



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:40 PM UTC

PDB ID : 4D9R / pdb_00004d9r
Title : Inhibiting Alternative Pathway Complement Activation by Targeting the Exosite on Factor D
Authors : Murray, J.M.; Wiesmann, C.
Deposited on : 2012-01-11
Resolution : 2.42 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

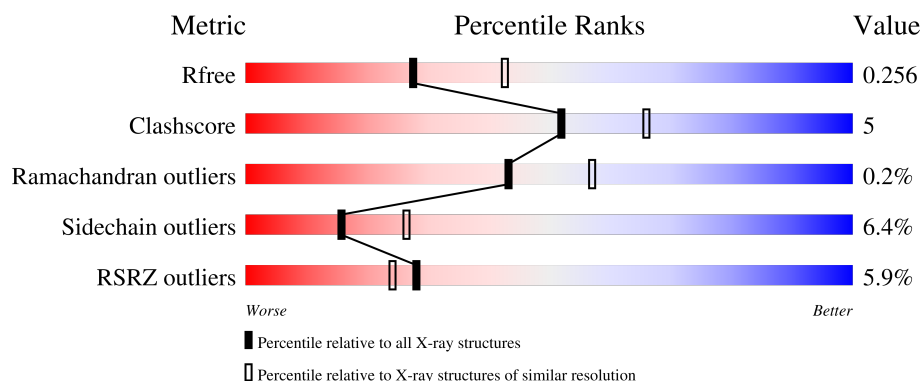
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	228	27% 87% 11% .
1	B	228	27% 85% 14% .
2	D	214	% 82% 16% .
2	L	214	% 82% 15% ..
3	E	218	% 86% 11% ..

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Mol	Chain	Length	Quality of chain
3	H	218	4% 81% 17%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10296 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 Complement factor D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	3	0
			1721	1063	327	321	10			
1	B	228	Total	C	N	O	S	0	3	0
			1721	1063	327	321	10			

- Molecule 2 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1630	1014	271	339	6			
2	D	213	Total	C	N	O	S	0	0	0
			1624	1011	270	338	5			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	105	GLU	-	linker	UNP P01834
L	106	ILE	-	linker	UNP P01834
L	107	LYS	-	linker	UNP P01834
L	108	ARG	-	linker	UNP P01834
D	105	GLU	-	linker	UNP P01834
D	106	ILE	-	linker	UNP P01834
D	107	LYS	-	linker	UNP P01834
D	108	ARG	-	linker	UNP P01834

- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	218	Total	C	N	O	S	19	0	0
			1631	1030	267	327	7			
3	E	216	Total	C	N	O	S	0	0	0
			1618	1024	265	323	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	117	VAL	-	linker	UNP P01857
H	118	THR	-	linker	UNP P01857
H	119	VAL	-	linker	UNP P01857
H	120	SER	-	linker	UNP P01857
H	121	SER	-	linker	UNP P01857
E	117	VAL	-	linker	UNP P01857
E	118	THR	-	linker	UNP P01857
E	119	VAL	-	linker	UNP P01857
E	120	SER	-	linker	UNP P01857
E	121	SER	-	linker	UNP P01857

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	2	Total Cl 2 2	0	0

- Molecule 5 is water.

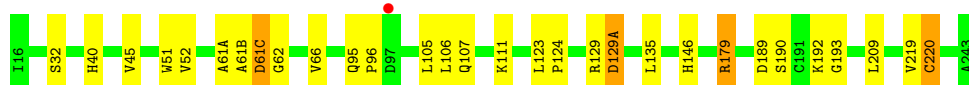
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	75	Total O 75 75	0	0
5	L	63	Total O 63 63	0	0
5	H	75	Total O 75 75	0	0
5	B	16	Total O 16 16	0	0
5	E	60	Total O 60 60	0	0
5	D	60	Total O 60 60	0	0

3 Residue-property plots

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.

