Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2017 – 06:24 PM EST

PDB ID	:	5HI3
Title	:	Binding site elucidation and structure guided design of macrocyclic IL-17A antagonists
Authors	:	Liu, S.
Deposited on	:	unknown
Resolution	:	2.15 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
http://wwpdb.org/validation/2016/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:

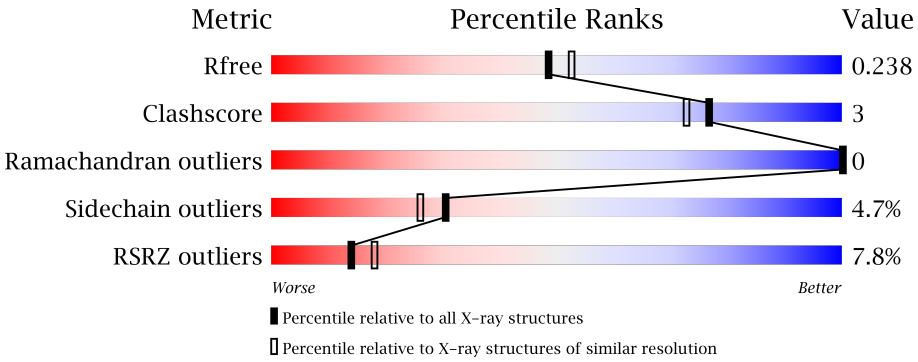
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

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 2.15 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.



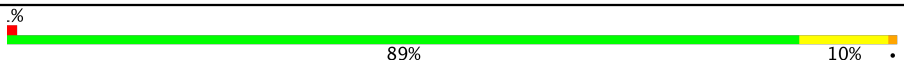
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	132	26% 68% 7% • 24%
1	B	132	17% 58% 8% • 33%
2	C	237	.% 83% 9% • 7%
2	H	237	.% 80% 11% • 7%
3	D	214	2% 89% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	L	214	
4	I	16	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	63O	B	400[A]	-	-	-	X
5	63O	B	400[B]	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8343 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 Interleukin-17A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	0	0
			806	503	151	146	6			
1	B	88	Total	C	N	O	S	0	0	0
			708	442	132	129	5			

- Molecule 2 is a protein called CAT-2000 FAB heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	220	Total	C	N	O	S	0	0	0
			1622	1017	278	321	6			
2	H	220	Total	C	N	O	S	0	0	0
			1622	1017	278	321	6			

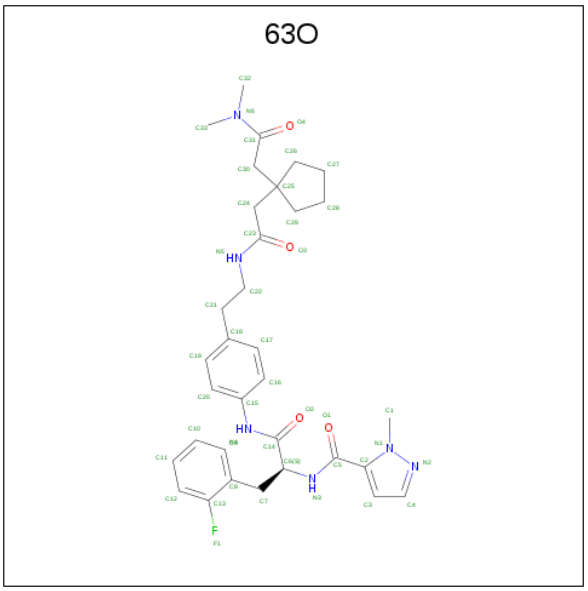
- Molecule 3 is a protein called CAT-2000 FAB light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	213	Total	C	N	O	S	0	1	0
			1618	1015	267	331	5			
3	L	213	Total	C	N	O	S	0	1	0
			1618	1015	267	331	5			

- Molecule 4 is a protein called synthetic IL-17A peptide inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	14	Total	C	N	O	0	0	0
			120	81	19	20			

- Molecule 5 is N-(4-{2-[({1-[2-(dimethylamino)-2-oxoethyl]cyclopentyl}acetyl)amino]ethyl}phenyl)-2-fluoro-Nalpha-[(1-methyl-1H-pyrazol-5-yl)carbonyl]-L-phenylalaninamide (three-letter code: 63O) (formula: $C_{33}H_{41}FN_6O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C F N O 88 66 2 12 8	0	1

