Full wwPDB X-ray Structure Validation Report (i)

Sep 17, 2023 – 06:30 PM EDT

PDB ID	:	4YPG
Title	:	Structural Insights Into the Neutralization Properties of a Human Anti-Interferon Monoclonal Antibody
Authors	:	Oganesyan, V.; Dall'Acqua, W.F.
Deposited on	:	2015-03-12
Resolution	:	3.00 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:

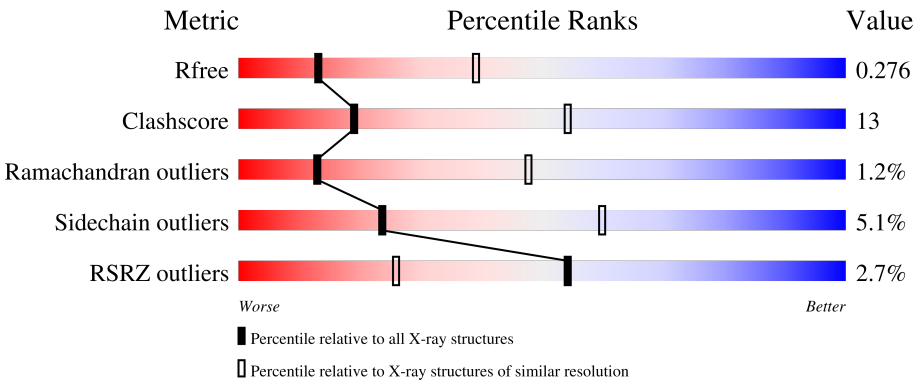
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	215	76% 21% •
1	L	215	2% 68% 28% •
2	B	219	3% 76% 21% •
2	H	219	5% 79% 19% •
3	C	161	4% 63% 34% •••

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Mol	Chain	Length	Quality of chain
3	D	161	3% 77% 20%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9219 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 Sifalimumab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1647	1027	281	334	5	0	0	0
1	L	215	1647	1027	281	334	5	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	ALA	conflict	UNP Q6PJF2
A	28	SER	ILE	conflict	UNP Q6PJF2
A	32	THR	ALA	conflict	UNP Q6PJF2
A	49	ILE	MET	conflict	UNP Q6PJF2
A	50	TYR	PHE	conflict	UNP Q6PJF2
A	52	ALA	SER	conflict	UNP Q6PJF2
A	96	PRO	GLN	conflict	UNP Q6PJF2
A	97	ARG	GLY	conflict	UNP Q6PJF2
A	101	GLN	PRO	conflict	UNP Q6PJF2
A	106	GLU	ASP	conflict	UNP Q6PJF2
L	9	GLY	ALA	conflict	UNP Q6PJF2
L	28	SER	ILE	conflict	UNP Q6PJF2
L	32	THR	ALA	conflict	UNP Q6PJF2
L	49	ILE	MET	conflict	UNP Q6PJF2
L	50	TYR	PHE	conflict	UNP Q6PJF2
L	52	ALA	SER	conflict	UNP Q6PJF2
L	96	PRO	GLN	conflict	UNP Q6PJF2
L	97	ARG	GLY	conflict	UNP Q6PJF2
L	101	GLN	PRO	conflict	UNP Q6PJF2
L	106	GLU	ASP	conflict	UNP Q6PJF2

- Molecule 2 is a protein called Sifalimumab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	219	1631	1027	273	324	7	0	0	0
2	H	219	1631	1027	273	324	7	0	0	0

- Molecule 3 is a protein called Interferon alpha-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	159	1296	828	216	243	9	0	0	0
3	D	161	1314	838	219	248	9	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	THR	-	expression tag	UNP P01563
C	0	SER	-	expression tag	UNP P01563
D	-1	THR	-	expression tag	UNP P01563
D	0	SER	-	expression tag	UNP P01563

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ni		
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0
4	D	1	1	1	0	0
4	H	1	1	1	0	0
4	L	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	18	18	18	0	0

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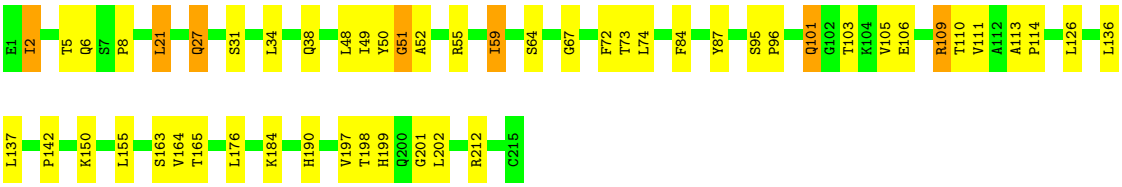
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	B	7	7	7	0	0
			Total	O		
5	C	7	7	7	0	0
			Total	O		
5	D	4	4	4	0	0
			Total	O		
5	H	6	6	6	0	0
			Total	O		
5	L	5	5	5	0	0

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.