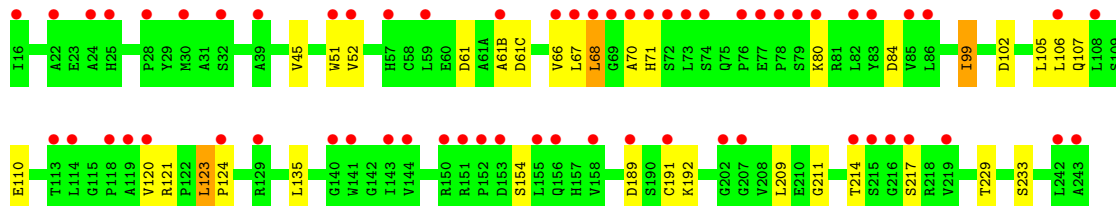
• Molecule 1: Complement factor D

Chain A: 



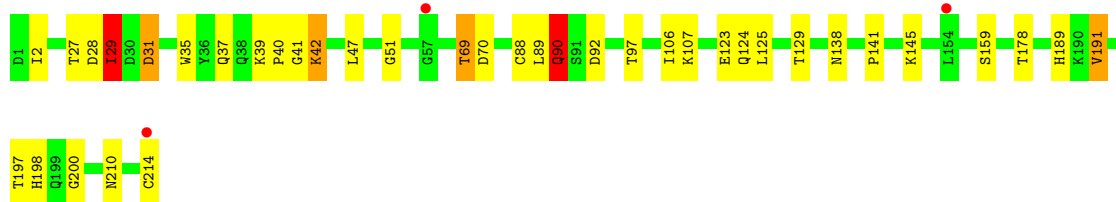
• Molecule 1: Complement factor D

Chain B: 



• Molecule 2: Fab light chain

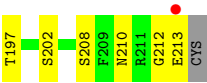
Chain L: 



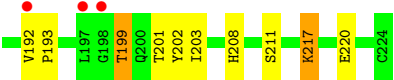
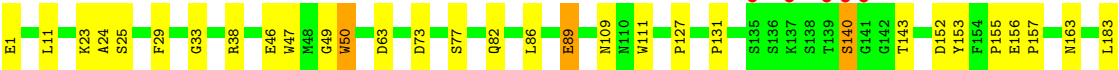
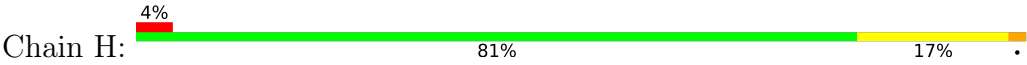
• Molecule 2: Fab light chain

Chain D: 

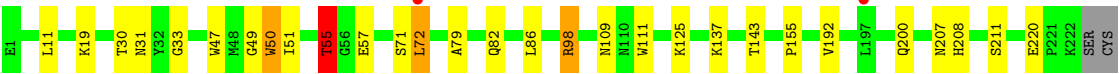
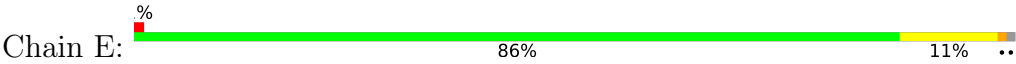




● Molecule 3: Fab heavy chain



● Molecule 3: Fab heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.05Å 132.05Å 180.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 2.42 19.84 – 2.42	Depositor EDS
% Data completeness (in resolution range)	98.7 (19.84-2.42) 98.4 (19.84-2.42)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.41Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.9.6, BUSTER 2.11.2	Depositor
R, R_{free}	0.213 , 0.251 0.215 , 0.256	Depositor DCC
R_{free} test set	3064 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	46.2	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10296	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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:
CL

