



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:57 PM GMT

PDB ID : 6FAB  
Title : THREE-DIMENSIONAL STRUCTURE OF MURINE ANTI-P-AZOPHENYLARSONATE FAB 36-71. 1. X-RAY CRYSTALLOGRAPHY, SITE-DIRECTED MUTAGENESIS, AND MODELING OF THE COMPLEX WITH HAPTEN  
Authors : Strong, R.K.; Rose, D.R.; Petsko, G.A.; Sharon, J.; Margolies, M.N.  
Deposited on : 1991-01-17  
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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

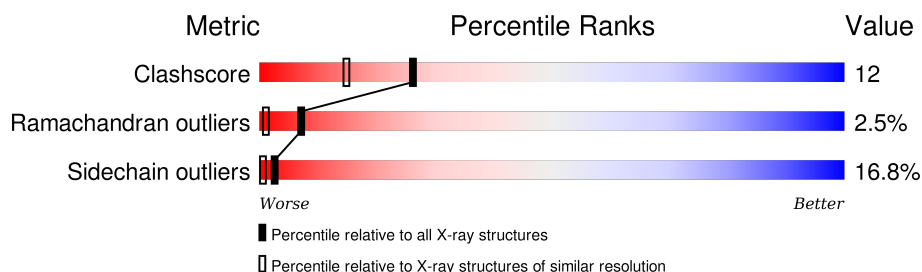
# 1 Overall quality at a glance

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))
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (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  $\geq 3$ , 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  $\leq 5\%$ . 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	214	
2	H	222	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3409 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 IGG1-KAPPA 36-71 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	214	Total	C	N	O	S	0	0	0
			1660	1026	284	343	7			

- Molecule 2 is a protein called IGG1-KAPPA 36-71 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	222	Total	C	N	O	S	0	0	0
			1679	1057	279	336	7			

- Molecule 3 is water.

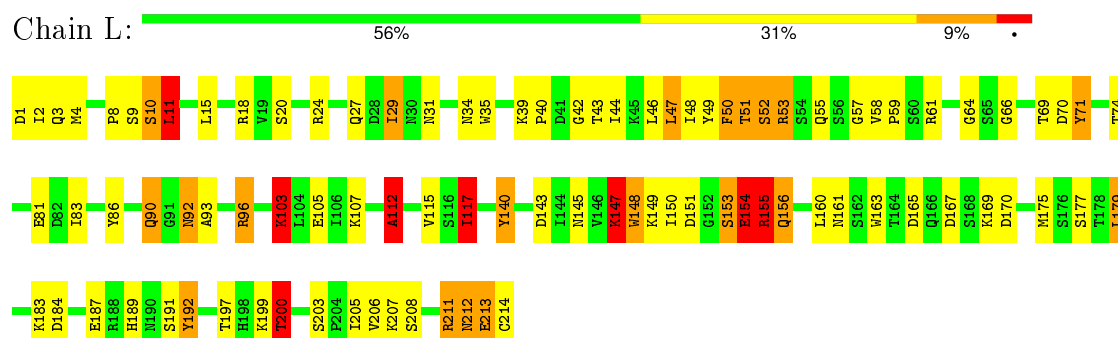
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	38	Total	O	0	0
			38	38		
3	L	32	Total	O	0	0
			32	32		

### 3 Residue-property plots [i](#)

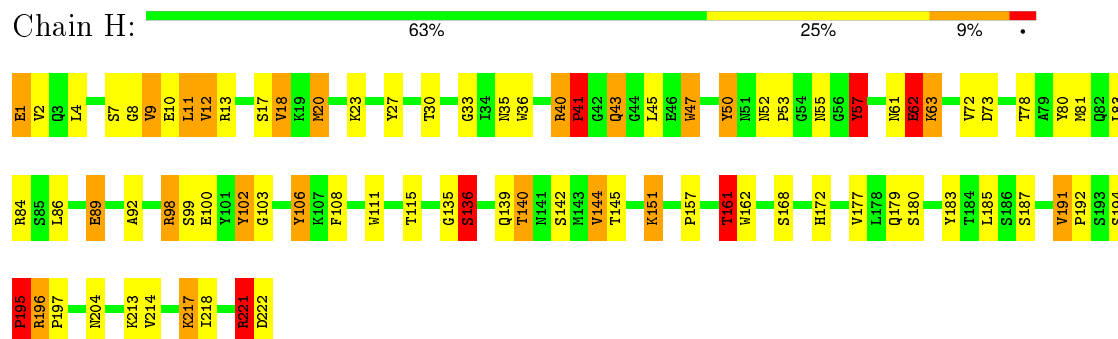
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

#### • Molecule 1: IGG1-KAPPA 36-71 FAB (LIGHT CHAIN)



#### • Molecule 2: IGG1-KAPPA 36-71 FAB (HEAVY CHAIN)



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.13Å 73.05Å 46.78Å 90.00° 104.48° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.209 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3409	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	L	1.04	0/1693	1.96	57/2293 (2.5%)
2	H	0.98	0/1721	1.86	44/2345 (1.9%)
All	All	1.01	0/3414	1.91	101/4638 (2.2%)

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
1	L	0	2
2	H	0	1
All	All	0	3

There are no bond length outliers.

