	1.65	0.60
2:F:685:GLU:HA	2:F:687:HIS:H	1.66	0.60
1:A:423:GLN:HE22	1:A:426:ASN:ND2	1.97	0.60
2:E:692:ARG:HE	2:E:693:LEU:CA	2.14	0.60
1:B:455:ARG:HA	1:B:455:ARG:NE	2.16	0.60
1:A:372:ILE:HD13	1:A:436:ARG:HG2	1.84	0.59
1:B:402:GLU:OE2	1:B:406:LYS:NZ	2.29	0.59
1:B:421:ILE:O	1:B:422:HIS:CB	2.50	0.59
1:B:278:PHE:HE2	1:B:354:ASN:HD22	1.47	0.59
1:B:293:ASN:HB2	5:B:649:HOH:O	2.02	0.59
1:B:423:GLN:CB	1:B:424:PRO:CD	2.77	0.59
1:B:268:GLU:O	1:B:272:LYS:HG3	2.02	0.58
1:B:385:LEU:HD21	1:B:437:LEU:HD21	1.85	0.58
1:A:284:PHE:CE2	1:A:459:HIS:HB3	2.38	0.58
1:A:437:LEU:O	1:A:441:ARG:HG2	2.03	0.58
2:F:694:LEU:O	2:F:695:GLN:HB2	2.03	0.58
1:A:269:ILE:HD12	1:A:269:ILE:N	2.18	0.58
1:B:455:ARG:CG	1:B:455:ARG:HH11	2.12	0.57
1:A:313:HIS:HD2	5:A:599:HOH:O	1.87	0.57
2:E:693:LEU:HD12	2:E:693:LEU:N	2.20	0.57
1:B:425:GLU:OE2	1:B:425:GLU:HA	2.03	0.57
1:B:402:GLU:HG3	1:B:406:LYS:HE3	1.85	0.57
1:B:421:ILE:HG22	1:B:422:HIS:N	2.18	0.56
1:A:401:ARG:HD3	5:A:612:HOH:O	2.04	0.56
2:E:685:GLU:CB	2:E:687:HIS:H	2.19	0.56
1:A:399:LYS:CG	1:A:400:ASP:H	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:GLU:O	1:A:285:LEU:HD13	2.06	0.56
1:B:340:LEU:HD12	1:B:340:LEU:N	2.20	0.55
1:B:299:VAL:HG21	2:F:693:LEU:HD13	1.89	0.55
1:A:294:HIS:CD2	1:A:298:LEU:CD2	2.89	0.55
1:B:299:VAL:CG1	1:B:303:LYS:HD2	2.37	0.55
1:B:405:GLU:HG2	1:B:409:GLU:OE2	2.07	0.54
1:A:326:GLU:OE2	1:A:441:ARG:NH1	2.41	0.54
1:A:298:LEU:HD22	1:A:298:LEU:N	2.22	0.53
1:A:314:GLU:HG3	5:E:327:HOH:O	2.06	0.53
1:A:455:ARG:HD3	1:A:461:PHE:CE1	2.40	0.53
1:A:262:LYS:O	1:A:262:LYS:HG3	2.08	0.53
1:A:339:LYS:O	1:A:343:GLY:O	2.26	0.53
1:B:303:LYS:O	1:B:309:GLN:OE1	2.25	0.53
2:F:685:GLU:CA	2:F:687:HIS:H	2.21	0.53
2:F:685:GLU:HA	2:F:687:HIS:N	2.24	0.53
1:B:273:ILE:O	1:B:347:LEU:HD12	2.09	0.53
1:A:308:PHE:O	1:A:311:LEU:HB2	2.09	0.53
1:B:276:GLU:HG3	1:B:277:GLU:N	2.23	0.52
1:B:379:GLN:HG2	5:B:681:HOH:O	2.09	0.52
1:A:343:GLY:O	1:A:345:SER:N	2.35	0.52
1:A:384:LEU:CD1	1:A:418:LEU:HD22	2.40	0.52
1:A:462:THR:HG22	1:A:465:LEU:H	1.72	0.52
1:B:271:ASN:O	1:B:275:LYS:HG2	2.10	0.52
1:B:385:LEU:HD13	1:B:385:LEU:C	2.29	0.52
1:A:396:GLN:HG2	1:A:397:TYR:CD2	2.45	0.52
1:B:418:LEU:HD12	1:B:418:LEU:N	2.24	0.52
2:E:692:ARG:HE	2:E:693:LEU:HA	1.74	0.51
1:A:466:CYS:HA	1:A:471:VAL:HG13	1.92	0.51
1:B:421:ILE:HD11	5:B:710:HOH:O	2.11	0.51
1:A:441:ARG:NE	5:A:526:HOH:O	2.33	0.51
1:A:311:LEU:HD12	1:A:407:LEU:HD11	1.93	0.51
1:A:287:LEU:HB3	4:A:473:MUF:H53	1.93	0.51
1:B:313:HIS:HD2	5:F:229:HOH:O	1.93	0.50
1:A:385:LEU:CD2	1:A:415:LEU:HD21	2.41	0.50
1:A:375:LEU:HD11	1:A:436:ARG:HD3	1.94	0.50
1:B:256:ILE:HD12	1:B:305:LEU:HD23	1.94	0.49
