Full wwPDB X-ray Structure Validation Report (i)

Dec 15, 2016 – 03:45 PM EST

PDB ID	:	2WUC
Title	:	Crystal structure of HGFA in complex with the allosteric non- inhibitory antibody Fab40.deltaTrp and Ac-KQLR-chloromethylketone
Authors	:	Ganesan, R.; Eigenbrot, C.; Shia, S.
Deposited on	:	2009-10-01
Resolution	:	2.70 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

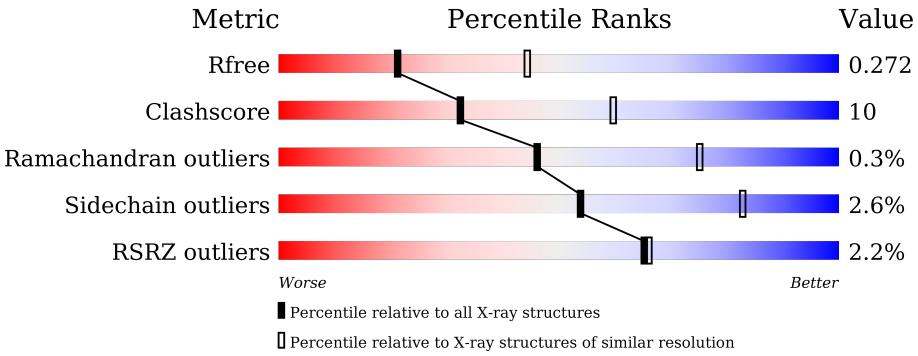
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

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 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	257	3%, 72%, 21%, 7%
2	B	35	3%, 11%, 9%, 80%
3	H	224	3%, 71%, 25%
4	I	6	50%, 50%
5	L	214	82%, 17%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5319 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 HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	1
			1825	1156	317	339	13			

- Molecule 2 is a protein called HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	S	0	0	1
			48	26	15	6	1			

- Molecule 3 is a protein called FAB FRAGMENT FAB40.DELTATRP HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	0	1
			1613	1025	268	314	6			

- Molecule 4 is a protein called ACE-KQLR-CHLOROMETHYLKETONE INHIBITOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	6	Total	C	N	O	0	0	1
			41	26	9	6			

- Molecule 5 is a protein called FAB FRAGMENT FAB40.DELTATRP LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	L	214	Total	C	N	O	S	0	0	0
			1633	1018	275	334	6			

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is water.

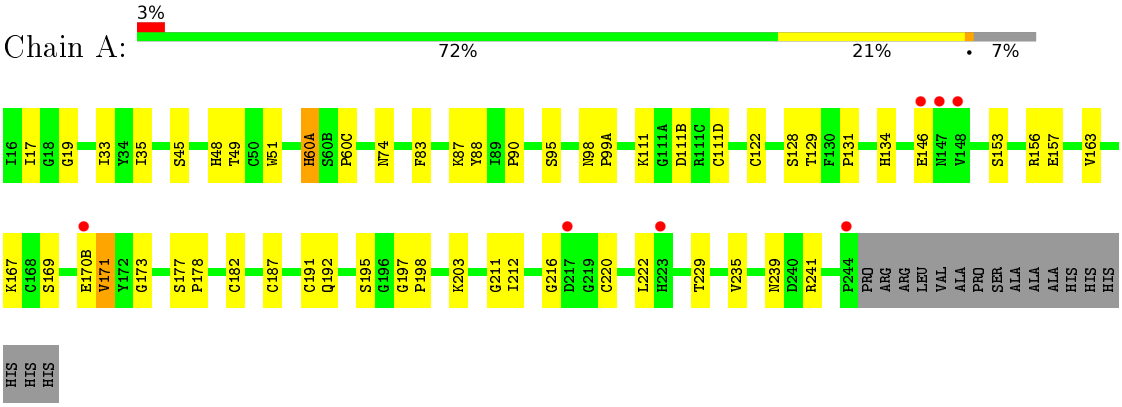
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	42	Total	O	0	0
			42	42		
7	B	1	Total	O	0	0
			1	1		
7	H	30	Total	O	0	0
			30	30		
7	I	2	Total	O	0	0
			2	2		
7	L	56	Total	O	0	0
			56	56		

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 errors 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.