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	L	163	TRP	CD1-CG-CD2	11.03	115.12	106.30
1	L	175	MET	CG-SD-CE	-9.75	84.59	100.20
2	H	151	LYS	CA-C-N	9.53	135.27	116.20
2	H	57	TYR	N-CA-C	9.48	136.59	111.00
1	L	154	GLU	CA-C-N	-9.34	96.65	117.20
1	L	192	TYR	CB-CG-CD2	-8.54	115.88	121.00
1	L	170	ASP	O-C-N	-8.43	109.20	122.70
1	L	96	ARG	NE-CZ-NH2	-8.35	116.13	120.30
1	L	163	TRP	CE2-CD2-CG	-8.32	100.64	107.30
2	H	185	LEU	CA-CB-CG	8.26	134.31	115.30
1	L	148	TRP	CE2-CD2-CG	-8.24	100.71	107.30
1	L	148	TRP	CD1-CG-CD2	8.15	112.82	106.30
1	L	112	ALA	N-CA-CB	8.06	121.39	110.10
2	H	111	TRP	CD1-CG-CD2	7.99	112.69	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	102	TYR	CB-CG-CD2	-7.99	116.21	121.00
2	H	111	TRP	CE2-CD2-CG	-7.90	100.98	107.30
1	L	154	GLU	N-CA-C	7.71	131.83	111.00
1	L	170	ASP	CA-C-N	7.70	134.13	117.20
1	L	11	LEU	CA-CB-CG	7.61	132.80	115.30
1	L	155	ARG	NE-CZ-NH2	-7.48	116.56	120.30
2	H	11	LEU	CA-CB-CG	7.47	132.49	115.30
1	L	140	TYR	CB-CG-CD1	-7.40	116.56	121.00
1	L	51	THR	CA-CB-CG2	7.13	122.39	112.40
2	H	47	TRP	CD1-CG-CD2	7.04	111.94	106.30
2	H	162	TRP	CD1-CG-CD2	7.01	111.91	106.30
1	L	35	TRP	CG-CD1-NE1	-6.95	103.15	110.10
1	L	112	ALA	CB-CA-C	-6.95	99.67	110.10
1	L	35	TRP	CD1-CG-CD2	6.83	111.77	106.30
2	H	80	TYR	CB-CG-CD2	-6.78	116.94	121.00
1	L	167	ASP	CB-CG-OD2	6.76	124.39	118.30
1	L	117	ILE	CB-CA-C	-6.72	98.17	111.60
1	L	163	TRP	CG-CD1-NE1	-6.71	103.39	110.10
2	H	36	TRP	CD1-CG-CD2	6.67	111.64	106.30
1	L	211	ARG	NE-CZ-NH2	-6.62	116.99	120.30
2	H	50	TYR	CB-CG-CD1	-6.57	117.06	121.00
2	H	135	GLY	CA-C-N	-6.57	102.75	117.20
1	L	52	SER	CA-C-N	6.55	131.61	117.20
2	H	43	GLN	N-CA-C	6.53	128.64	111.00
1	L	70	ASP	CB-CG-OD1	6.51	124.16	118.30
2	H	81	MET	CG-SD-CE	-6.49	89.81	100.20
2	H	36	TRP	CE2-CD2-CG	-6.46	102.13	107.30
2	H	214	VAL	CG1-CB-CG2	-6.44	100.60	110.90
2	H	89	GLU	CA-CB-CG	6.39	127.45	113.40
1	L	86	TYR	CB-CG-CD2	-6.36	117.19	121.00
2	H	162	TRP	CE2-CD2-CG	-6.33	102.23	107.30
2	H	136	SER	N-CA-CB	-6.33	101.01	110.50
1	L	51	THR	CA-C-N	-6.26	103.44	117.20
2	H	9	VAL	CG1-CB-CG2	-6.19	101.00	110.90
1	L	51	THR	CA-CB-OG1	-6.18	96.02	109.00
1	L	18	ARG	NE-CZ-NH1	6.15	123.37	120.30
2	H	1	GLU	N-CA-C	-6.06	94.64	111.00
2	H	135	GLY	O-C-N	6.04	132.36	122.70