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	0.85	0/1770	1.32	7/2408 (0.3%)
1	B	0.82	0/1770	1.26	5/2408 (0.2%)
2	D	0.81	0/1656	1.16	5/2252 (0.2%)
2	L	0.78	0/1662	1.18	4/2260 (0.2%)
3	E	0.81	1/1658 (0.1%)	1.17	4/2261 (0.2%)
3	H	0.78	0/1671	1.16	4/2277 (0.2%)
All	All	0.81	1/10187 (0.0%)	1.21	29/13866 (0.2%)

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
2	L	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	192	VAL	CA-C	5.05	1.56	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	GLY	N-CA-C	8.71	121.91	112.33
3	E	82	GLN	CB-CG-CD	6.75	124.08	112.60
1	B	189	ASP	CA-CB-CG	6.16	118.75	112.60
2	D	141	PRO	CA-C-N	6.12	128.48	120.28
2	D	141	PRO	C-N-CA	6.12	128.48	120.28
1	B	99	ILE	N-CA-C	-6.08	107.07	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	189	ASP	CA-CB-CG	6.04	118.64	112.60
2	L	90	GLN	CB-CG-CD	5.96	122.74	112.60
1	A	129(A)	ASP	CA-CB-CG	5.92	118.52	112.60
1	A	61(C)	ASP	CA-C-N	5.89	126.86	120.44
1	A	61(C)	ASP	C-N-CA	5.89	126.86	120.44
3	E	55	THR	N-CA-CB	-5.86	101.91	110.47
1	B	189	ASP	CA-C-N	5.86	129.19	120.87
1	B	189	ASP	C-N-CA	5.86	129.19	120.87
1	A	219	VAL	CA-C-N	-5.79	112.72	122.92
1	A	219	VAL	C-N-CA	-5.79	112.72	122.92
2	D	5	THR	CB-CA-C	5.61	119.10	110.62
3	H	73	ASP	CA-C-N	5.45	127.84	120.38
3	H	73	ASP	C-N-CA	5.45	127.84	120.38
3	E	31	ASN	CA-CB-CG	5.32	117.92	112.60
2	D	212	GLY	N-CA-C	5.28	125.70	113.18
2	L	29	ILE	N-CA-CB	-5.23	105.36	112.16
3	H	29	PHE	CA-CB-CG	5.21	119.01	113.80
2	L	191	VAL	N-CA-C	5.20	115.59	107.99
1	B	70	ALA	N-CA-C	5.20	117.72	109.50
3	E	207	ASN	OD1-CG-ND2	-5.16	117.44	122.60
2	D	191	VAL	N-CA-C	5.15	115.19	107.51
2	L	189	HIS	N-CA-C	5.10	118.01	110.46
3	H	1	GLU	CB-CG-CD	5.02	121.13	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	138	ASN	Sidechain

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	1721	0	1704	10	0
1	B	1721	0	1704	15	0
2	D	1624	0	1582	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	1630	0	1586	23	0
3	E	1618	0	1579	15	0
3	H	1631	0	1588	22	0
4	D	2	0	0	0	0
5	A	75	0	0	0	0
5	B	16	0	0	0	0
5	D	60	0	0	1	0
5	E	60	0	0	2	0
5	H	75	0	0	2	0
5	L	63	0	0	1	0
All	All	10296	0	9743	100	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 5.