1:B:385:LEU:HD21	1:B:437:LEU:CG	2.41	0.49
1:B:394:ASP:HA	1:B:401:ARG:NH1	2.27	0.49
1:A:303:LYS:HZ1	2:E:695:GLN:N	2.10	0.49
1:A:416:GLN:NE2	5:A:529:HOH:O	2.46	0.49
1:A:399:LYS:CG	1:A:400:ASP:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:467:GLU:OE2	2:F:689:ILE:HG13	2.12	0.49
1:A:245:LEU:N	5:A:539:HOH:O	2.45	0.49
1:A:298:LEU:CD2	1:A:298:LEU:N	2.76	0.49
1:B:256:ILE:HD12	1:B:305:LEU:CD2	2.42	0.49
2:F:690:LEU:O	2:F:693:LEU:HD12	2.12	0.48
1:A:409:GLU:HB3	1:A:410:PRO:HD3	1.96	0.48
1:A:288:THR:HG21	1:A:461:PHE:O	2.13	0.48
2:E:692:ARG:O	2:E:694:LEU:N	2.47	0.48
1:A:320:LEU:HD12	2:E:690:LEU:HD21	1.96	0.48
1:B:244:GLU:N	5:B:742:HOH:O	2.47	0.47
2:E:692:ARG:NE	2:E:693:LEU:N	2.55	0.47
2:F:692:ARG:HG3	2:F:692:ARG:HH11	1.78	0.47
1:A:311:LEU:HD12	1:A:407:LEU:CD1	2.45	0.47
1:B:385:LEU:HD21	1:B:437:LEU:CD2	2.44	0.47
1:B:421:ILE:N	1:B:421:ILE:CD1	2.73	0.47
1:A:423:GLN:NE2	1:A:426:ASN:HB3	2.22	0.47
1:B:347:LEU:HD13	1:B:351:ARG:NE	2.30	0.47
1:A:269:ILE:HG21	1:A:290:MET:HG2	1.97	0.47
1:B:407:LEU:O	1:B:410:PRO:HD2	2.14	0.47
1:A:317:ILE:CG2	2:E:685:GLU:HG3	2.26	0.47
1:B:341:PRO:O	1:B:344:HIS:HB3	2.15	0.46
1:B:299:VAL:HG11	2:F:693:LEU:HD13	1.97	0.46
1:A:391:LEU:CD2	1:A:411:LEU:HD11	2.45	0.46
2:E:692:ARG:NH2	2:E:693:LEU:HA	2.30	0.46
2:F:693:LEU:HD12	2:F:693:LEU:C	2.36	0.46
1:A:321:LYS:HA	1:A:468:ILE:CD1	2.43	0.46
1:A:423:GLN:NE2	1:A:426:ASN:HD22	2.06	0.46
1:A:344:HIS:HD2	5:A:616:HOH:O	1.99	0.46
1:B:273:ILE:O	1:B:351:ARG:NH2	2.42	0.46
1:B:385:LEU:CD2	1:B:437:LEU:HD21	2.46	0.46
1:B:338:LYS:O	1:B:344:HIS:CE1	2.65	0.46
1:B:417:LYS:HE3	5:B:717:HOH:O	2.15	0.46
1:B:422:HIS:ND1	1:B:423:GLN:CG	2.78	0.46
2:E:690:LEU:HA	2:E:693:LEU:HD11	1.98	0.46
1:A:343:GLY:HA3	1:A:346:ASP:OD1	2.17	0.46
1:A:302:THR:HG22	1:A:308:PHE:CE2	2.51	0.45
2:E:689:ILE:CG2	2:E:690:LEU:N	2.79	0.45
1:A:299:VAL:CG2	1:A:320:LEU:HD11	2.46	0.45
1:A:343:GLY:O	1:A:344:HIS:HB3	2.16	0.45
1:A:311:LEU:CD1	1:A:407:LEU:CD1	2.94	0.45
2:F:684:THR:HB	5:F:183:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:GLN:HG2	5:A:582:HOH:O	2.17	0.45
1:A:375:LEU:HD11	1:A:436:ARG:CD	2.47	0.45
1:A:321:LYS:CE	2:E:687:HIS:NE2	2.76	0.45
1:A:377:MET:HA	1:A:381:GLU:OE1	2.17	0.45
1:B:264:ARG:CG	1:B:264:ARG:NH1	2.72	0.45
1:A:257:MET:O	1:A:261:ASN:HB2	2.17	0.45
1:A:274:LEU:HB3	1:A:275:LYS:HG2	1.99	0.45
1:A:293:ASN:O	1:A:297:VAL:HG13	2.17	0.45
1:A:385:LEU:HD22	1:A:415:LEU:HD22	1.99	0.45
1:A:455:ARG:CD	1:A:461:PHE:HE1	2.27	0.45
2:E:689:ILE:HG23	2:E:690:LEU:N	2.31	0.45
1:A:409:GLU:HB3	1:A:410:PRO:CD	2.47	0.45
1:B:455:ARG:CG	1:B:455:ARG:NH1	2.74	0.45
1:B:283:ASN:OD1	1:B:351:ARG:HG2	2.17	0.44
