



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:56 PM GMT

PDB ID : 1DBJ
Title : MOLECULAR BASIS OF CROSS-REACTIVITY AND THE LIMITS OF
ANTIBODY-ANTIGEN COMPLEMENTARITY
Authors : Arevalo, J.H.; Wilson, I.A.
Deposited on : 1993-08-24
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 ⓘ 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 (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

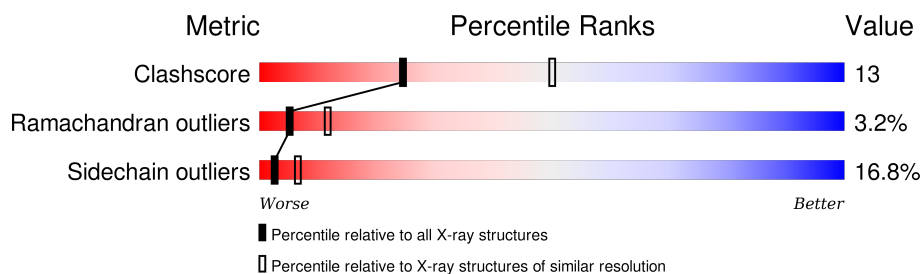
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (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 $\leq 5\%$. 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	216	
2	H	219	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3376 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 DB3 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	216	Total	C	N	O	S	0	0	0
			1679	1051	286	335	7			

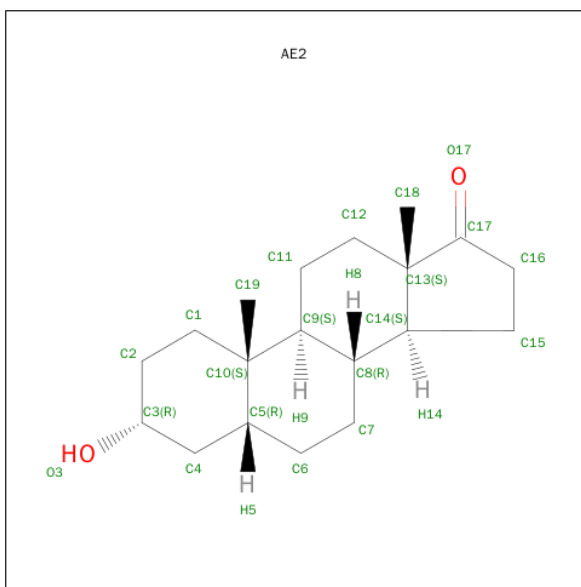
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	2	VAL	ILE	CONFLICT	GB 1589925
L	7	ILE	SER	CONFLICT	GB 1589925
L	14	ASN	SER	CONFLICT	GB 1589925
L	27B	LEU	VAL	CONFLICT	GB 1589925
L	27C	ILE	VAL	CONFLICT	GB 1589925
L	34	HIS	GLU	CONFLICT	GB 1589925
L	36	TYR	PHE	CONFLICT	GB 1589925
L	48	MET	ILE	CONFLICT	GB 1589925
L	56	TYR	SER	CONFLICT	GB 1589925
L	85	ILE	VAL	CONFLICT	GB 1589925
L	87	PHE	TYR	CONFLICT	GB 1589925
L	89	SER	PHE	CONFLICT	GB 1589925
L	91	SER	ALA	CONFLICT	GB 1589925
L	96	PRO	TRP	CONFLICT	GB 1589925

- Molecule 2 is a protein called IGG1-KAPPA DB3 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	0	0
			1675	1071	270	328	6			

- Molecule 3 is AETIOCHOLANOLONE (three-letter code: AE2) (formula: C₁₉H₃₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			21	19	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total	O	0	0
			1	1		