All (100) 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:D:108:ARG:HH21	2:D:109:THR:HG22	1.07	1.16
3:H:156:GLU:HG3	3:H:157:PRO:HA	1.27	1.13
3:H:156:GLU:HG3	3:H:157:PRO:CA	1.98	0.94
2:D:108:ARG:NH2	2:D:109:THR:HG22	1.81	0.93
1:B:71:HIS:HE2	1:B:154:SER:HB2	1.39	0.85
1:B:71:HIS:NE2	1:B:154:SER:HB2	1.92	0.84
2:L:39:LYS:HB2	2:L:42:LYS:HG3	1.61	0.80
3:H:156:GLU:CG	3:H:157:PRO:HA	2.12	0.77
3:H:192:VAL:HG22	3:H:193:PRO:HD2	1.68	0.74
2:L:198:HIS:CD2	2:L:200:GLY:H	2.07	0.72
3:E:137:LYS:HE2	2:D:208:SER:O	1.94	0.68
3:E:109:ASN:HD21	3:E:111:TRP:HE1	1.41	0.66
2:L:29:ILE:HG13	2:L:92:ASP:HB2	1.77	0.66
2:D:161:GLU:HG3	5:D:405:HOH:O	1.95	0.66
1:B:71:HIS:CD2	1:B:154:SER:HB2	2.32	0.65
1:B:102:ASP:OD2	1:B:214:THR:HG23	1.95	0.65
3:H:109:ASN:HD21	3:H:111:TRP:HE1	1.43	0.64
1:A:52:VAL:HG21	1:A:66:VAL:HG11	1.80	0.64
2:L:198:HIS:HD2	2:L:200:GLY:H	1.46	0.63
1:A:40:HIS:HE1	1:A:193:GLY:O	1.83	0.62
3:E:55:THR:HG22	3:E:57:GLU:H	1.63	0.62
3:H:38:ARG:NH1	3:H:46:GLU:OE1	2.32	0.62
3:H:192:VAL:HG21	3:H:202:TYR:OH	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:LEU:HD12	1:A:124:PRO:HD2	1.85	0.58
1:B:102:ASP:HB3	1:B:214:THR:HG23	1.85	0.58
3:E:51:ILE:HD13	3:E:72:LEU:HD13	1.85	0.58
1:B:123:LEU:HD13	1:B:209:LEU:HB2	1.86	0.57
1:A:146:HIS:HE1	1:A:220:CYS:O	1.88	0.56
3:H:38:ARG:NH2	3:H:89:GLU:O	2.39	0.56
3:H:155:PRO:O	3:H:208:HIS:HE1	1.90	0.55
3:H:11:LEU:HB2	3:H:155:PRO:HG3	1.89	0.54
2:D:145:LYS:HB3	2:D:197:THR:HB	1.90	0.53
1:B:67:LEU:HD11	1:B:80:LYS:HG3	1.91	0.53
3:E:11:LEU:HB2	3:E:155:PRO:HG3	1.91	0.53
2:L:41:GLY:H	2:L:42:LYS:HE3	1.74	0.52
3:E:208:HIS:HD2	3:E:211:SER:OG	1.92	0.52
3:E:155:PRO:O	3:E:208:HIS:HE1	1.92	0.52
1:A:61(A):ALA:O	1:A:61(C):ASP:N	2.43	0.51
3:H:208:HIS:HD2	3:H:211:SER:OG	1.93	0.51
2:L:145:LYS:HB3	2:L:197:THR:HB	1.93	0.51
2:L:141:PRO:O	2:L:198:HIS:HE1	1.94	0.50
2:L:2:ILE:HD13	2:L:29:ILE:HD11	1.92	0.50
1:B:102:ASP:HB3	1:B:214:THR:CG2	2.42	0.50
3:E:72:LEU:HD12	3:E:79:ALA:HA	1.93	0.50
3:H:33:GLY:HA3	3:H:50:TRP:CZ3	2.47	0.49
3:E:33:GLY:HA3	3:E:50:TRP:CZ3	2.48	0.48
1:B:123:LEU:HD23	1:B:124:PRO:HD2	1.94	0.48
2:L:31:ASP:OD1	2:L:51:GLY:HA2	2.13	0.48
2:L:90:GLN:HE21	2:L:92:ASP:HB3	1.78	0.48
2:D:163:VAL:HG22	2:D:175:LEU:HD12	1.94	0.48
2:L:29:ILE:HG13	2:L:92:ASP:CB	2.43	0.48
2:D:108:ARG:HH21	2:D:109:THR:CG2	2.00	0.48
2:L:35:TRP:CZ3	2:L:88:CYS:HB3	2.49	0.47
2:D:40:PRO:HG3	2:D:165:GLU:HG3	1.97	0.47