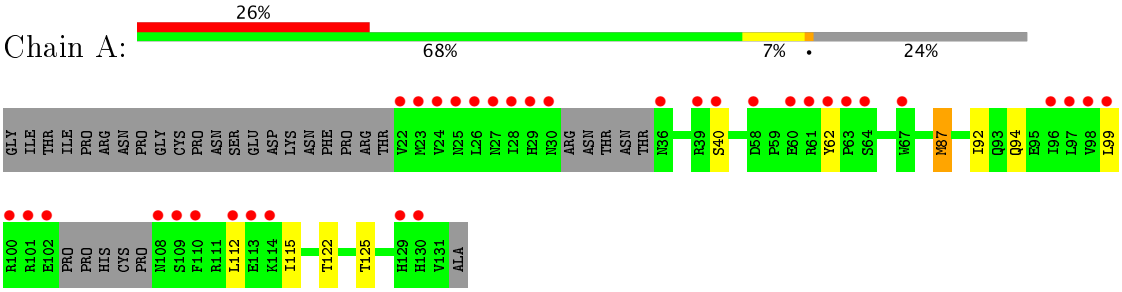
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	3	Total O 3 3	0	0
6	B	7	Total O 7 7	0	0
6	C	31	Total O 31 31	0	0
6	D	22	Total O 22 22	0	0
6	H	40	Total O 40 40	0	0
6	L	38	Total O 38 38	0	0

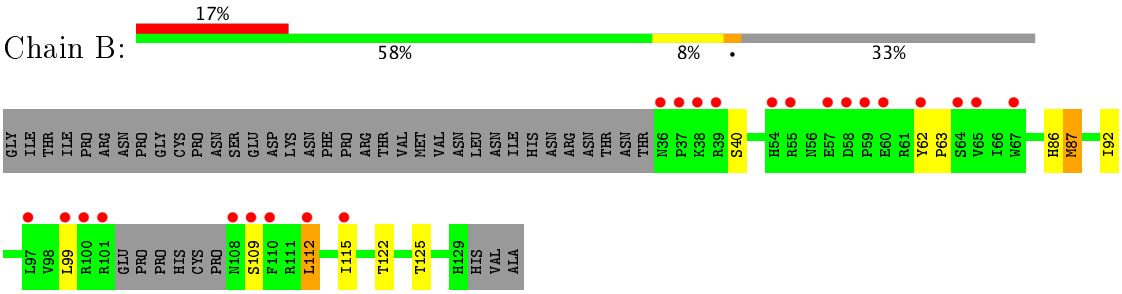
3 Residue-property plots (i)

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.