3 Residue-property plots

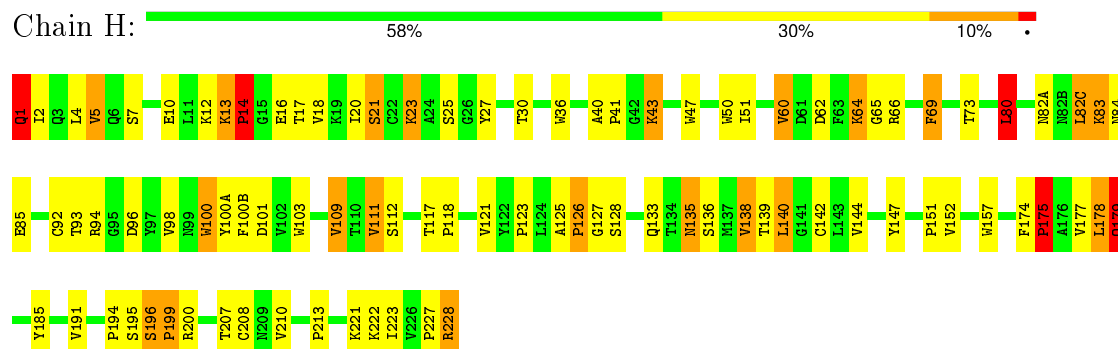
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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 DB3 FAB (LIGHT CHAIN)



• Molecule 2: IGG1-KAPPA DB3 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 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	134.76Å 134.76Å 124.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.214 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3376	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: AE2

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	1.00	0/1719	1.77	25/2331 (1.1%)
2	H	1.13	3/1723 (0.2%)	1.91	50/2358 (2.1%)
All	All	1.07	3/3442 (0.1%)	1.84	75/4689 (1.6%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	195	SER	CA-CB	-6.31	1.43	1.52
2	H	157	TRP	CG-CD2	-5.52	1.34	1.43
2	H	196	SER	CA-CB	-5.25	1.45	1.52