1:A:270:THR:HG23	1:A:344:HIS:NE2	2.31	0.44
1:B:340:LEU:HB3	1:B:341:PRO:HA	1.99	0.44
1:A:455:ARG:HA	1:A:455:ARG:HD2	1.63	0.44
1:A:321:LYS:HA	1:A:468:ILE:CG1	2.47	0.44
1:A:371:SER:O	1:A:436:ARG:NH2	2.47	0.44
1:A:423:GLN:NE2	1:A:426:ASN:CB	2.80	0.44
1:B:424:PRO:HB2	5:B:685:HOH:O	2.18	0.44
1:B:423:GLN:OE1	1:B:424:PRO:HD2	2.17	0.44
1:B:424:PRO:O	1:B:425:GLU:CB	2.64	0.44
1:A:321:LYS:HE3	2:E:687:HIS:CD2	2.52	0.44
1:A:343:GLY:C	1:A:345:SER:H	2.18	0.44
1:A:265:MET:HE2	5:A:570:HOH:O	2.17	0.44
1:A:381:GLU:OE2	1:A:429:HIS:HE1	2.00	0.44
1:B:385:LEU:HD21	1:B:437:LEU:HG	1.99	0.44
1:B:423:GLN:CD	1:B:424:PRO:HD2	2.38	0.44
1:A:303:LYS:HZ1	2:E:695:GLN:HB2	1.83	0.43
1:A:436:ARG:HD2	5:A:530:HOH:O	2.17	0.43
1:B:299:VAL:HG21	2:F:693:LEU:CD1	2.49	0.43
2:E:685:GLU:HB2	2:E:687:HIS:H	1.82	0.43
1:A:269:ILE:HD12	1:A:269:ILE:H	1.84	0.43
1:A:423:GLN:HE21	1:A:426:ASN:CB	2.23	0.43
2:F:690:LEU:CD2	2:F:693:LEU:HD11	2.49	0.43
1:A:317:ILE:O	1:A:321:LYS:HB3	2.19	0.43
1:A:460:LYS:HE3	1:A:460:LYS:HB3	1.36	0.43
1:B:274:LEU:N	1:B:274:LEU:CD1	2.82	0.43
1:A:265:MET:CE	1:A:290:MET:HE2	2.47	0.43
1:A:409:GLU:CB	1:A:410:PRO:CD	2.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:346:ASP:O	1:B:350:GLU:HG2	2.19	0.42
1:B:299:VAL:HG12	1:B:303:LYS:CD	2.49	0.42
1:A:423:GLN:HB3	1:A:423:GLN:HE21	1.54	0.42
1:A:339:LYS:HB2	5:A:540:HOH:O	2.20	0.42
1:B:436:ARG:HD3	1:B:436:ARG:HA	1.77	0.42
1:A:253:LEU:O	1:A:257:MET:HG2	2.20	0.42
2:F:684:THR:O	2:F:686:ARG:HB2	2.20	0.42
1:A:265:MET:CE	1:A:290:MET:CE	2.98	0.41
1:B:308:PHE:HA	1:B:311:LEU:HD23	2.01	0.41
1:B:347:LEU:HA	1:B:347:LEU:HD23	1.74	0.41
1:A:319:LEU:HD21	1:A:404:VAL:HG11	2.02	0.41
1:A:381:GLU:O	1:A:385:LEU:HD23	2.20	0.41
1:A:245:LEU:HD21	1:A:418:LEU:CD1	2.51	0.41
1:B:340:LEU:HA	1:B:341:PRO:C	2.40	0.41
1:B:406:LYS:HD3	1:B:406:LYS:HA	1.60	0.41
1:B:263:GLN:OE1	1:B:263:GLN:N	2.48	0.41
1:B:416:GLN:O	1:B:420:LYS:HD2	2.20	0.41
1:B:311:LEU:N	1:B:311:LEU:CD2	2.81	0.41
1:A:311:LEU:CD1	1:A:407:LEU:HD12	2.50	0.41
1:A:461:PHE:O	1:A:462:THR:CB	2.69	0.41
1:A:270:THR:HG23	1:A:344:HIS:CE1	2.56	0.41
1:A:385:LEU:CD2	1:A:415:LEU:CD2	2.98	0.41
1:A:265:MET:HE1	1:A:290:MET:CE	2.50	0.40
1:A:456:VAL:CG1	1:A:457:ASN:N	2.84	0.40
1:B:426:ASN:N	5:B:685:HOH:O	2.46	0.40
1:A:435:GLY:O	1:A:438:THR:HB	2.22	0.40
1:B:311:LEU:HD21	1:B:407:LEU:CD1	2.47	0.40
1:A:418:LEU:HD12	1:A:418:LEU:N	2.37	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	220/238 (92%)	207 (94%)	9 (4%)	4 (2%)	8 2
1	B	226/238 (95%)	216 (96%)	7 (3%)	3 (1%)	12 4
2	E	9/25 (36%)	5 (56%)	1 (11%)	3 (33%)	0 0
2	F	10/25 (40%)	7 (70%)	3 (30%)	0	100 100
All	All	465/526 (88%)	435 (94%)	20 (4%)	10 (2%)	6 1