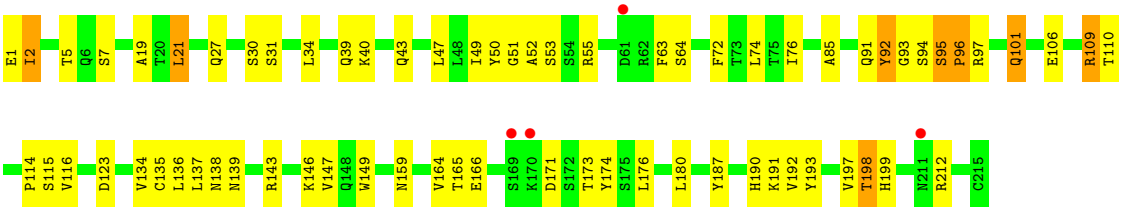
• Molecule 1: Sifalimumab light chain

Chain A:



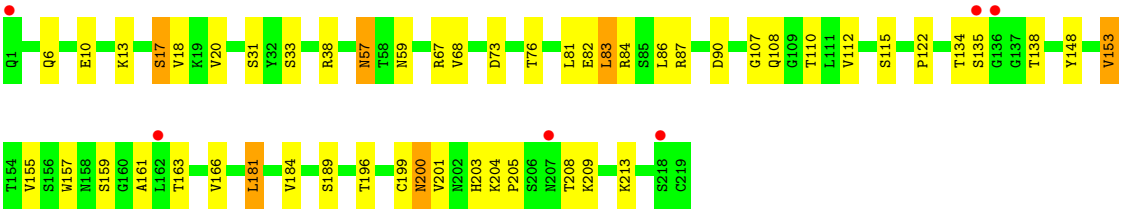
• Molecule 1: Sifalimumab light chain

Chain L:



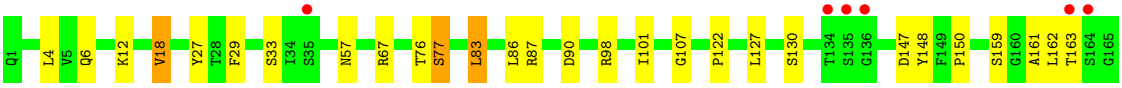
• Molecule 2: Sifalimumab heavy chain

Chain B:

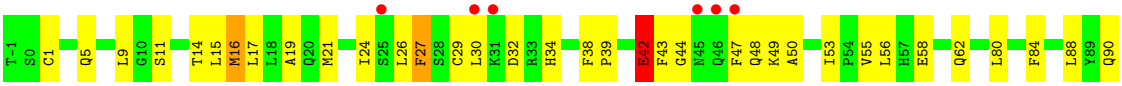


• Molecule 2: Sifalimumab heavy chain

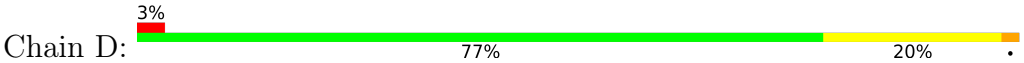
Chain H:

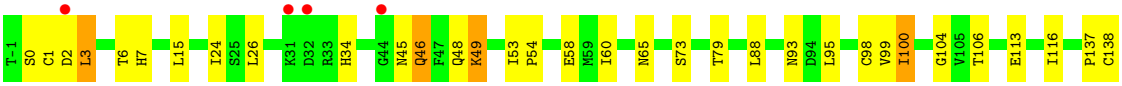


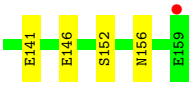
• Molecule 3: Interferon alpha-2



• Molecule 3: Interferon alpha-2







4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	134.82Å 153.26Å 163.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 21.70 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-3.00) 99.7 (21.70-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	2.62 (at 2.99Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.272 0.231 , 0.276	Depositor DCC
R_{free} test set	1719 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	66.9	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 57.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9219	wwPDB-VP
Average B, all atoms (Å^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NI

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	0.45	0/1682	0.65	0/2283
1	L	0.43	0/1682	0.63	0/2283
2	B	0.43	0/1670	0.59	0/2279
2	H	0.43	0/1670	0.62	0/2279
3	C	0.47	0/1322	0.65	0/1783
3	D	0.46	0/1340	0.60	0/1807
All	All	0.44	0/9366	0.62	0/12714