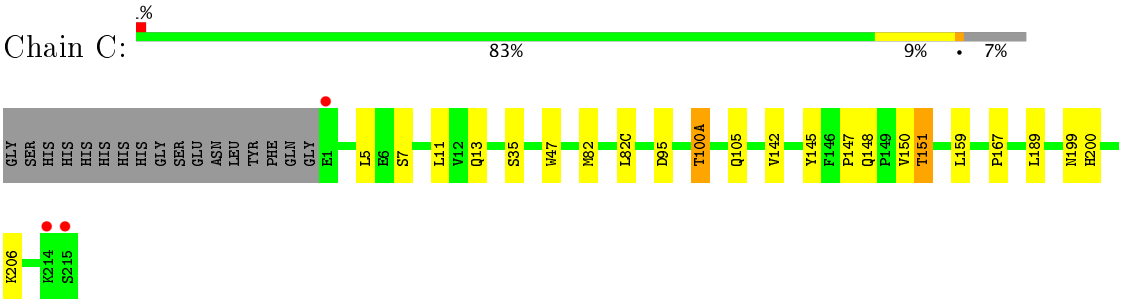
- Molecule 1: Interleukin-17A



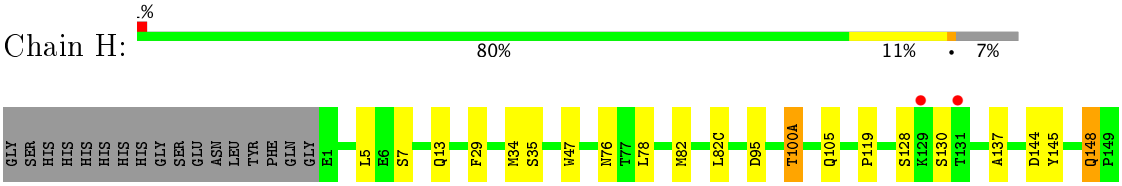
- Molecule 1: Interleukin-17A

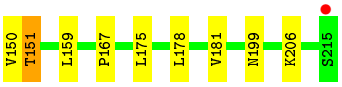


- Molecule 2: CAT-2000 FAB heavy chain



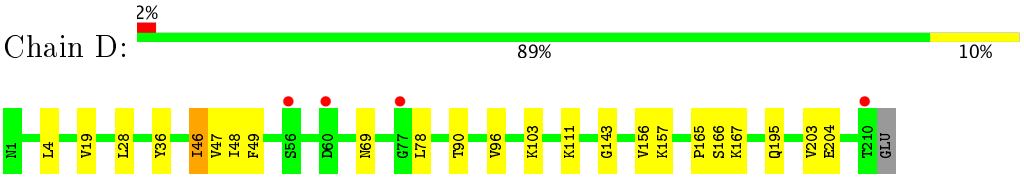
- Molecule 2: CAT-2000 FAB heavy chain





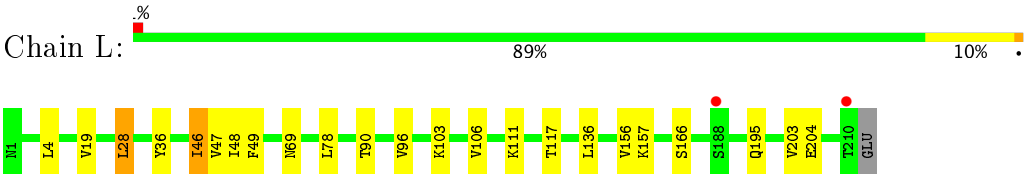
• Molecule 3: CAT-2000 FAB light chain

Chain D:



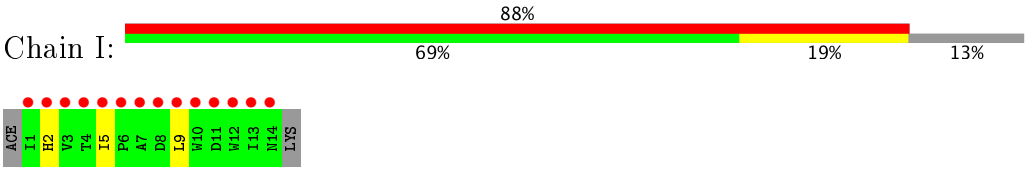
• Molecule 3: CAT-2000 FAB light chain

Chain L:



• Molecule 4: synthetic IL-17A peptide inhibitor

Chain I:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	91.11Å 68.32Å 100.45Å 90.00° 90.82° 90.00°	Depositor
Resolution (Å)	47.80 – 2.15 47.84 – 2.15	Depositor EDS
% Data completeness (in resolution range)	94.5 (47.80-2.15) 94.5 (47.84-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.24 (at 2.16Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.197 , 0.231 0.201 , 0.238	Depositor DCC
R_{free} test set	3146 reflections (5.19%)	DCC
Wilson B-factor (Å^2)	33.0	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 38.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8343	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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: 63O

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	0.42	0/824	0.59	0/1120
1	B	0.43	0/725	0.59	0/986
2	C	0.58	0/1658	0.73	0/2256
2	H	0.55	0/1658	0.73	0/2256
3	D	0.50	0/1660	0.70	0/2269
3	L	0.52	0/1660	0.70	0/2269
4	I	0.47	0/125	0.58	0/174
All	All	0.52	0/8310	0.69	0/11330

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	806	0	775	3	0
1	B	708	0	680	7	0
2	C	1622	0	1601	11	0
2	H	1622	0	1601	16	0
3	D	1618	0	1555	11	0
3	L	1618	0	1555	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	120	0	115	3	0
5	B	88	0	0	1	0
6	A	3	0	0	0	0
6	B	7	0	0	0	0
6	C	31	0	0	1	0
6	D	22	0	0	0	0
6	H	40	0	0	0	0
6	L	38	0	0	2	0
All	All	8343	0	7882	56	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 3.