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	B	423	GLN
1	B	425	GLU
2	E	692	ARG
2	E	686	ARG
2	E	693	LEU
1	A	309	GLN
1	A	314	GLU
1	A	462	THR
1	B	422	HIS

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	207/221 (94%)	182 (88%)	25 (12%)	5 1
1	B	211/221 (96%)	190 (90%)	21 (10%)	7 3
2	E	11/24 (46%)	7 (64%)	4 (36%)	0 0
2	F	12/24 (50%)	6 (50%)	6 (50%)	0 0
All	All	441/490 (90%)	385 (87%)	56 (13%)	4 1

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	262	LYS

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Mol	Chain	Res	Type
1	A	274	LEU
1	A	275	LYS
1	A	285	LEU
1	A	297	VAL
1	A	311	LEU
1	A	315	ASP
1	A	320	LEU
1	A	321	LYS
1	A	335	ILE
1	A	344	HIS
1	A	347	LEU
1	A	391	LEU
1	A	400	ASP
1	A	402	GLU
1	A	406	LYS
1	A	409	GLU
1	A	420	LYS
1	A	425	GLU
1	A	441	ARG
1	A	456	VAL
1	A	458	ASP
1	A	462	THR
1	A	464	LEU
1	A	471	VAL
1	B	262	LYS
1	B	264	ARG
1	B	267	GLN
1	B	285	LEU
1	B	312	ASP
1	B	314	GLU
1	B	339	LYS
1	B	340	LEU
1	B	342	SER
1	B	347	LEU
1	B	385	LEU
1	B	394	ASP
1	B	406	LYS
1	B	420	LYS
1	B	421	ILE
1	B	422	HIS
1	B	423	GLN
1	B	451	LEU