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 (i)

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	1647	0	1601	45	0
1	L	1647	0	1601	59	4
2	B	1631	0	1603	39	0
2	H	1631	0	1603	35	0
3	C	1296	0	1294	44	4
3	D	1314	0	1308	31	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	H	1	0	0	0	0
4	L	1	0	0	0	0
5	A	18	0	0	1	0
5	B	7	0	0	0	0
5	C	7	0	0	0	0
5	D	4	0	0	0	0
5	H	6	0	0	1	0
5	L	5	0	0	1	0
All	All	9219	0	9010	233	4

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 13.

All (233) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:162:LEU:HD12	2:H:195:GLN:NE2	1.40	1.33
3:D:48:GLN:O	3:D:49:LYS:HG2	1.40	1.19
3:C:130:LEU:HD21	3:C:143:VAL:HG21	1.24	1.10
2:H:162:LEU:CD1	2:H:195:GLN:NE2	2.14	1.10
3:C:47:PHE:CE1	3:C:48:GLN:NE2	2.22	1.05
2:B:18:VAL:HG23	2:B:86:LEU:HD11	1.37	1.04
1:L:31:SER:O	1:L:52:ALA:HB2	1.60	1.02
3:C:47:PHE:HE1	3:C:48:GLN:NE2	1.60	0.94
3:D:99:VAL:HG12	1:L:93:GLY:O	1.68	0.93
2:H:163:THR:O	2:H:166:VAL:HG22	1.66	0.93
2:H:162:LEU:HD12	2:H:195:GLN:HE22	1.28	0.93
2:H:162:LEU:CD1	2:H:195:GLN:HE22	1.79	0.91
3:C:47:PHE:HE1	3:C:48:GLN:HE21	0.92	0.90
3:C:47:PHE:CD1	3:C:48:GLN:HG3	2.07	0.90
2:H:162:LEU:HD12	2:H:195:GLN:HE21	1.29	0.90
3:C:130:LEU:HD21	3:C:143:VAL:CG2	2.01	0.89
3:C:43:PHE:CZ	3:C:55:VAL:HG12	2.09	0.87
3:D:99:VAL:CG1	1:L:93:GLY:O	2.23	0.86
1:A:137:LEU:CD2	1:A:197:VAL:HG21	2.05	0.86
1:A:137:LEU:HD22	1:A:197:VAL:HG21	1.57	0.84
2:B:18:VAL:CG2	2:B:86:LEU:HD11	2.08	0.83
3:C:43:PHE:CE2	3:C:55:VAL:HG12	2.15	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:83:LEU:HD23	2:H:86:LEU:HD23	1.60	0.81
3:D:48:GLN:O	3:D:49:LYS:CG	2.26	0.80
2:B:155:VAL:HG22	2:B:201:VAL:HG22	1.62	0.79
1:A:136:LEU:HD22	2:B:184:VAL:HG21	1.68	0.76
1:L:47:LEU:HD21	1:L:50:TYR:HB3	1.68	0.75
1:L:95:SER:O	1:L:96:PRO:C	2.26	0.73
1:L:31:SER:O	1:L:52:ALA:CB	2.37	0.71
3:D:65:ASN:HB2	1:L:50:TYR:OH	1.90	0.71
1:A:51:GLY:O	1:A:52:ALA:HB3	1.91	0.70
2:B:83:LEU:HD22	2:B:86:LEU:HD23	1.71	0.70
1:A:137:LEU:HD21	1:A:197:VAL:CG2	2.21	0.70
3:C:42:GLU:O	3:C:43:PHE:CG	2.45	0.70
2:B:68:VAL:HG23	2:B:82:GLU:O	1.92	0.69
2:H:166:VAL:HG12	2:H:185:VAL:HB	1.74	0.69
1:A:50:TYR:O	1:A:52:ALA:N	2.25	0.69
3:C:53:ILE:HG23	3:C:95:LEU:HD22	1.74	0.68
3:D:60:ILE:HG23	3:D:88:LEU:HD22	1.74	0.68
2:H:83:LEU:HD23	2:H:86:LEU:CD2	2.23	0.68
2:H:194:THR:O	2:H:194:THR:HG22	1.93	0.68
1:L:34:LEU:CD2	1:L:72:PHE:CG	2.78	0.67
3:C:53:ILE:HD12	3:C:104:GLY:HA3	1.76	0.67
3:C:47:PHE:O	3:C:48:GLN:HB2	1.95	0.67
2:B:68:VAL:HG21	2:B:81:LEU:HD11	1.78	0.66
1:L:95:SER:O	1:L:97:ARG:N	2.29	0.66
3:D:0:SER:HB2	2:H:57:ASN:HD22	1.61	0.66
1:L:51:GLY:O	1:L:52:ALA:HB3	1.95	0.66