1	L	154	GLU	CA-C-O	6.03	132.76	120.10
2	H	43	GLN	CA-C-N	6.03	128.25	116.20
1	L	52	SER	CB-CA-C	5.98	121.46	110.10
2	H	47	TRP	CE2-CD2-CG	-5.95	102.54	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	102	TYR	CB-CG-CD1	5.91	124.54	121.00
1	L	52	SER	CA-CB-OG	5.89	127.11	111.20
1	L	213	GLU	N-CA-C	-5.88	95.14	111.00
1	L	57	GLY	CA-C-O	5.83	131.09	120.60
2	H	217	LYS	CA-CB-CG	-5.83	100.58	113.40
1	L	53	ARG	CA-C-N	5.79	129.94	117.20
1	L	117	ILE	CA-CB-CG1	-5.74	100.09	111.00
2	H	151	LYS	O-C-N	-5.71	113.49	123.20
2	H	151	LYS	N-CA-C	5.71	126.41	111.00
1	L	4	MET	CA-CB-CG	5.66	122.92	113.30
1	L	52	SER	O-C-N	-5.65	113.66	122.70
1	L	42	GLY	N-CA-C	5.62	127.15	113.10
2	H	98	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	L	51	THR	O-C-N	5.61	131.68	122.70
1	L	96	ARG	NE-CZ-NH1	5.61	123.10	120.30
2	H	221	ARG	NE-CZ-NH1	5.59	123.09	120.30
2	H	180	SER	CA-C-N	-5.57	104.95	117.20
2	H	162	TRP	CG-CD1-NE1	-5.54	104.56	110.10
1	L	154	GLU	CA-CB-CG	5.54	125.58	113.40
1	L	57	GLY	CA-C-N	-5.53	105.03	117.20
1	L	155	ARG	CA-CB-CG	5.52	125.55	113.40
1	L	103	LYS	CA-CB-CG	5.50	125.51	113.40
1	L	153	SER	CA-C-N	5.45	129.19	117.20
2	H	62	GLU	OE1-CD-OE2	-5.45	116.76	123.30
2	H	106	TYR	CB-CG-CD2	-5.45	117.73	121.00
1	L	154	GLU	CB-CA-C	-5.43	99.54	110.40
1	L	163	TRP	CB-CG-CD1	-5.43	119.94	127.00
1	L	147	LYS	CA-CB-CG	5.34	125.16	113.40
2	H	73	ASP	N-CA-C	-5.33	96.60	111.00
1	L	151	ASP	CB-CG-OD2	5.33	123.10	118.30
1	L	117	ILE	CA-CB-CG2	5.32	121.54	110.90
2	H	221	ARG	CA-CB-CG	5.31	125.08	113.40
1	L	71	TYR	CB-CG-CD1	-5.29	117.82	121.00
2	H	111	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	L	206	VAL	N-CA-CB	-5.28	99.89	111.50
1	L	15	LEU	CB-CG-CD2	-5.25	102.08	111.00
2	H	12	VAL	CG1-CB-CG2	-5.24	102.51	110.90
2	H	183	TYR	CB-CG-CD2	-5.17	117.89	121.00
2	H	20	MET	CG-SD-CE	-5.15	91.95	100.20
1	L	92	ASN	O-C-N	-5.13	114.50	122.70
1	L	156	GLN	N-CA-C	5.13	124.84	111.00
2	H	161	THR	N-CA-CB	-5.12	100.57	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	195	PRO	CA-N-CD	-5.07	104.41	111.50
2	H	18	VAL	CG1-CB-CG2	-5.06	102.80	110.90
1	L	61	ARG	NE-CZ-NH1	5.03	122.81	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	106	TYR	Sidechain
1	L	155	ARG	Peptide
1	L	192	TYR	Sidechain