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Mol	Chain	Res	Type
1	B	455	ARG
1	B	460	LYS
1	B	470	ASP
2	E	685	GLU
2	E	690	LEU
2	E	692	ARG
2	E	693	LEU
2	F	685	GLU
2	F	686	ARG
2	F	690	LEU
2	F	692	ARG
2	F	693	LEU
2	F	695	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	296	GLN
1	A	423	GLN
1	A	429	HIS
1	A	457	ASN
1	A	459	HIS
1	B	250	GLN
1	B	267	GLN
1	B	344	HIS
1	B	379	GLN
2	E	695	GLN
2	F	687	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	MUF	B	1	-	32,35,35	1.63	8 (25%)	45,55,55	1.80	12 (26%)
4	MUF	A	473	-	32,35,35	1.77	11 (34%)	45,55,55	1.72	8 (17%)

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	MUF	B	1	-	-	0/8/70/70	0/5/5/5
4	MUF	A	473	-	-	1/8/70/70	0/5/5/5

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	473	MUF	C6-C5	3.04	1.36	1.33
4	A	473	MUF	C7-C8	3.02	1.58	1.53
4	A	473	MUF	C19-C10	2.88	1.59	1.54
4	B	1	MUF	C1-C10	2.84	1.59	1.54
4	A	473	MUF	C10-C5	2.84	1.56	1.52
4	B	1	MUF	C6-C5	2.80	1.36	1.33
4	A	473	MUF	C1-C10	2.75	1.59	1.54
4	A	473	MUF	C12-C13	2.61	1.58	1.54
4	B	1	MUF	C12-C13	2.59	1.58	1.54
4	A	473	MUF	C18-C13	2.57	1.58	1.54
4	A	473	MUF	C10-C9	2.57	1.60	1.56
4	B	1	MUF	C7-C8	2.55	1.57	1.53
4	B	1	MUF	C19-C10	2.39	1.58	1.54
4	A	473	MUF	C53-C52	2.30	1.43	1.39
4	B	1	MUF	C57-C52	2.24	1.43	1.39
4	B	1	MUF	C8-C9	2.09	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1	MUF	C4-C5	2.08	1.48	1.43
4	A	473	MUF	C57-C52	2.07	1.42	1.39
4	A	473	MUF	C57-C56	2.00	1.42	1.38

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	473	MUF	C13-C17-C20	-5.37	106.86	114.93
4	B	1	MUF	C13-C17-C20	-4.94	107.51	114.93
4	A	473	MUF	C16-C17-C13	-4.81	99.92	104.21
4	B	1	MUF	C1-C10-C5	-3.54	105.24	108.62
4	A	473	MUF	C8-C7-C6	3.30	117.47	112.73
4	B	1	MUF	C8-C7-C6	3.14	117.24	112.73
4	B	1	MUF	C18-C13-C12	-3.05	105.77	110.59
4	B	1	MUF	C9-C10-C5	2.97	112.31	108.29
4	B	1	MUF	C12-C13-C17	2.69	119.38	116.10
4	B	1	MUF	C17-C13-C14	-2.61	96.94	99.72
4	B	1	MUF	C18-C13-C14	2.48	116.35	111.71
4	A	473	MUF	O52-C20-C52	-2.47	117.47	120.66
4	A	473	MUF	C18-C13-C12	-2.43	106.75	110.59
4	A	473	MUF	C17-C13-C14	-2.40	97.16	99.72
4	B	1	MUF	C12-C11-C9	-2.36	109.02	113.11
4	B	1	MUF	C16-C17-C13	-2.30	102.16	104.21
4	B	1	MUF	C54-C53-C52	-2.27	118.14	120.78
4	B	1	MUF	O52-C20-C52	-2.17	117.85	120.66
4	A	473	MUF	C1-C10-C5	-2.16	106.55	108.62
4	A	473	MUF	C52-C20-C17	2.11	122.44	119.44

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	473	MUF	C13-C17-C20-C52

There are no ring outliers.