2:B:33:SER:H	3:C:93:ASN:HD21	1.41	0.65
1:A:95:SER:OG	1:A:96:PRO:HD3	1.97	0.64
1:L:21:LEU:N	1:L:21:LEU:HD23	2.13	0.64
1:L:159:ASN:ND2	1:L:180:LEU:HD11	2.14	0.63
2:B:122:PRO:HB3	2:B:148:TYR:HB3	1.80	0.63
2:H:101:ILE:HD12	1:L:92:TYR:CG	2.34	0.63
1:A:6:GLN:H	1:A:101:GLN:HE22	1.47	0.63
1:L:40:LYS:HB2	1:L:43:GLN:HE21	1.64	0.63
2:B:73:ASP:OD1	2:B:76:THR:HG23	2.00	0.62
2:B:10:GLU:HB2	2:B:112:VAL:HG22	1.82	0.62
1:L:1:GLU:O	1:L:1:GLU:HG2	1.99	0.62
1:A:113:ALA:HB2	1:A:201:GLY:O	2.00	0.61
1:L:49:ILE:O	1:L:49:ILE:HG22	2.00	0.61
1:A:34:LEU:HD22	1:A:72:PHE:CG	2.37	0.60
2:H:162:LEU:HD11	2:H:195:GLN:HE22	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:LEU:HD21	1:A:197:VAL:HG21	1.81	0.59
2:B:196:THR:HG23	2:B:213:LYS:HE3	1.85	0.59
1:L:34:LEU:HD22	1:L:72:PHE:CD1	2.38	0.59
3:C:11:SER:H	3:C:91:GLN:NE2	2.00	0.59
2:B:163:THR:O	2:B:166:VAL:HG23	2.02	0.58
1:A:95:SER:OG	1:A:96:PRO:CD	2.51	0.58
1:A:136:LEU:HD21	2:B:184:VAL:HG11	1.84	0.58
2:H:6:GLN:HE21	2:H:107:GLY:HA3	1.69	0.58
2:H:163:THR:O	2:H:166:VAL:CG2	2.48	0.58
1:L:187:TYR:O	1:L:193:TYR:OH	2.22	0.58
1:L:190:HIS:O	1:L:212:ARG:HD3	2.04	0.57
1:L:138:ASN:HB3	1:L:139:ASN:HD22	1.69	0.57
3:D:93:ASN:HD21	2:H:33:SER:H	1.52	0.57
1:L:159:ASN:HD21	1:L:180:LEU:HD11	1.70	0.56
3:C:114:ASP:OD1	3:C:115:SER:N	2.38	0.56
2:H:12:LYS:HG3	2:H:18:VAL:HG13	1.87	0.56
2:H:76:THR:O	2:H:77:SER:HB2	2.05	0.56
3:C:32:ASP:O	3:C:142:VAL:HG21	2.06	0.56
1:A:21:LEU:HD13	1:A:103:THR:HB	1.86	0.56
1:A:136:LEU:CD2	2:B:184:VAL:HG11	2.36	0.56
2:H:216:PRO:O	2:H:217:LYS:HG2	2.06	0.56
3:C:48:GLN:C	3:C:50:ALA:H	2.09	0.55
3:D:54:PRO:HG3	3:D:106:THR:HG21	1.88	0.55
3:C:91:GLN:HE22	3:C:151:PHE:HZ	1.54	0.55
3:C:43:PHE:CZ	3:C:55:VAL:CG1	2.87	0.55
1:L:116:VAL:HG22	1:L:197:VAL:HG21	1.88	0.54
2:H:167:HIS:NE2	5:H:401:HOH:O	2.13	0.54
3:C:17:LEU:HD13	3:C:84:PHE:HA	1.88	0.54
1:A:55:ARG:HD2	1:A:59:ILE:HG22	1.89	0.53
3:C:56:LEU:HD13	3:C:154:SER:HB2	1.89	0.53
3:D:0:SER:HB2	2:H:57:ASN:ND2	2.22	0.53
3:C:110:LEU:H	3:C:110:LEU:HD12	1.73	0.53
3:D:99:VAL:HG11	1:L:93:GLY:O	2.06	0.53
1:L:171:ASP:OD1	1:L:173:THR:HG23	2.09	0.53
1:L:5:THR:HA	1:L:101:GLN:HE22	1.73	0.53
1:A:21:LEU:HD23	1:A:21:LEU:N	2.24	0.53
3:C:11:SER:OG	3:C:14:THR:OG1	2.27	0.53
1:L:1:GLU:N	5:L:401:HOH:O	2.40	0.53
3:D:2:ASP:C	3:D:3:LEU:HD23	2.29	0.52
1:L:39:GLN:O	1:L:85:ALA:HB1	2.09	0.52
3:D:6:THR:HG22	3:D:7:HIS:ND1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ILE:HG12	1:A:27:GLN:HG2	1.90	0.52
1:A:49:ILE:HD12	1:A:74:LEU:CD1	2.39	0.52
1:A:137:LEU:CD2	1:A:197:VAL:CG2	2.77	0.52
1:A:164:VAL:HG22	1:A:176:LEU:HD12	1.91	0.52
1:A:114:PRO:HD3	1:A:199:HIS:CD2	2.45	0.52