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	94	ARG	NE-CZ-NH1	11.04	125.82	120.30
2	H	80	LEU	CA-CB-CG	10.03	138.37	115.30
2	H	227	PRO	CA-C-N	-9.07	97.24	117.20
1	L	163	TRP	CD1-CG-CD2	9.01	113.50	106.30
1	L	211	ARG	NE-CZ-NH2	-8.95	115.83	120.30
2	H	66	ARG	NE-CZ-NH2	-8.93	115.84	120.30
2	H	200	ARG	NE-CZ-NH1	8.87	124.73	120.30
2	H	36	TRP	CD1-CG-CD2	8.85	113.38	106.30
1	L	211	ARG	NE-CZ-NH1	8.65	124.63	120.30
1	L	35	TRP	CD1-CG-CD2	8.55	113.14	106.30
1	L	160	LEU	CA-CB-CG	8.53	134.91	115.30
1	L	163	TRP	CE2-CD2-CG	-8.09	100.83	107.30
2	H	94	ARG	NE-CZ-NH2	-8.09	116.26	120.30
1	L	48	MET	CA-CB-CG	8.08	127.03	113.30
2	H	36	TRP	CE2-CD2-CG	-8.05	100.86	107.30
2	H	50	TRP	CD1-CG-CD2	7.88	112.60	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	148	TRP	CD1-CG-CD2	7.66	112.43	106.30
2	H	228	ARG	N-CA-C	-7.45	90.89	111.00
2	H	103	TRP	CD1-CG-CD2	7.34	112.17	106.30
2	H	47	TRP	CD1-CG-CD2	7.23	112.08	106.30
1	L	148	TRP	CE2-CD2-CG	-7.13	101.60	107.30
2	H	157	TRP	CD1-CG-CD2	6.95	111.86	106.30
2	H	66	ARG	NE-CZ-NH1	6.87	123.73	120.30
1	L	163	TRP	CG-CD2-CE3	6.85	140.07	133.90
2	H	98	VAL	CG1-CB-CG2	-6.75	100.10	110.90
1	L	163	TRP	CB-CG-CD1	-6.69	118.30	127.00
2	H	157	TRP	CE2-CD2-CG	-6.67	101.96	107.30
2	H	103	TRP	CE2-CD2-CG	-6.65	101.98	107.30
2	H	50	TRP	CE2-CD2-CG	-6.60	102.02	107.30
2	H	179	GLN	N-CA-CB	-6.49	98.92	110.60
1	L	35	TRP	CE2-CD2-CG	-6.48	102.11	107.30
2	H	138	VAL	CA-CB-CG1	-6.48	101.18	110.90
1	L	86	TYR	CB-CG-CD2	-6.38	117.17	121.00
2	H	27	TYR	CB-CG-CD1	-6.35	117.19	121.00
2	H	147	TYR	CB-CG-CD2	-6.32	117.21	121.00
2	H	100	TRP	CD1-CG-CD2	6.30	111.34	106.30
2	H	83	LYS	O-C-N	-6.25	112.70	122.70
2	H	177	VAL	CA-CB-CG2	-6.11	101.74	110.90
2	H	100	TRP	CE2-CD2-CG	-6.08	102.44	107.30
2	H	103	TRP	CG-CD2-CE3	6.08	139.37	133.90
2	H	60	VAL	CG1-CB-CG2	-6.01	101.28	110.90
2	H	100	TRP	CG-CD2-CE3	6.00	139.31	133.90
2	H	4	LEU	N-CA-C	-5.85	95.19	111.00
1	L	35	TRP	CG-CD1-NE1	-5.81	104.29	110.10
2	H	199	PRO	N-CD-CG	5.76	111.85	103.20
1	L	9	LEU	CA-CB-CG	5.74	128.50	115.30
1	L	154	GLU	OE1-CD-OE2	5.74	130.19	123.30
2	H	111	VAL	CG1-CB-CG2	-5.73	101.73	110.90
2	H	47	TRP	CG-CD1-NE1	-5.70	104.40	110.10
1	L	45	LYS	CA-CB-CG	5.68	125.90	113.40
2	H	47	TRP	CG-CD2-CE3	5.68	139.01	133.90
1	L	77	ARG	N-CA-C	-5.67	95.68	111.00
2	H	177	VAL	CA-CB-CG1	5.67	119.41	110.90
1	L	49	TYR	CB-CG-CD1	-5.64	117.61	121.00
2	H	100(A)	TYR	CB-CG-CD2	-5.63	117.62	121.00
1	L	23	CYS	CA-CB-SG	5.59	124.07	114.00
2	H	1	GLN	N-CA-C	-5.58	95.95	111.00
2	H	47	TRP	CE2-CD2-CG	-5.54	102.87	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	47	TRP	CB-CG-CD1	-5.53	119.81	127.00
1	L	35	TRP	CD2-CE2-CZ2	-5.41	115.80	122.30
2	H	101	ASP	N-CA-C	5.39	125.54	111.00
1	L	163	TRP	CG-CD1-NE1	-5.35	104.75	110.10
1	L	58	VAL	CA-CB-CG2	-5.34	102.89	110.90
2	H	96	ASP	N-CA-CB	-5.27	101.11	110.60
2	H	100	TRP	N-CA-C	5.26	125.20	111.00
2	H	83	LYS	N-CA-CB	-5.22	101.20	110.60
1	L	8	PRO	O-C-N	-5.18	114.42	122.70
2	H	208	CYS	CA-CB-SG	-5.15	104.73	114.00
2	H	36	TRP	CG-CD1-NE1	-5.13	104.97	110.10
2	H	36	TRP	CG-CD2-CE3	5.12	138.51	133.90
2	H	50	TRP	CG-CD2-CE3	5.11	138.50	133.90
2	H	69	PHE	CB-CG-CD2	-5.09	117.23	120.80
2	H	199	PRO	CA-N-CD	-5.08	104.39	111.50
2	H	175	PRO	O-C-N	5.06	130.80	122.70
1	L	35	TRP	CA-CB-CG	5.05	123.29	113.70

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	L	1679	0	1625	43	0
2	H	1675	0	1633	44	0
3	H	21	0	30	0	0
4	H	1	0	0	0	0
All	All	3376	0	3288	86	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 13.