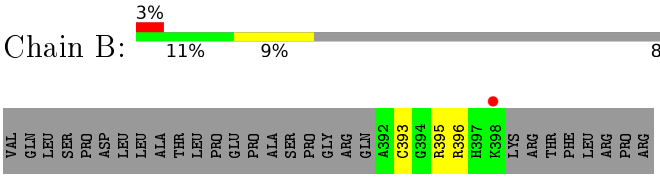
- Molecule 1: HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG CHAIN

Chain A:



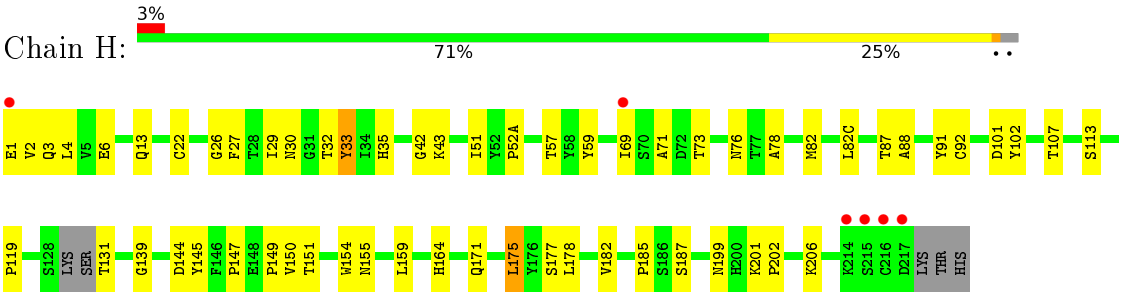
- Molecule 2: HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT CHAIN

Chain B:



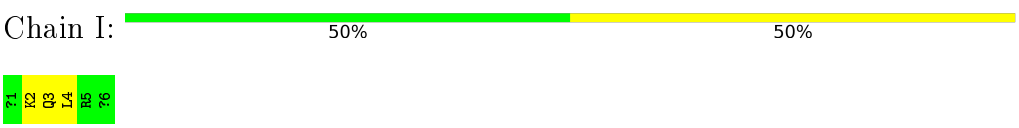
- Molecule 3: FAB FRAGMENT FAB40.DELTATRP HEAVY CHAIN

Chain H:



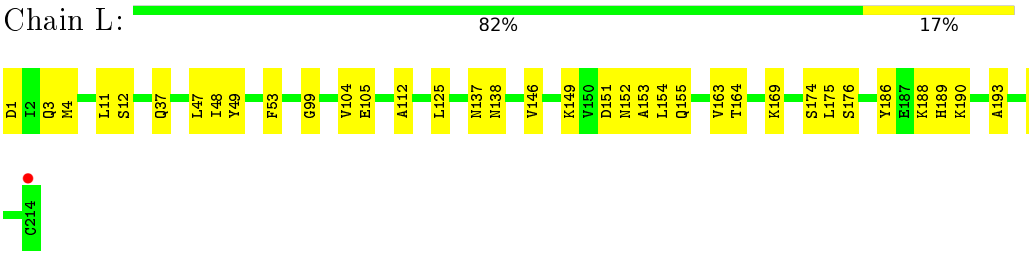
- Molecule 4: ACE-KQLR-CHLOROMETHYLKETONE INHIBITOR

Chain I:



- Molecule 5: FAB FRAGMENT FAB40.DELTATRP LIGHT CHAIN

Chain L:


82%
17%
D1
T2
Q3
M4
L11
S12
Q37
L47
I48
Y49
F53
G99
V104
E105
A112
L125
N137
N138
V146
K149
V150
D151
N152
A153
L154
Q155
V163
T164
K169
S174
L175
S176
Y186
E187
K188
H189
K190
A193
V196
L201
S208
C214

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	80.36Å 147.89Å 146.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 2.70 29.47 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.93-2.70) 99.4 (29.47-2.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.00 (at 2.72Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.226 , 0.274 0.222 , 0.272	Depositor DCC
R_{free} test set	2388 reflections (10.99%)	DCC
Wilson B-factor (Å^2)	40.3	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 37.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5319	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: AR7, 0QE, ACE, NAG

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	0.40	0/1879	0.62	0/2560
2	B	0.65	0/48	0.45	0/62
3	H	0.42	0/1656	0.62	0/2263
4	I	0.25	0/26	0.89	0/33
5	L	0.42	0/1667	0.63	0/2262
All	All	0.41	0/5276	0.62	0/7180

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	I	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	I	4	LEU	Mainchain

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	1825	0	1736	39	0
2	B	48	0	44	3	0
3	H	1613	0	1568	43	0
4	I	41	0	46	3	0
5	L	1633	0	1585	23	0
6	A	28	0	25	2	0
7	A	42	0	0	3	0
7	B	1	0	0	0	0
7	H	30	0	0	4	0
7	I	2	0	0	0	0
7	L	56	0	0	0	1
All	All	5319	0	5004	107	1

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 10.