1:A:32:SER:OG	1:A:40:HIS:HD2	1.98	0.46
3:H:140:SER:N	3:H:143:THR:O	2.38	0.46
1:B:51:TRP:CH2	1:B:107:GLN:HB2	2.51	0.45
2:D:35:TRP:CZ3	2:D:88:CYS:HB3	2.51	0.45
3:H:47:TRP:CZ3	3:H:49:GLY:HA2	2.52	0.45
2:L:159:SER:HA	2:L:178:THR:O	2.17	0.45
3:E:98:ARG:HD2	5:E:301:HOH:O	2.17	0.44
3:E:137:LYS:CE	2:D:208:SER:O	2.63	0.44
2:D:37:GLN:HB2	2:D:47:LEU:HD11	2.00	0.44
1:B:102:ASP:CB	1:B:214:THR:HG23	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:28:ASP:OD1	2:D:68:GLY:HA2	2.17	0.44
2:D:191:VAL:HG22	2:D:210:ASN:ND2	2.33	0.44
1:A:51:TRP:CH2	1:A:107:GLN:HB2	2.53	0.43
2:L:123:GLU:HB2	5:L:309:HOH:O	2.18	0.43
1:B:52:VAL:HG21	1:B:66:VAL:HG11	2.00	0.43
2:D:83:VAL:HG21	2:D:166:GLN:HB3	1.99	0.43
3:H:192:VAL:HG21	3:H:202:TYR:CZ	2.54	0.43
2:L:39:LYS:CB	2:L:42:LYS:HG3	2.39	0.43
1:B:68:LEU:HD22	1:B:120:VAL:HG13	2.00	0.43
3:E:47:TRP:CZ3	3:E:49:GLY:HA2	2.53	0.43
2:D:159:SER:HA	2:D:178:THR:O	2.19	0.43
3:H:152:ASP:HB3	3:H:183:LEU:HD13	2.01	0.43
2:L:191:VAL:HG22	2:L:210:ASN:ND2	2.34	0.42
1:B:71:HIS:CD2	1:B:154:SER:CB	3.02	0.42
1:B:211:GLY:HA2	1:B:229:THR:O	2.18	0.42
2:L:29:ILE:CG1	2:L:92:ASP:HB2	2.48	0.42
1:A:95:GLN:HB2	1:A:96:PRO:CD	2.50	0.42
2:L:31:ASP:CG	2:L:51:GLY:HA2	2.45	0.42
1:A:123:LEU:CD2	1:A:209:LEU:HB2	2.49	0.42
3:E:51:ILE:HG21	5:E:306:HOH:O	2.18	0.42
3:H:127:PRO:HB3	3:H:153:TYR:HB3	2.02	0.42
3:H:163:ASN:ND2	3:H:203:ILE:H	2.18	0.42
2:L:37:GLN:HB2	2:L:47:LEU:HD11	2.02	0.41
3:H:199:THR:HB	5:H:317:HOH:O	2.19	0.41
2:L:27:THR:HG22	2:L:28:ASP:N	2.35	0.41
2:L:2:ILE:HG21	2:L:29:ILE:HD11	2.02	0.41
3:H:24:ALA:O	3:H:77:SER:OG	2.38	0.41
3:H:131:PRO:HD3	3:H:217:LYS:HE2	2.02	0.41
3:E:109:ASN:HD21	3:E:111:TRP:NE1	2.14	0.41
1:A:179:ARG:H	1:A:179:ARG:HG2	1.82	0.41
2:D:35:TRP:CD2	2:D:73:LEU:HB2	2.55	0.41
2:L:69:THR:HG22	2:L:70:ASP:OD1	2.21	0.40
3:E:71:SER:O	3:E:72:LEU:CD1	2.69	0.40
2:D:116:PHE:HD2	2:D:135:LEU:HD23	1.86	0.40
2:L:124:GLN:HE21	2:L:129:THR:HG23	1.86	0.40
3:H:23:LYS:HD3	5:H:301:HOH:O	2.20	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	A	229/228 (100%)	219 (96%)	9 (4%)	1 (0%)	30	42
1	B	229/228 (100%)	222 (97%)	6 (3%)	1 (0%)	30	42
2	D	211/214 (99%)	203 (96%)	8 (4%)	0	100	100
2	L	212/214 (99%)	205 (97%)	6 (3%)	1 (0%)	24	35
3	E	214/218 (98%)	210 (98%)	4 (2%)	0	100	100
3	H	216/218 (99%)	209 (97%)	7 (3%)	0	100	100
All	All	1311/1320 (99%)	1268 (97%)	40 (3%)	3 (0%)	43	57