All (86) 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:194:PRO:O	2:H:199:PRO:HD2	1.56	1.03
1:L:14:ASN:OD1	1:L:107:LYS:HD3	1.94	0.68
2:H:83:LYS:HZ3	2:H:85:GLU:HB3	1.59	0.68
2:H:93:THR:HG21	2:H:100(B):PHE:HB3	1.77	0.67
1:L:113:PRO:HG3	1:L:144:ILE:HD11	1.77	0.66
1:L:133:VAL:HG13	1:L:178:THR:HG22	1.78	0.66
2:H:51:ILE:HD11	2:H:69:PHE:HB3	1.77	0.65
2:H:93:THR:CG2	2:H:100(B):PHE:HB3	2.26	0.64
1:L:108:ARG:HG2	1:L:171:SER:HB2	1.80	0.64
2:H:12:LYS:O	2:H:111:VAL:HA	2.00	0.61
1:L:61:ARG:HB2	1:L:76:SER:HB2	1.83	0.60
1:L:193:THR:HB	1:L:208:SER:OG	2.03	0.58
1:L:155:ARG:HH21	1:L:185:GLU:HG2	1.67	0.58
2:H:83:LYS:HD3	2:H:85:GLU:H	1.68	0.58
2:H:194:PRO:O	2:H:199:PRO:CD	2.42	0.57
2:H:40:ALA:HB3	2:H:43:LYS:HB2	1.87	0.57
2:H:83:LYS:NZ	2:H:85:GLU:HB3	2.20	0.56
1:L:151:ASP:HA	1:L:191:SER:OG	2.07	0.55
2:H:18:VAL:HG12	2:H:82(C):LEU:HD21	1.88	0.55
1:L:108:ARG:HH12	1:L:111:ALA:HB2	1.72	0.55
2:H:207:THR:HG23	2:H:222:LYS:HD3	1.89	0.55
1:L:6:GLN:NE2	1:L:101:GLY:H	2.04	0.55
2:H:5:VAL:HG13	2:H:23:LYS:HB2	1.89	0.54
2:H:14:PRO:HD3	2:H:111:VAL:HG12	1.90	0.54
1:L:27(B):LEU:HD11	1:L:90:GLN:HG3	1.90	0.54
1:L:8:PRO:O	1:L:102:THR:HB	2.08	0.54
1:L:50:LYS:HB2	1:L:53:ASN:HD22	1.73	0.52
2:H:178:LEU:HA	2:H:185:TYR:HA	1.92	0.52
1:L:47:LEU:HA	1:L:58:VAL:HG21	1.92	0.52
2:H:5:VAL:HG22	2:H:23:LYS:HD2	1.92	0.51
1:L:108:ARG:HD3	1:L:109:ALA:O	2.10	0.51
2:H:21:SER:HB2	2:H:23:LYS:HZ2	1.75	0.51
2:H:13:LYS:O	2:H:16:GLU:HG3	2.11	0.50
1:L:117:ILE:HD13	1:L:194:CYS:HB3	1.93	0.50
1:L:182:THR:HG23	1:L:185:GLU:H	1.77	0.50
2:H:13:LYS:HE3	2:H:13:LYS:N	2.27	0.49
2:H:140:LEU:HG	2:H:223:ILE:HG21	1.93	0.49
2:H:14:PRO:HG3	2:H:84:ASN:OD1	2.13	0.49
1:L:120:PRO:HG2	1:L:130:ALA:HB1	1.94	0.49
1:L:6:GLN:CD	1:L:88:CYS:SG	2.91	0.49
2:H:21:SER:HB2	2:H:23:LYS:NZ	2.28	0.49
2:H:17:THR:OG1	2:H:82(A):ASN:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:144:ILE:HD12	1:L:198:HIS:HB2	1.95	0.48
1:L:21:ILE:HG23	1:L:102:THR:HG21	1.94	0.48