All (107) 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)
5:L:112:ALA:HB1	5:L:201:LEU:HD13	1.68	0.75
4:I:2:LYS:HA	4:I:2:LYS:HE3	1.73	0.71
3:H:119:PRO:HB3	3:H:145:TYR:HB3	1.75	0.69
1:A:167:LYS:O	1:A:171:VAL:HG21	1.95	0.67
1:A:45:SER:OG	1:A:198:PRO:HB3	1.94	0.67
1:A:170(B):GLU:H	1:A:170(B):GLU:CD	2.00	0.65
5:L:190:LYS:HD2	5:L:190:LYS:N	2.15	0.62
1:A:216:GLY:O	4:I:3:GLN:HB3	1.98	0.62
1:A:222:LEU:HD12	1:A:222:LEU:H	1.64	0.61
3:H:82:MET:HE2	3:H:82(C):LEU:HD21	1.82	0.61
1:A:187:CYS:SG	1:A:222:LEU:HG	2.40	0.61
3:H:144:ASP:HB3	3:H:175:LEU:HD23	1.82	0.60
3:H:151:THR:HG22	7:H:2027:HOH:O	2.01	0.59
4:I:2:LYS:CE	4:I:2:LYS:HA	2.30	0.59
3:H:178:LEU:HD12	3:H:178:LEU:C	2.23	0.59
5:L:188:LYS:HG3	5:L:189:HIS:ND1	2.18	0.58
1:A:48:HIS:CE1	1:A:49:THR:HG22	2.38	0.58
1:A:222:LEU:N	1:A:222:LEU:HD12	2.20	0.57
1:A:60(A):HIS:H	1:A:60(A):HIS:CD2	2.22	0.56
5:L:47:LEU:O	5:L:48:ILE:HD13	2.04	0.56
3:H:30:ASN:HD22	3:H:73:THR:HG21	1.70	0.56
3:H:59:TYR:CZ	3:H:69:ILE:HG22	2.42	0.55
3:H:6:GLU:OE2	3:H:91:TYR:HA	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:51:ILE:HD13	3:H:71:ALA:HB2	1.89	0.54
5:L:193:ALA:HB2	5:L:208:SER:HB3	1.89	0.54
3:H:13:GLN:OE1	3:H:113:SER:HA	2.07	0.54
2:B:396:ARG:HG3	2:B:396:ARG:HH11	1.73	0.54
3:H:87:THR:O	3:H:88:ALA:HB2	2.07	0.53
3:H:42:GLY:O	3:H:43:LYS:HD2	2.09	0.53
3:H:82:MET:HB3	3:H:82(C):LEU:HD21	1.91	0.52
1:A:146:GLU:HB2	1:A:220:CYS:HB2	1.92	0.52
5:L:112:ALA:CB	5:L:201:LEU:HD13	2.38	0.52
1:A:177:SER:HB2	1:A:178:PRO:HD2	1.92	0.52
1:A:60(A):HIS:CD2	1:A:60(C):PRO:HD3	2.44	0.51
1:A:156:ARG:HD3	7:A:2024:HOH:O	2.11	0.51
5:L:12:SER:HA	5:L:105:GLU:O	2.10	0.51
3:H:2:VAL:HG13	3:H:27:PHE:CE1	2.45	0.51
3:H:33:TYR:HD2	3:H:33:TYR:N	2.09	0.51
1:A:163:VAL:HB	1:A:182:CYS:HB2	1.93	0.51
3:H:33:TYR:CD2	3:H:33:TYR:N	2.77	0.51
1:A:49:THR:O	1:A:111(D):CYS:HB2	2.11	0.51
3:H:30:ASN:HA	3:H:52(A):PRO:HB2	1.93	0.50
1:A:241:ARG:NH2	3:H:57:THR:O	2.43	0.50
1:A:211:GLY:HA2	1:A:229:THR:O	2.11	0.50
5:L:154:LEU:HD13	5:L:155:GLN:O	2.12	0.49
2:B:396:ARG:HG3	2:B:396:ARG:NH1	2.27	0.49
3:H:4:LEU:HD12	3:H:22:CYS:SG	2.52	0.49
3:H:171:GLN:NE2	3:H:177:SER:HB2	2.27	0.49
5:L:175:LEU:HD23	5:L:175:LEU:C	2.32	0.49
3:H:59:TYR:CE1	3:H:69:ILE:HG22	2.47	0.49
5:L:190:LYS:HD2	5:L:190:LYS:H	1.75	0.49
3:H:164:HIS:CD2	5:L:137:ASN:HD21	2.31	0.49
1:A:222:LEU:CD1	1:A:222:LEU:H	2.26	0.48
1:A:131:PRO:O	1:A:134:HIS:HB2	2.13	0.48