All (56) 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)
3:L:117:THR:HB	6:L:330:HOH:O	1.42	1.16
2:C:82:MET:HE2	2:C:82(C):LEU:HD21	1.77	0.66
2:C:11:LEU:HB2	2:C:147:PRO:HG3	1.85	0.58
1:A:92:ILE:HD11	1:A:122:THR:HB	1.84	0.58
1:B:92:ILE:HD11	1:B:122:THR:HB	1.86	0.57
3:L:28:LEU:H	3:L:69:ASN:ND2	2.04	0.56
3:L:28:LEU:H	3:L:69:ASN:HD21	1.53	0.55
3:D:195:GLN:HG2	3:D:204:GLU:HG3	1.90	0.54
3:L:195:GLN:HG2	3:L:204:GLU:HG3	1.90	0.54
2:C:148:GLN:NE2	6:C:301:HOH:O	2.41	0.53
2:H:150:VAL:HG23	2:H:178:LEU:HD21	1.91	0.53
2:H:181:VAL:HG11	3:L:136:LEU:CD1	2.39	0.52
3:D:47:VAL:HG12	3:D:48:ILE:HG12	1.93	0.51
3:L:47:VAL:HG12	3:L:48:ILE:HG12	1.92	0.51
2:H:82:MET:HE2	2:H:82(C):LEU:HD21	1.92	0.51
1:B:112:LEU:HD12	4:I:5:ILE:HG22	1.91	0.51
2:C:151:THR:HG22	2:C:199:ASN:HB3	1.93	0.50
2:H:5:LEU:HD23	2:H:105:GLN:HE22	1.76	0.50
2:C:5:LEU:HD23	2:C:105:GLN:HE22	1.76	0.50
2:H:130:SER:HB2	2:H:137:ALA:HB3	1.94	0.50
2:C:145:TYR:CE2	2:C:150:VAL:HG13	2.47	0.49
3:D:143:GLY:O	3:D:165:PRO:HG2	2.12	0.49
1:B:62:TYR:HB3	1:B:99:LEU:HB3	1.95	0.48
1:A:87:MET:HB3	1:A:125:THR:HG22	1.94	0.48
2:H:181:VAL:CG1	3:L:136:LEU:CD1	2.91	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:MET:HB3	1:B:125:THR:HG22	1.95	0.47
3:L:78:LEU:HD21	3:L:106:VAL:HG22	1.95	0.47
1:A:62:TYR:HB3	1:A:99:LEU:HB3	1.96	0.47
2:H:151:THR:HG22	2:H:199:ASN:HB3	1.97	0.46
2:H:144:ASP:HB3	2:H:175:LEU:HD13	1.97	0.46
2:H:181:VAL:HG11	3:L:136:LEU:HD12	1.98	0.46
3:D:28:LEU:H	3:D:69:ASN:HD21	1.63	0.45
3:D:36:TYR:CE1	3:D:46:ILE:HG22	2.52	0.44
1:B:86:HIS:HE1	6:L:319:HOH:O	2.00	0.44
1:B:63:PRO:HB3	5:B:400[A]:63O:C33	2.48	0.43
3:D:36:TYR:HE1	3:D:46:ILE:HG22	1.84	0.43
3:D:46:ILE:HD13	3:D:49:PHE:HB3	2.01	0.43
3:L:4:LEU:HD11	3:L:90:THR:HG22	2.01	0.42
2:H:119:PRO:HB3	2:H:145:TYR:HB3	2.00	0.42
2:C:47:TRP:CG	3:D:96:VAL:HB	2.55	0.42
2:C:95:ASP:OD1	2:C:100(A):THR:HB	2.20	0.42
2:H:47:TRP:CG	3:L:96:VAL:HB	2.54	0.42
2:C:150:VAL:HG12	2:C:200:HIS:CD2	2.55	0.42
4:I:5:ILE:HB	4:I:9:LEU:HD23	2.02	0.42
2:H:34:MET:HB3	2:H:78:LEU:HD22	2.02	0.41
3:D:4:LEU:HD11	3:D:90:THR:HG22	2.01	0.41
2:H:95:ASP:OD1	2:H:100(A):THR:HB	2.20	0.41
3:D:28:LEU:H	3:D:69:ASN:ND2	2.18	0.41
2:C:142:VAL:HG11	2:C:150:VAL:HG21	2.02	0.41
2:C:167:PRO:HG2	3:D:166:SER:OG	2.21	0.41
2:H:148:GLN:HE21	2:H:148:GLN:HA	1.84	0.41
1:B:109:SER:HA	4:I:2:HIS:O	2.21	0.40
3:L:46:ILE:HD13	3:L:49:PHE:HB3	2.02	0.40
3:L:36:TYR:CE1	3:L:46:ILE:HG22	2.56	0.40
2:H:167:PRO:HG2	3:L:166:SER:OG	2.21	0.40
2:H:29:PHE:CD2	2:H:76:ASN:HA	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	94/132 (71%)	91 (97%)	3 (3%)	0	100	100
1	B	84/132 (64%)	84 (100%)	0	0	100	100
2	C	218/237 (92%)	215 (99%)	3 (1%)	0	100	100
2	H	218/237 (92%)	214 (98%)	4 (2%)	0	100	100
3	D	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
3	L	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
4	I	12/16 (75%)	12 (100%)	0	0	100	100
All	All	1050/1182 (89%)	1028 (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	93/124 (75%)	88 (95%)	5 (5%)	26	20
1	B	81/124 (65%)	77 (95%)	4 (5%)	29	24
2	C	182/196 (93%)	174 (96%)	8 (4%)	33	29
2	H	182/196 (93%)	173 (95%)	9 (5%)	29	24
3	D	185/186 (100%)	176 (95%)	9 (5%)	29	24
3	L	185/186 (100%)	177 (96%)	8 (4%)	33	30
4	I	13/14 (93%)	13 (100%)	0	100	100
All	All	921/1026 (90%)	878 (95%)	43 (5%)	30	26