## 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	L	1660	0	1590	50	0
2	H	1679	0	1636	37	0
3	H	38	0	0	2	0
3	L	32	0	0	1	0
All	All	3409	0	3226	81	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 12.

All (81) 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:192:PRO:HB2	2:H:195:PRO:HD2	1.54	0.88
1:L:213:GLU:HG3	2:H:136:SER:HB3	1.63	0.80
1:L:52:SER:HB3	1:L:64:GLY:HA3	1.64	0.78
1:L:48:ILE:HG21	1:L:52:SER:HA	1.66	0.78
2:H:161:THR:HG22	2:H:204:ASN:HB2	1.64	0.77
1:L:47:LEU:HA	1:L:58:VAL:HG11	1.65	0.77
1:L:31:ASN:HB3	1:L:51:THR:HB	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:196:ARG:HG2	2:H:197:PRO:HA	1.66	0.75
2:H:140:THR:HB	2:H:144:VAL:HA	1.74	0.70
2:H:144:VAL:HG23	2:H:191:VAL:HG23	1.75	0.69
1:L:160:LEU:HD13	2:H:177:VAL:CG2	2.24	0.68
1:L:50:PHE:HD2	2:H:102:TYR:HE2	1.45	0.64
1:L:147:LYS:HA	1:L:155:ARG:HG2	1.80	0.64
2:H:2:VAL:HB	2:H:27:TYR:HD2	1.62	0.63
2:H:35:ASN:HD22	2:H:47:TRP:HE1	1.46	0.63
1:L:48:ILE:CG2	1:L:52:SER:HA	2.27	0.62
1:L:155:ARG:HB3	1:L:156:GLN:HG2	1.82	0.62
1:L:52:SER:HB3	1:L:64:GLY:CA	2.29	0.62
1:L:145:ASN:OD1	1:L:147:LYS:HE2	2.01	0.60
1:L:24:ARG:NH1	1:L:24:ARG:HB3	2.18	0.59
1:L:160:LEU:HD13	2:H:177:VAL:HG23	1.85	0.58
1:L:2:ILE:HG21	1:L:29:ILE:HD11	1.86	0.57
1:L:154:GLU:HA	3:L:637:HOH:O	2.05	0.57
1:L:149:LYS:HA	1:L:153:SER:O	2.05	0.56
2:H:53:PRO:HB3	2:H:72:VAL:HG21	1.87	0.56
2:H:35:ASN:ND2	2:H:47:TRP:HE1	2.05	0.55
2:H:13:ARG:HD2	3:H:629:HOH:O	2.06	0.55
1:L:2:ILE:HD13	1:L:29:ILE:HD11	1.88	0.55
1:L:90:GLN:HE22	1:L:93:ALA:H	1.53	0.54
2:H:8:GLY:HA3	2:H:20:MET:HA	1.90	0.53
1:L:112:ALA:HA	1:L:200:THR:HG21	1.91	0.53
1:L:189:HIS:O	1:L:211:ARG:HD3	2.09	0.53
2:H:172:HIS:O	2:H:187:SER:HA	2.11	0.51
1:L:160:LEU:HD13	2:H:177:VAL:HG21	1.92	0.51
1:L:148:TRP:H	1:L:155:ARG:HG2	1.76	0.50
1:L:52:SER:HB3	1:L:64:GLY:C	2.31	0.50
2:H:40:ARG:NH2	2:H:89:GLU:HA	2.26	0.50
2:H:62:GLU:O	2:H:63:LYS:HB2	2.11	0.49
1:L:145:ASN:HB3	1:L:197:THR:HB	1.94	0.49
1:L:31:ASN:O	1:L:51:THR:HB	2.13	0.49
1:L:90:GLN:NE2	1:L:92:ASN:H	2.11	0.48
2:H:41:PRO:HD3	2:H:92:ALA:HA	1.96	0.48
1:L:50:PHE:O	1:L:51:THR:HG22	2.13	0.48
1:L:2:ILE:HG21	1:L:29:ILE:CD1	2.44	0.48
2:H:83:LEU:HB3	2:H:86:LEU:HD21	1.97	0.47
2:H:139:GLN:HG2	2:H:140:THR:N	2.28	0.47
2:H:12:VAL:HG11	2:H:18:VAL:CG1	2.44	0.47
2:H:9:VAL:HG12	2:H:12:VAL:HG13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:34:ASN:HD22	1:L:49:TYR:HA	1.81	0.46
2:H:62:GLU:OE1	2:H:62:GLU:HA	2.16	0.46
1:L:39:LYS:HG3	1:L:40:PRO:HD2	1.98	0.46
1:L:24:ARG:HA	1:L:69:THR:O	2.15	0.45
2:H:98:ARG:O	2:H:108:PHE:HA	2.16	0.45
1:L:107:LYS:HD2	1:L:140:TYR:OH	2.16	0.45
2:H:33:GLY:HA3	2:H:50:TYR:CE1	2.51	0.45
1:L:52:SER:O	1:L:53:ARG:HB3	2.16	0.45
2:H:140:THR:HG21	2:H:145:THR:OG1	2.17	0.45
1:L:8:PRO:HG3	1:L:11:LEU:HD23	1.99	0.44
1:L:51:THR:O	1:L:52:SER:HB2	2.18	0.44
1:L:212:ASN:HD22	1:L:212:ASN:HA	1.70	0.44
2:H:23:LYS:HG2	2:H:78:THR:HG23	1.99	0.44
2:H:179:GLN:HG3	3:H:657:HOH:O	2.16	0.43
1:L:117:ILE:CG1	1:L:207:LYS:HB3	2.48	0.43
1:L:66:GLY:HA3	1:L:71:TYR:HA	2.00	0.43
1:L:55:GLN:NE2	1:L:59:PRO:O	2.51	0.43
1:L:183:LYS:NZ	1:L:187:GLU:OE1	2.52	0.43
2:H:17:SER:OG	2:H:84:ARG:NH1	2.51	0.43
1:L:50:PHE:CD2	2:H:102:TYR:HE2	2.31	0.43
2:H:2:VAL:HB	2:H:27:TYR:CD2	2.48	0.43
1:L:207:LYS:HD3	1:L:207:LYS:HA	1.83	0.43
1:L:115:VAL:HG12	1:L:207:LYS:HG3	2.00	0.42
1:L:117:ILE:O	1:L:117:ILE:HD12	2.19	0.42
1:L:31:ASN:HB3	1:L:51:THR:CB	2.44	0.42
1:L:150:ILE:HD11	1:L:179:LEU:HD11	2.02	0.42
1:L:10:SER:OG	1:L:103:LYS:HE3	2.20	0.42
2:H:52:ASN:ND2	2:H:55:ASN:HB2	2.35	0.41
2:H:196:ARG:HB3	2:H:196:ARG:HE	1.54	0.41
1:L:90:GLN:HE21	1:L:92:ASN:H	1.67	0.41
2:H:40:ARG:HH11	2:H:40:ARG:HD3	1.75	0.41
2:H:217:LYS:HG2	2:H:218:ILE:N	2.35	0.41
1:L:161:ASN:ND2	1:L:177:SER:OG	2.55	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	L	212/214 (99%)	198 (93%)	11 (5%)	3 (1%)	14	4
2	H	220/222 (99%)	199 (90%)	13 (6%)	8 (4%)	4	0
All	All	432/436 (99%)	397 (92%)	24 (6%)	11 (2%)	7	1