3:H:22:CYS:HB3	3:H:78:ALA:HB3	1.96	0.48
5:L:37:GLN:HB2	5:L:47:LEU:HD11	1.96	0.48
1:A:98:ASN:N	1:A:99(A):PRO:CD	2.76	0.47
1:A:212:ILE:HB	1:A:229:THR:HB	1.96	0.47
3:H:59:TYR:OH	3:H:69:ILE:HG22	2.15	0.47
1:A:48:HIS:HB3	1:A:51:TRP:HB2	1.96	0.47
5:L:146:VAL:HG22	5:L:196:VAL:HG22	1.96	0.47
1:A:156:ARG:NH1	7:A:2024:HOH:O	2.45	0.46
1:A:17:ILE:HD12	1:A:17:ILE:C	2.35	0.46
3:H:159:LEU:HD21	3:H:182:VAL:HG21	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:92:CYS:O	3:H:92:CYS:SG	2.74	0.46
5:L:49:TYR:O	5:L:53:PHE:HB2	2.15	0.46
5:L:193:ALA:CB	5:L:208:SER:HB3	2.45	0.46
3:H:29:ILE:HG23	3:H:76:ASN:ND2	2.30	0.46
3:H:2:VAL:HB	3:H:102:TYR:CE1	2.51	0.45
5:L:163:VAL:HG12	5:L:164:THR:O	2.16	0.45
1:A:60(A):HIS:H	1:A:60(A):HIS:HD2	1.62	0.45
5:L:154:LEU:HD13	5:L:155:GLN:N	2.32	0.45
1:A:235:VAL:HG12	1:A:239:ASN:ND2	2.31	0.45
1:A:19:GLY:HA3	1:A:157:GLU:O	2.18	0.44
3:H:82:MET:HE2	3:H:82(C):LEU:CD2	2.47	0.44
5:L:175:LEU:HD23	5:L:176:SER:N	2.33	0.44
3:H:35:HIS:O	3:H:92:CYS:HA	2.18	0.43
3:H:199:ASN:ND2	3:H:206:LYS:HE3	2.33	0.43
1:A:203:LYS:NZ	7:A:2033:HOH:O	2.51	0.43
3:H:201:LYS:N	3:H:202:PRO:CD	2.81	0.43
1:A:74:ASN:CG	6:A:1244:NAG:HN2	2.21	0.43
1:A:83:PHE:CE2	1:A:111:LYS:HE2	2.54	0.43
1:A:169:SER:O	1:A:173:GLY:HA2	2.18	0.43
5:L:125:LEU:HD21	5:L:186:TYR:HE2	1.83	0.43
1:A:88:TYR:O	1:A:90:PRO:HD3	2.19	0.43
1:A:74:ASN:CG	6:A:1244:NAG:N2	2.72	0.43
1:A:191:CYS:SG	1:A:192:GLN:N	2.91	0.42
5:L:4:MET:O	5:L:99:GLY:HA2	2.19	0.42
3:H:131:THR:N	7:H:2017:HOH:O	2.52	0.42
3:H:155:ASN:HA	7:H:2021:HOH:O	2.19	0.42
1:A:33:ILE:HG22	1:A:35:ILE:HG13	2.02	0.42
5:L:151:ASP:O	5:L:152:ASN:HB2	2.20	0.41
5:L:149:LYS:HA	5:L:153:ALA:O	2.20	0.41
3:H:32:THR:C	3:H:33:TYR:HD2	2.24	0.41
1:A:195:SER:C	1:A:197:GLY:H	2.23	0.41
5:L:11:LEU:HD21	5:L:104:VAL:HG22	2.02	0.41
3:H:145:TYR:CE2	3:H:150:VAL:HG23	2.55	0.41
3:H:185:PRO:C	3:H:187:SER:N	2.74	0.41
1:A:128:SER:O	1:A:129:THR:HG23	2.20	0.41
1:A:122:CYS:SG	2:B:393:CYS:O	2.79	0.41
3:H:107:THR:O	3:H:107:THR:HG23	2.20	0.41
3:H:2:VAL:HG13	3:H:27:PHE:CD1	2.56	0.41
3:H:32:THR:HG23	7:H:2002:HOH:O	2.21	0.41
3:H:26:GLY:O	3:H:27:PHE:HB3	2.21	0.40
3:H:139:GLY:HA2	3:H:154:TRP:CZ2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LYS:HB3	1:A:87:LYS:HE2	1.83	0.40
3:H:1:GLU:HG3	3:H:3:GLN:HG3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:2002:HOH:O	7:L:2002:HOH:O[4_545]	2.14	0.06