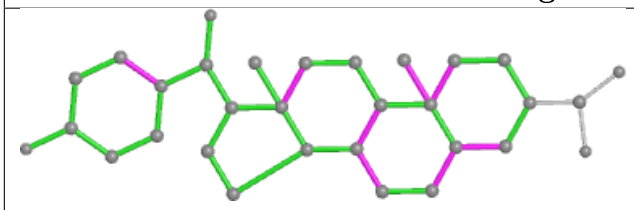
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	473	MUF	1	0

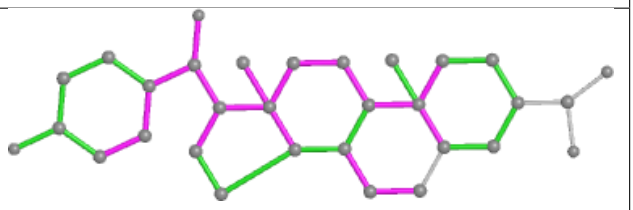
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

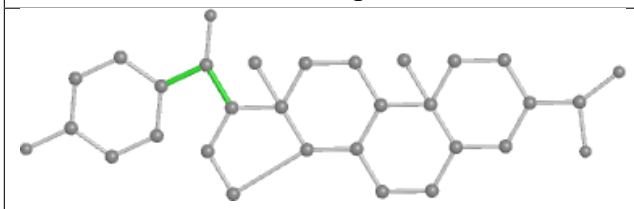
Ligand MUF B 1



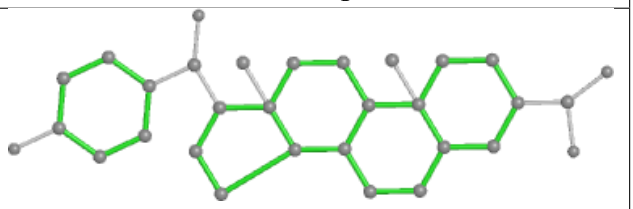
Bond lengths



Bond angles

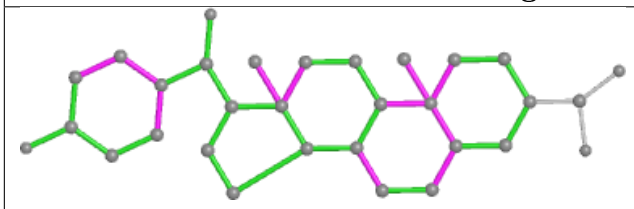


Torsions

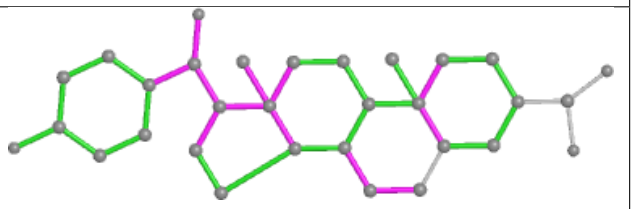


Rings

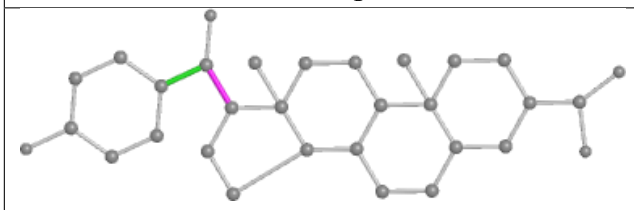
Ligand MUF A 473



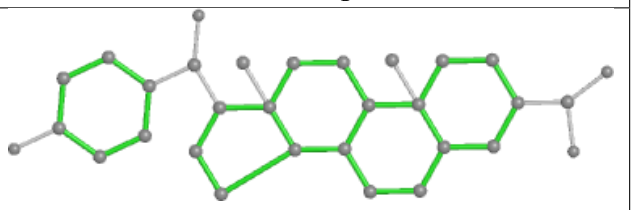
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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	224/238 (94%)	0.30	16 (7%) 16 17	16, 35, 61, 75	0
1	B	228/238 (95%)	0.01	5 (2%) 62 64	16, 25, 50, 78	0
2	E	11/25 (44%)	1.45	3 (27%) 0 0	46, 52, 67, 69	0
2	F	12/25 (48%)	0.55	0 100 100	30, 39, 62, 70	0