2:H:64:LYS:HD2	2:H:65:GLY:H	1.79	0.48
1:L:115:VAL:HG22	1:L:207:LYS:HZ2	1.79	0.48
2:H:151:PRO:O	2:H:213:PRO:HD2	2.15	0.47
1:L:7:ILE:HG22	1:L:8:PRO:HA	1.97	0.47
1:L:143:ASP:O	1:L:198:HIS:HD2	1.98	0.47
2:H:83:LYS:HD3	2:H:84:ASN:N	2.30	0.47
2:H:179:GLN:HB3	2:H:179:GLN:HE21	1.62	0.47
2:H:69:PHE:CE1	2:H:80:LEU:HD23	2.50	0.46
1:L:161:ASN:HB2	1:L:163:TRP:CH2	2.50	0.46
2:H:139:THR:HA	2:H:191:VAL:O	2.15	0.46
1:L:7:ILE:CG2	1:L:8:PRO:HA	2.46	0.46
2:H:41:PRO:O	2:H:43:LYS:HD2	2.17	0.45
1:L:189:HIS:HB2	1:L:192:TYR:OH	2.17	0.45
2:H:60:VAL:HG12	2:H:62:ASP:H	1.82	0.44
1:L:37:LEU:HD21	1:L:39:LYS:HE3	1.99	0.44
1:L:58:VAL:HA	1:L:59:PRO:HD3	1.75	0.44
1:L:145:ASN:O	1:L:196:ALA:HA	2.18	0.44
1:L:135:PHE:HD1	1:L:176:SER:HB3	1.83	0.44
2:H:20:ILE:HD12	2:H:80:LEU:HD12	1.99	0.44
1:L:18:GLN:OE1	1:L:74:LYS:HE2	2.17	0.44
1:L:117:ILE:O	1:L:117:ILE:HG23	2.19	0.43
2:H:83:LYS:HD2	2:H:85:GLU:HG2	2.00	0.43
2:H:13:LYS:HA	2:H:112:SER:O	2.19	0.43
1:L:48:MET:SD	1:L:54:ARG:HG2	2.57	0.43
1:L:54:ARG:HH11	1:L:54:ARG:HD2	1.69	0.43
1:L:27(D):HIS:ND1	1:L:28:ASN:OD1	2.51	0.43
2:H:5:VAL:O	2:H:23:LYS:HD2	2.18	0.43
2:H:126:PRO:O	2:H:128:SER:N	2.52	0.42
1:L:3:VAL:HB	1:L:26:SER:HB3	2.02	0.42
2:H:194:PRO:C	2:H:199:PRO:HD2	2.34	0.42
2:H:117:THR:HA	2:H:118:PRO:HD2	1.82	0.42
2:H:1:GLN:OE1	2:H:1:GLN:N	2.47	0.41
1:L:6:GLN:CG	1:L:88:CYS:SG	3.08	0.41
1:L:170:ASP:O	1:L:172:THR:HG23	2.21	0.41
1:L:13:VAL:HG11	1:L:78:VAL:HG21	2.03	0.41
1:L:33:LEU:HD22	1:L:89:SER:O	2.20	0.41
1:L:146:VAL:HG11	1:L:161:ASN:ND2	2.36	0.41
2:H:10:GLU:HB2	2:H:109:VAL:HG13	2.03	0.41
1:L:164:THR:HG23	2:H:174:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:121:VAL:HG12	2:H:221:LYS:HG3	2.03	0.40
2:H:83:LYS:HD2	2:H:85:GLU:OE2	2.21	0.40
2:H:125:ALA:O	2:H:228:ARG:NH1	2.55	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	L	214/216 (99%)	191 (89%)	16 (8%)	7 (3%)	5	11
2	H	217/219 (99%)	188 (87%)	22 (10%)	7 (3%)	5	12
All	All	431/435 (99%)	379 (88%)	38 (9%)	14 (3%)	5	12