1:L:1:GLU:O	1:L:2:ILE:HB	2.10	0.52
1:A:150:LYS:NZ	5:A:402:HOH:O	2.43	0.51
2:B:122:PRO:HD2	2:B:208:THR:HG21	1.91	0.51
1:L:146:LYS:HB3	1:L:198:THR:HG23	1.91	0.51
1:L:2:ILE:HD12	1:L:94:SER:OG	2.10	0.51
1:A:113:ALA:HB1	1:A:202:LEU:CD2	2.40	0.51
2:H:194:THR:O	2:H:194:THR:CG2	2.58	0.50
2:B:83:LEU:HD22	2:B:86:LEU:CD2	2.39	0.50
2:B:181:LEU:HD23	2:B:181:LEU:C	2.32	0.50
1:L:136:LEU:HD23	1:L:138:ASN:HD21	1.76	0.50
1:L:143:ARG:HD2	1:L:174:TYR:CE2	2.46	0.50
1:A:8:PRO:O	1:A:103:THR:HG23	2.11	0.50
3:D:3:LEU:O	3:D:6:THR:HB	2.11	0.50
3:C:29:CYS:SG	3:C:138:CYS:SG	3.09	0.50
1:A:21:LEU:O	1:A:73:THR:HG23	2.11	0.49
1:A:109:ARG:HD3	1:A:110:THR:O	2.12	0.49
3:C:1:CYS:HG	3:C:98:CYS:HG	0.56	0.49
3:D:58:GLU:HG2	3:D:116:ILE:HG23	1.95	0.49
2:H:127:LEU:HD21	1:L:134:VAL:HG21	1.94	0.49
1:A:137:LEU:HD21	1:A:197:VAL:HG22	1.92	0.49
3:C:47:PHE:O	3:C:48:GLN:CB	2.58	0.49
3:D:100:ILE:HD13	1:L:95:SER:HA	1.94	0.49
1:A:51:GLY:O	3:C:120:ARG:NH2	2.46	0.49
1:L:55:ARG:HD3	1:L:63:PHE:O	2.12	0.49
2:H:196:THR:HG23	2:H:213:LYS:HE2	1.95	0.49
3:C:1:CYS:SG	3:C:98:CYS:CB	3.00	0.49
3:C:15:LEU:HD22	3:C:148:MET:HG2	1.94	0.49
3:C:47:PHE:HD1	3:C:48:GLN:HG3	1.71	0.49
1:A:51:GLY:O	1:A:52:ALA:CB	2.59	0.48
3:D:1:CYS:CB	3:D:98:CYS:HG	2.22	0.48
2:H:159:SER:H	2:H:200:ASN:HD21	1.60	0.48
3:D:15:LEU:HD21	3:D:152:SER:OG	2.13	0.48
2:B:57:ASN:N	2:B:57:ASN:HD22	2.11	0.48
2:B:67:ARG:NH2	2:B:90:ASP:OD2	2.47	0.48
3:C:27:PHE:N	3:C:27:PHE:CD2	2.82	0.48
1:L:34:LEU:CD2	1:L:72:PHE:CD1	2.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:29:CYS:CB	3:C:138:CYS:HG	2.26	0.48
1:L:137:LEU:HD11	1:L:147:VAL:HG22	1.95	0.48
1:L:137:LEU:HD22	1:L:197:VAL:HG21	1.94	0.48
3:D:65:ASN:CB	1:L:50:TYR:OH	2.61	0.47
2:B:204:LYS:N	2:B:205:PRO:CD	2.78	0.47
2:B:31:SER:O	3:C:90:GLN:NE2	2.46	0.47
2:B:68:VAL:HG21	2:B:81:LEU:CD1	2.45	0.47
1:A:142:PRO:O	1:A:199:HIS:HE1	1.98	0.47
3:C:84:PHE:CE2	3:C:88:LEU:HD11	2.50	0.47
1:A:34:LEU:HD22	1:A:72:PHE:CD2	2.50	0.47
3:C:38:PHE:CD1	3:C:39:PRO:HD2	2.50	0.47
3:C:21:MET:HA	3:C:80:LEU:HD12	1.96	0.47
3:D:60:ILE:HG23	3:D:88:LEU:CD2	2.43	0.46
1:L:49:ILE:HD12	1:L:74:LEU:CD1	2.45	0.46
1:L:137:LEU:CD2	1:L:197:VAL:HG21	2.46	0.46
2:B:134:THR:CG2	2:B:135:SER:N	2.79	0.46
1:L:34:LEU:HD22	1:L:72:PHE:CG	2.48	0.46
2:B:157:TRP:CH2	2:B:199:CYS:HB3	2.51	0.46
1:L:109:ARG:HD3	1:L:110:THR:O	2.15	0.46
2:B:134:THR:HG22	2:B:135:SER:N	2.30	0.46
1:L:2:ILE:HG21	1:L:91:GLN:HG2	1.98	0.46
1:L:64:SER:O	1:L:74:LEU:HD12	2.15	0.46
2:B:6:GLN:HE21	2:B:107:GLY:HA3	1.80	0.46
2:H:159:SER:N	2:H:200:ASN:HD21	2.13	0.46
3:D:113:GLU:OE2	1:L:31:SER:OG	2.32	0.45
2:B:159:SER:H	2:B:200:ASN:HD21	1.62	0.45