All	All	475/526 (90%)	0.19	24 (5%) 28 31	16, 31, 61, 78	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	343	GLY	10.4
1	B	424	PRO	7.9
1	B	423	GLN	6.0
1	A	344	HIS	4.5
1	A	400	ASP	4.2
1	A	397	TYR	3.2
1	A	458	ASP	3.0
2	E	693	LEU	2.9
1	A	305	LEU	2.8
1	A	310	THR	2.8
1	A	308	PHE	2.7
1	B	278	PHE	2.6
1	A	399	LYS	2.6
1	A	299	VAL	2.4
1	B	264	ARG	2.4
1	A	398	ILE	2.3
2	E	694	LEU	2.3
1	A	406	LYS	2.2
1	A	302	THR	2.2
1	A	309	GLN	2.1
1	B	262	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	691	HIS	2.0
1	A	311	LEU	2.0
1	A	306	PRO	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 carbohydrates in this entry.

6.4 Ligands (i)

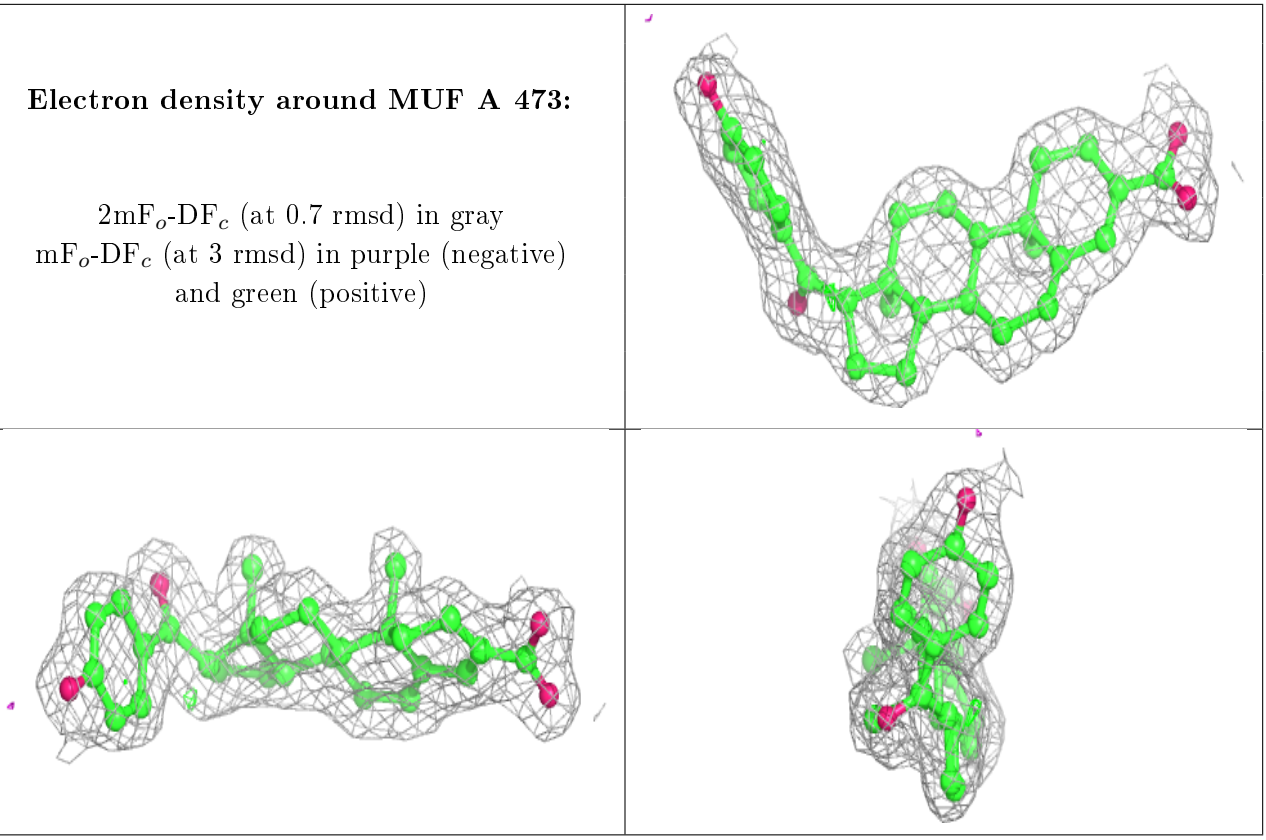
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	MUF	A	473	31/31	0.95	0.10	20,28,37,38	0
4	MUF	B	1	31/31	0.96	0.10	12,20,26,32	0
3	YT3	B	2	1/1	1.00	0.09	18,18,18,18	0
3	YT3	A	1	1/1	1.00	0.09	19,19,19,19	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.