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	127	GLY
1	L	27(E)	SER
1	L	28	ASN
1	L	153	SER
1	L	171	SER
2	H	14	PRO
2	H	136	SER
1	L	17	ASP
1	L	68	GLY
2	H	7	SER
2	H	100	TRP
2	H	135	ASN
2	H	175	PRO
1	L	51	VAL

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	194/194 (100%)	160 (82%)	34 (18%)	2	6
2	H	188/188 (100%)	158 (84%)	30 (16%)	3	8
All	All	382/382 (100%)	318 (83%)	64 (17%)	2	6

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

Mol	Chain	Res	Type
1	L	1	ASP
1	L	9	LEU
1	L	13	VAL
1	L	14	ASN
1	L	15	LEU
1	L	18	GLN
1	L	24	ARG
1	L	27(E)	SER
1	L	31	THR
1	L	46	LEU
1	L	52	SER
1	L	78	VAL
1	L	81	GLU
1	L	90	GLN
1	L	95	PRO
1	L	102	THR
1	L	108	ARG
1	L	120	PRO
1	L	125	LEU
1	L	145	ASN
1	L	156	GLN
1	L	157	ASN
1	L	160	LEU
1	L	168	SER
1	L	175	MET
1	L	177	SER
1	L	184	ASP

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Mol	Chain	Res	Type
1	L	190	ASN
1	L	193	THR
1	L	194	CYS
1	L	203	SER
1	L	206	VAL
1	L	207	LYS
1	L	210	ASN
2	H	1	GLN
2	H	2	ILE
2	H	5	VAL
2	H	13	LYS
2	H	14	PRO
2	H	21	SER
2	H	23	LYS
2	H	25	SER
2	H	30	THR
2	H	43	LYS
2	H	64	LYS
2	H	73	THR
2	H	80	LEU
2	H	82(C)	LEU
2	H	92	CYS
2	H	109	VAL
2	H	123	PRO
2	H	126	PRO
2	H	133	GLN
2	H	135	ASN
2	H	138	VAL
2	H	140	LEU
2	H	142	CYS
2	H	144	VAL
2	H	152	VAL
2	H	175	PRO
2	H	178	LEU
2	H	179	GLN
2	H	196	SER
2	H	210	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	6	GLN

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Mol	Chain	Res	Type
1	L	34	HIS
1	L	53	ASN
1	L	161	ASN
2	H	82(A)	ASN
2	H	135	ASN
2	H	179	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
3	AE2	H	229	-	24,24,24	1.21	4 (16%)	39,39,39	1.64	10 (25%)

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
3	AE2	H	229	-	-	0/0/58/58	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	229	AE2	C13-C17	-2.32	1.49	1.52
3	H	229	AE2	C11-C9	-2.21	1.49	1.53
3	H	229	AE2	C12-C13	-2.06	1.50	1.54
3	H	229	AE2	C4-C3	2.74	1.57	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	229	AE2	C19-C10-C1	-3.63	102.10	108.20
3	H	229	AE2	C5-C4-C3	-3.32	107.98	112.91
3	H	229	AE2	C4-C5-C10	-2.48	109.92	112.66
3	H	229	AE2	C13-C14-C8	-2.13	110.83	113.12
3	H	229	AE2	C10-C9-C8	-2.11	110.04	112.40
3	H	229	AE2	C12-C13-C17	-2.08	113.06	116.60
3	H	229	AE2	C4-C5-C6	-2.02	107.88	111.66
3	H	229	AE2	C18-C13-C14	2.05	116.27	112.94
3	H	229	AE2	C19-C10-C9	2.58	115.05	111.18
3	H	229	AE2	C15-C14-C8	5.10	127.08	119.03

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 ⓘ

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 ⓘ

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

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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