2:B:17:SER:HB3	2:B:84:ARG:HA	1.99	0.45
2:B:153:VAL:HG23	2:B:203:HIS:HB2	1.99	0.45
1:A:64:SER:O	1:A:74:LEU:HD12	2.16	0.45
3:C:9:LEU:HD21	3:C:49:LYS:NZ	2.32	0.45
1:L:191:LYS:HG2	1:L:192:VAL:HG23	1.98	0.45
1:L:51:GLY:O	1:L:52:ALA:CB	2.61	0.45
3:D:53:ILE:HD13	3:D:104:GLY:HA3	1.98	0.45
1:A:31:SER:O	1:A:52:ALA:HB2	2.17	0.45
2:B:68:VAL:CG2	2:B:81:LEU:CD1	2.95	0.44
2:B:18:VAL:HG23	2:B:86:LEU:CD1	2.27	0.44
3:C:53:ILE:CD1	3:C:104:GLY:HA3	2.47	0.44
1:L:165:THR:HG22	1:L:166:GLU:N	2.32	0.44
3:C:126:ILE:HD13	3:C:147:ILE:HD11	2.00	0.44
1:L:114:PRO:HD3	1:L:199:HIS:CD2	2.53	0.44
1:L:137:LEU:HD23	1:L:137:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:TYR:C	1:A:52:ALA:N	2.70	0.44
2:H:130:SER:CB	2:H:217:LYS:O	2.65	0.44
1:A:38:GLN:HB2	1:A:48:LEU:HD11	1.99	0.44
1:A:48:LEU:HD11	1:A:87:TYR:CE1	2.53	0.43
2:H:204:LYS:N	2:H:205:PRO:CD	2.82	0.43
1:L:159:ASN:ND2	1:L:180:LEU:CD1	2.81	0.43
2:B:20:VAL:HG22	2:B:110:THR:HG21	2.01	0.43
3:C:5:GLN:OE1	3:C:5:GLN:N	2.41	0.43
3:D:49:LYS:HE3	3:D:156:ASN:HD21	1.83	0.43
1:L:137:LEU:HD13	1:L:197:VAL:HG11	1.99	0.43
3:D:24:ILE:HD13	3:D:137:PRO:HB2	2.01	0.43
2:H:122:PRO:HB3	2:H:148:TYR:HB3	2.00	0.43
2:H:67:ARG:NH2	2:H:90:ASP:OD2	2.51	0.43
1:A:50:TYR:O	1:A:51:GLY:C	2.56	0.42
1:A:50:TYR:C	1:A:52:ALA:H	2.23	0.42
2:H:147:ASP:HB3	2:H:178:LEU:HD12	2.02	0.42
3:C:58:GLU:O	3:C:62:GLN:HG2	2.20	0.42
3:D:24:ILE:HD11	3:D:138:CYS:HA	2.02	0.42
3:D:3:LEU:HD23	3:D:3:LEU:N	2.35	0.42
3:D:45:ASN:O	3:D:46:GLN:C	2.58	0.42
3:D:65:ASN:CA	1:L:50:TYR:OH	2.68	0.42
2:B:68:VAL:CG2	2:B:81:LEU:HD11	2.48	0.41
2:H:216:PRO:O	2:H:217:LYS:CG	2.67	0.41
3:C:24:ILE:HD13	3:C:137:PRO:HB2	2.02	0.41
3:D:26:LEU:HD13	3:D:141:GLU:HG3	2.03	0.41
1:A:111:VAL:HG13	1:A:142:PRO:HD2	2.02	0.41
1:A:126:LEU:HB3	1:A:184:LYS:HE3	2.02	0.41
3:D:95:LEU:O	3:D:99:VAL:HG23	2.21	0.41
1:A:190:HIS:O	1:A:212:ARG:HD3	2.20	0.41
2:B:159:SER:N	2:B:200:ASN:HD21	2.19	0.41
3:C:133:LYS:O	3:C:134:LYS:C	2.58	0.41
2:H:4:LEU:HD11	2:H:98:ARG:HB2	2.03	0.41
2:H:27:TYR:CE1	2:H:29:PHE:HA	2.56	0.41
2:H:150:PRO:O	2:H:203:HIS:HE1	2.04	0.41
1:L:34:LEU:HD22	1:L:72:PHE:CE1	2.56	0.41
2:B:18:VAL:CG2	2:B:86:LEU:CD1	2.91	0.41
1:L:135:CYS:HB2	1:L:149:TRP:CZ2	2.56	0.41
1:A:67:GLY:HA3	1:A:72:PHE:HA	2.02	0.40
2:B:157:TRP:HB2	2:B:163:THR:HG22	2.03	0.40
1:A:95:SER:O	2:B:59:ASN:ND2	2.54	0.40
2:B:13:LYS:HA	2:B:115:SER:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:49:LYS:NZ	3:D:156:ASN:HD21	2.18	0.40
1:L:19:ALA:HB3	1:L:76:ILE:HB	2.04	0.40
1:L:21:LEU:N	1:L:21:LEU:CD2	2.81	0.40
3:C:16:MET:O	3:C:19:ALA:HB3	2.21	0.40
1:L:164:VAL:HG22	1:L:176:LEU:HD12	2.03	0.40
1:A:84:PHE:CD2	1:A:105:VAL:HG12	2.57	0.40