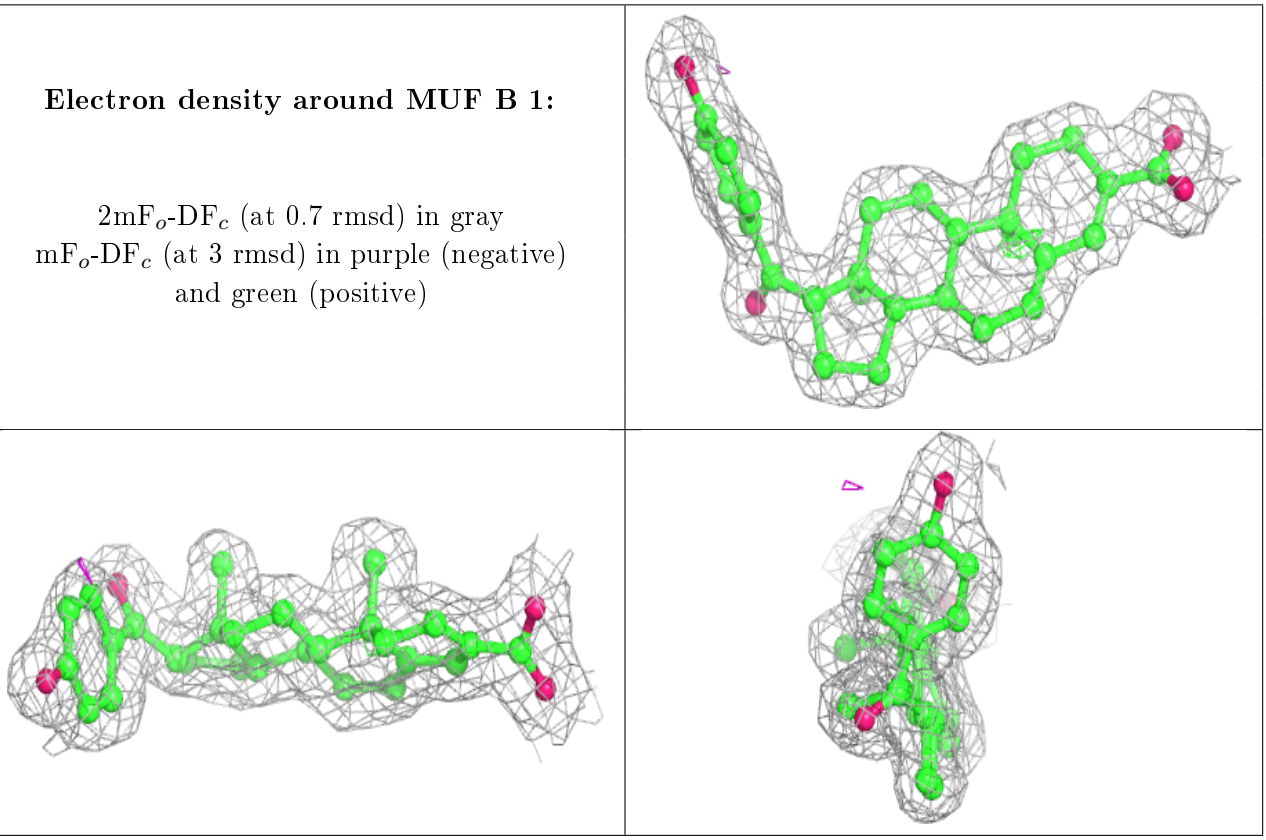
Electron density around MUF A 473:

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



Electron density around MUF B 1:

$2mF_o$-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.