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	238/257 (93%)	218 (92%)	19 (8%)	1 (0%)	39 69
2	B	5/35 (14%)	3 (60%)	2 (40%)	0	100 100
3	H	215/224 (96%)	198 (92%)	17 (8%)	0	100 100
4	I	3/6 (50%)	2 (67%)	1 (33%)	0	100 100
5	L	212/214 (99%)	200 (94%)	11 (5%)	1 (0%)	34 63
All	All	673/736 (91%)	621 (92%)	50 (7%)	2 (0%)	46 75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	L	138	ASN
1	A	171	VAL

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	199/213 (93%)	195 (98%)	4 (2%)	63 87
2	B	4/30 (13%)	3 (75%)	1 (25%)	1 2
3	H	175/181 (97%)	170 (97%)	5 (3%)	50 80
4	I	3/3 (100%)	3 (100%)	0	100 100
5	L	186/186 (100%)	181 (97%)	5 (3%)	52 82
All	All	567/613 (92%)	552 (97%)	15 (3%)	54 83

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60(A)	HIS
1	A	95	SER
1	A	111(B)	ASP
1	A	153	SER
2	B	395	ARG
3	H	33	TYR
3	H	101	ASP
3	H	147	PRO
3	H	149	PRO
3	H	175	LEU
5	L	1	ASP
5	L	3	GLN
5	L	169	LYS
5	L	174	SER
5	L	201	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60(A)	HIS
1	A	70	GLN
1	A	71	HIS

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Mol	Chain	Res	Type
1	A	116	GLN
1	A	204	ASN
1	A	239	ASN
3	H	3	GLN
3	H	30	ASN
3	H	39	GLN
3	H	105	GLN
3	H	171	GLN
3	H	199	ASN
3	H	204	ASN
5	L	38	GLN
5	L	137	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	AR7	I	5	1,4	5,8,11	0.60	0	4,8,13	0.38	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	AR7	I	5	1,4	-	0/4/6/11	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

2 carbohydrates 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	$\#\|Z\| > 2$
6	NAG	A	1244	1,6	14,14,15	1.12	1 (7%)	15,19,21	0.97	2 (13%)
6	NAG	A	1245	6	14,14,15	0.47	0	15,19,21	2.24	4 (26%)

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
6	NAG	A	1244	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	1245	6	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1244	NAG	O5-C5	3.76	1.51	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	1245	NAG	C4-C3-C2	-5.83	102.30	111.34
6	A	1245	NAG	C2-N2-C7	-3.17	118.98	123.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	1244	NAG	C1-O5-C5	-2.33	108.72	112.14
6	A	1244	NAG	C2-N2-C7	-2.32	120.08	123.11
6	A	1245	NAG	O4-C4-C5	2.35	115.42	109.23
6	A	1245	NAG	C1-O5-C5	3.76	117.67	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1244	NAG	2	0

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	240/257 (93%)	0.15	7 (2%) 55 55	20, 39, 72, 83	1 (0%)
2	B	7/35 (20%)	1.09	1 (14%) 4 3	54, 65, 90, 91	0
3	H	219/224 (97%)	-0.07	6 (2%) 58 58	18, 35, 57, 97	1 (0%)
4	I	3/6 (50%)	0.94	0 100 100	57, 57, 70, 76	0
5	L	214/214 (100%)	-0.41	1 (0%) 91 93	18, 31, 55, 87	0
All	All	683/736 (92%)	-0.08	15 (2%) 65 66	18, 35, 65, 97	2 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	217	ASP	13.3
3	H	216	CYS	5.9
1	A	148	VAL	5.2
3	H	215	SER	4.9
1	A	244	PRO	3.9
1	A	147	ASN	3.6
3	H	1	GLU	3.3
3	H	214	LYS	3.3
1	A	223	HIS	2.9
1	A	170(B)	GLU	2.7
3	H	69	ILE	2.7
5	L	214	CYS	2.4
1	A	146	GLU	2.3
1	A	217	ASP	2.2
2	B	398	LYS	2.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
4	AR7	I	5	11/12	0.88	0.21	-	36,41,49,50	0

6.3 Carbohydrates (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
6	NAG	A	1244	14/15	0.59	0.30	-	53,63,68,68	0
6	NAG	A	1245	14/15	0.45	0.61	-	70,75,83,83	0

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.