All (4) 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)
3:C:48:GLN:NE2	1:L:115:SER:OG[2_565]	1.20	1.00
3:C:47:PHE:CE1	1:L:115:SER:CB[2_565]	1.77	0.43
3:C:47:PHE:CD1	1:L:115:SER:OG[2_565]	1.97	0.23
3:C:48:GLN:NE2	1:L:115:SER:CB[2_565]	2.15	0.05

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	213/215 (99%)	199 (93%)	12 (6%)	2 (1%)	17 55
1	L	213/215 (99%)	200 (94%)	9 (4%)	4 (2%)	8 36
2	B	217/219 (99%)	198 (91%)	18 (8%)	1 (0%)	29 68
2	H	217/219 (99%)	204 (94%)	11 (5%)	2 (1%)	17 55
3	C	157/161 (98%)	144 (92%)	10 (6%)	3 (2%)	8 36
3	D	159/161 (99%)	147 (92%)	10 (6%)	2 (1%)	12 45
All	All	1176/1190 (99%)	1092 (93%)	70 (6%)	14 (1%)	13 48

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	49	LYS
1	L	95	SER
1	A	51	GLY
2	B	161	ALA
3	C	30	LEU
3	C	44	GLY
3	D	46	GLN
2	H	77	SER
2	H	161	ALA
1	L	53	SER
3	C	42	GLU
1	L	2	ILE
1	L	96	PRO
1	A	2	ILE

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	186/186 (100%)	175 (94%)	11 (6%)	19	54
1	L	186/186 (100%)	176 (95%)	10 (5%)	22	57
2	B	184/184 (100%)	172 (94%)	12 (6%)	17	50
2	H	184/184 (100%)	177 (96%)	7 (4%)	33	69
3	C	146/148 (99%)	139 (95%)	7 (5%)	25	62
3	D	148/148 (100%)	142 (96%)	6 (4%)	30	67
All	All	1034/1036 (100%)	981 (95%)	53 (5%)	24	60