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	43	GLN
2	H	136	SER
2	H	142	SER
2	H	221	ARG
1	L	200	THR
2	H	63	LYS
2	H	103	GLY
1	L	112	ALA
2	H	57	TYR
1	L	50	PHE
2	H	41	PRO

### 5.3.2 Protein sidechains

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	L	191/191 (100%)	155 (81%)	36 (19%)	2	0
2	H	190/190 (100%)	162 (85%)	28 (15%)	4	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	381/381 (100%)	317 (83%)	64 (17%)	<b>2</b> <b>0</b>

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1	ASP
1	L	3	GLN
1	L	9	SER
1	L	10	SER
1	L	11	LEU
1	L	20	SER
1	L	27	GLN
1	L	29	ILE
1	L	43	THR
1	L	44	ILE
1	L	46	LEU
1	L	47	LEU
1	L	74	THR
1	L	81	GLU
1	L	83	ILE
1	L	90	GLN
1	L	96	ARG
1	L	103	LYS
1	L	105	GLU
1	L	117	ILE
1	L	143	ASP
1	L	147	LYS
1	L	154	GLU
1	L	155	ARG
1	L	165	ASP
1	L	169	LYS
1	L	179	LEU
1	L	184	ASP
1	L	191	SER
1	L	199	LYS
1	L	200	THR
1	L	203	SER
1	L	205	ILE
1	L	208	SER
1	L	212	ASN
1	L	214	CYS
2	H	1	GLU

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Mol	Chain	Res	Type
2	H	4	LEU
2	H	7	SER
2	H	10	GLU
2	H	11	LEU
2	H	30	THR
2	H	40	ARG
2	H	41	PRO
2	H	45	LEU
2	H	57	TYR
2	H	61	ASN
2	H	62	GLU
2	H	99	SER
2	H	100	GLU
2	H	115	THR
2	H	140	THR
2	H	144	VAL
2	H	151	LYS
2	H	157	PRO
2	H	161	THR
2	H	168	SER
2	H	191	VAL
2	H	194	SER
2	H	195	PRO
2	H	196	ARG
2	H	213	LYS
2	H	221	ARG
2	H	222	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	34	ASN
1	L	90	GLN
1	L	161	ASN
1	L	212	ASN
2	H	35	ASN
2	H	61	ASN

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.