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	SER
1	A	87	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	94	GLN
1	A	112	LEU
1	A	115	ILE
1	B	40	SER
1	B	87	MET
1	B	112	LEU
1	B	115	ILE
2	C	7	SER
2	C	13	GLN
2	C	35	SER
2	C	100(A)	THR
2	C	151	THR
2	C	159	LEU
2	C	189	LEU
2	C	206	LYS
3	D	19	VAL
3	D	46	ILE
3	D	78	LEU
3	D	103	LYS
3	D	111	LYS
3	D	156	VAL
3	D	157	LYS
3	D	167	LYS
3	D	203	VAL
2	H	7	SER
2	H	13	GLN
2	H	35	SER
2	H	100(A)	THR
2	H	128	SER
2	H	148	GLN
2	H	151	THR
2	H	159	LEU
2	H	206	LYS
3	L	19	VAL
3	L	28	LEU
3	L	46	ILE
3	L	103	LYS
3	L	111	LYS
3	L	156	VAL
3	L	157	LYS
3	L	203	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	36	ASN
1	B	36	ASN
1	B	86	HIS
2	C	13	GLN
2	C	76	ASN
2	C	82(A)	ASN
2	C	105	GLN
2	C	148	GLN
3	D	69	ASN
3	D	89	GLN
3	D	127	GLN
3	D	195	GLN
2	H	76	ASN
2	H	82(A)	ASN
2	H	105	GLN
2	H	148	GLN
4	I	14	ASN
3	L	69	ASN
3	L	89	GLN
3	L	127	GLN
3	L	195	GLN

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

2 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	$\#\|Z\| > 2$
5	63O	B	400[A]	-	46,47,47	0.57	1 (2%)	54,65,65	0.68	1 (1%)
5	63O	B	400[B]	-	46,47,47	0.51	1 (2%)	54,65,65	0.57	1 (1%)

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
5	63O	B	400[A]	-	-	0/37/49/49	0/4/4/4
5	63O	B	400[B]	-	-	0/37/49/49	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	400[B]	63O	C2-N1	2.50	1.40	1.36
5	B	400[A]	63O	C2-N1	2.97	1.40	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	400[B]	63O	C25-C30-C31	2.06	119.75	116.31
5	B	400[A]	63O	C25-C30-C31	3.01	121.33	116.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	400[A]	63O	1	0