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	21	LEU
1	A	27	GLN
1	A	59	ILE
1	A	101	GLN

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Mol	Chain	Res	Type
1	A	106	GLU
1	A	109	ARG
1	A	155	LEU
1	A	163	SER
1	A	165	THR
1	A	198	THR
2	B	17	SER
2	B	38	ARG
2	B	57	ASN
2	B	83	LEU
2	B	87	ARG
2	B	108	GLN
2	B	138	THR
2	B	153	VAL
2	B	181	LEU
2	B	189	SER
2	B	200	ASN
2	B	209	LYS
3	C	16	MET
3	C	26	LEU
3	C	27	PHE
3	C	34	HIS
3	C	42	GLU
3	C	100	ILE
3	C	128	LEU
3	D	3	LEU
3	D	34	HIS
3	D	73	SER
3	D	79	THR
3	D	100	ILE
3	D	146	GLU
2	H	18	VAL
2	H	83	LEU
2	H	87	ARG
2	H	199	CYS
2	H	200	ASN
2	H	209	LYS
2	H	215	GLU
1	L	7	SER
1	L	21	LEU
1	L	27	GLN
1	L	30	SER

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Mol	Chain	Res	Type
1	L	92	TYR
1	L	101	GLN
1	L	106	GLU
1	L	109	ARG
1	L	123	ASP
1	L	198	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	101	GLN
1	A	156	GLN
1	A	199	HIS
2	B	6	GLN
2	B	57	ASN
2	B	59	ASN
2	B	174	GLN
2	B	195	GLN
2	B	200	ASN
2	B	202	ASN
3	C	91	GLN
3	C	93	ASN
3	C	124	GLN
3	D	93	ASN
3	D	124	GLN
2	H	6	GLN
2	H	55	ASN
2	H	57	ASN
2	H	59	ASN
2	H	174	GLN
2	H	195	GLN
2	H	200	ASN
2	H	202	ASN
2	H	203	HIS
1	L	27	GLN
1	L	43	GLN
1	L	101	GLN
1	L	138	ASN
1	L	139	ASN
1	L	211	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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	215/215 (100%)	-0.18	0	100	100	44, 56, 76, 93	0
1	L	215/215 (100%)	-0.06	4 (1%)	66	37	43, 60, 95, 128	0
2	B	219/219 (100%)	-0.19	6 (2%)	54	26	44, 58, 94, 113	0
2	H	219/219 (100%)	0.13	11 (5%)	28	10	49, 69, 118, 135	0
3	C	159/161 (98%)	-0.06	6 (3%)	40	16	46, 62, 112, 141	0
3	D	161/161 (100%)	-0.09	5 (3%)	49	21	47, 63, 104, 131	0
All	All	1188/1190 (99%)	-0.08	32 (2%)	54	26	43, 61, 104, 141	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	219	CYS	4.7
2	H	207	ASN	3.7
3	D	32	ASP	3.3
2	B	135	SER	3.2
2	H	164	SER	3.1
2	B	162	LEU	3.0
2	B	1	GLN	3.0
3	D	159	GLU	3.0
2	B	218	SER	2.9
3	C	25	SER	2.8
2	H	163	THR	2.8
2	H	194	THR	2.7
3	C	31	LYS	2.7
3	D	44	GLY	2.6
2	B	207	ASN	2.6
3	C	46	GLN	2.6
2	H	135	SER	2.5
2	H	218	SER	2.4
2	H	35	SER	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	30	LEU	2.3
3	D	31	LYS	2.3
2	H	134	THR	2.3
1	L	169	SER	2.3
2	H	189	SER	2.2
3	C	47	PHE	2.2
2	H	136	GLY	2.1
1	L	61	ASP	2.1
2	B	136	GLY	2.1
1	L	211	ASN	2.1
1	L	170	LYS	2.1
3	C	45	ASN	2.1
3	D	2	ASP	2.1

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, 95th 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	NI	A	301	1/1	0.82	0.22	84,84,84,84	0
4	NI	B	301	1/1	0.86	0.10	84,84,84,84	1
4	NI	L	301	1/1	0.93	0.18	77,77,77,77	1
4	NI	H	301	1/1	0.96	0.10	72,72,72,72	1
4	NI	C	201	1/1	0.97	0.06	69,69,69,69	0
4	NI	D	201	1/1	0.97	0.05	64,64,64,64	0

6.5 Other polymers (i)

There are no such residues in this entry.