5.7 Other polymers

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	100/132 (75%)	1.70	34 (34%) 0 1	31, 66, 190, 216	0
1	B	88/132 (66%)	1.54	23 (26%) 1 1	28, 55, 132, 173	0
2	C	220/237 (92%)	0.13	3 (1%) 75 80	20, 32, 54, 112	0
2	H	220/237 (92%)	-0.00	3 (1%) 75 80	23, 33, 59, 85	0
3	D	213/214 (99%)	0.20	4 (1%) 67 74	20, 43, 72, 103	0
3	L	213/214 (99%)	-0.17	2 (0%) 84 87	25, 36, 53, 97	0
4	I	14/16 (87%)	6.85	14 (100%) 0 0	105, 112, 131, 131	0
All	All	1068/1182 (90%)	0.41	83 (7%) 14 18	20, 37, 101, 216	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	I	10	TRP	13.3
4	I	1	ILE	11.4
4	I	2	HIS	10.2
2	C	215	SER	10.2
1	A	30	ASN	10.1
1	B	37	PRO	9.6
3	D	210	THR	8.8
1	B	62	TYR	8.6
1	A	29	HIS	8.5
1	B	59	PRO	8.2
4	I	13	ILE	8.1
1	A	26	LEU	7.9
1	A	22	VAL	7.4
1	B	55	ARG	7.2
1	A	110	PHE	7.1
1	A	62	TYR	7.0
4	I	5	ILE	6.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	I	12	TRP	6.6
1	A	64	SER	6.6
1	B	36	ASN	6.5
1	B	39	ARG	6.4
1	B	110	PHE	6.2
1	A	24	VAL	6.1
4	I	3	VAL	5.9
4	I	4	THR	5.9
1	A	130	HIS	5.7
1	A	108	ASN	5.7
4	I	14	ASN	5.7
1	A	25	ASN	5.5
4	I	9	LEU	5.5
1	A	28	ILE	5.4
1	B	101	ARG	5.3
1	B	60	GLU	5.3
1	B	67	TRP	5.3
4	I	7	ALA	5.3
1	A	23	MET	5.3
1	B	64	SER	5.2
1	A	98	VAL	5.1
1	B	99	LEU	5.1
1	B	97	LEU	4.9
1	A	101	ARG	4.9
1	A	27	ASN	4.7
3	L	210	THR	4.6
1	B	100	ARG	4.6
1	A	109	SER	4.5
1	B	108	ASN	4.5
1	B	38	LYS	4.4
1	B	57	GLU	4.3
4	I	8	ASP	4.3
3	D	60	ASP	4.2
4	I	11	ASP	4.1
2	C	214	LYS	4.1
2	H	215	SER	4.0
1	A	39	ARG	3.8
1	B	65	VAL	3.8
1	A	112	LEU	3.8
1	B	112	LEU	3.6
1	B	109	SER	3.6
2	H	131	THR	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	C	1	GLU	3.5
1	A	102	GLU	3.3
1	A	97	LEU	3.2
1	B	58	ASP	2.9
1	A	60	GLU	2.9
1	A	67	TRP	2.6
1	B	54	HIS	2.6
1	B	115	ILE	2.6
4	I	6	PRO	2.6
1	A	100	ARG	2.6
1	A	36	ASN	2.5
1	A	61	ARG	2.4
1	A	114	LYS	2.4
3	L	188	SER	2.4
1	A	96	ILE	2.4
1	A	63	PRO	2.3
2	H	129	LYS	2.3
1	A	99	LEU	2.3
1	A	58	ASP	2.2
1	A	129	HIS	2.1
1	A	113	GLU	2.1
1	A	40	SER	2.1
3	D	77	GLY	2.1
3	D	56	SER	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
5	63O	B	400[B]	44/44	0.73	0.41	1.78	60,66,75,76	44
5	63O	B	400[A]	44/44	0.73	0.41	1.31	74,85,87,88	44

6.5 Other polymers (i)

There are no such residues in this entry.