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61(B)	ALA
1	B	61(B)	ALA
2	L	40	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	A	185/182 (102%)	174 (94%)	11 (6%)	18	30
1	B	185/182 (102%)	168 (91%)	17 (9%)	8	13
2	D	190/191 (100%)	179 (94%)	11 (6%)	18	30
2	L	191/191 (100%)	180 (94%)	11 (6%)	18	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	182/184 (99%)	171 (94%)	11 (6%)	17	29
3	H	184/184 (100%)	173 (94%)	11 (6%)	17	29
All	All	1117/1114 (100%)	1045 (94%)	72 (6%)	16	26

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	VAL
1	A	105	LEU
1	A	106	LEU
1	A	111	LYS
1	A	129	ARG
1	A	129(A)	ASP
1	A	135	LEU
1	A	179	ARG
1	A	190	SER
1	A	192	LYS
1	A	220	CYS
2	L	29	ILE
2	L	31	ASP
2	L	42	LYS
2	L	69	THR
2	L	89	LEU
2	L	90	GLN
2	L	97	THR
2	L	106	ILE
2	L	107	LYS
2	L	125	LEU
2	L	214	CYS
3	H	25	SER
3	H	50	TRP
3	H	63	ASP
3	H	82	GLN
3	H	86	LEU
3	H	89	GLU
3	H	140	SER
3	H	199	THR
3	H	201	THR
3	H	217	LYS
3	H	220	GLU
1	B	45	VAL

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Mol	Chain	Res	Type
1	B	61	ASP
1	B	61(C)	ASP
1	B	68	LEU
1	B	84	ASP
1	B	99	ILE
1	B	105	LEU
1	B	106	LEU
1	B	110	GLU
1	B	121	ARG
1	B	123	LEU
1	B	135	LEU
1	B	191	CYS
1	B	192	LYS
1	B	217	SER
1	B	233[A]	SER
1	B	233[B]	SER
3	E	19	LYS
3	E	30	THR
3	E	50	TRP
3	E	55	THR
3	E	72	LEU
3	E	86	LEU
3	E	98	ARG
3	E	125	LYS
3	E	143	THR
3	E	200	GLN
3	E	220	GLU
2	D	89	LEU
2	D	90	GLN
2	D	97	THR
2	D	106	ILE
2	D	109	THR
2	D	125	LEU
2	D	154	LEU
2	D	165	GLU
2	D	188	LYS
2	D	202	SER
2	D	213	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	40	HIS
1	A	50	GLN
1	A	146	HIS
1	A	157	HIS
2	L	90	GLN
2	L	147	GLN
2	L	198	HIS
2	L	210	ASN
3	H	31	ASN
3	H	43	GLN
3	H	109	ASN
3	H	163	ASN
3	H	179	GLN
3	H	208	HIS
1	B	25	HIS
1	B	95	GLN
1	B	157	HIS
3	E	39	GLN
3	E	109	ASN
3	E	179	GLN
3	E	208	HIS
2	D	37	GLN
2	D	38	GLN
2	D	79	GLN
2	D	210	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	228/228 (100%)	-0.14	1 (0%) 88 87	23, 42, 69, 92	3 (1%)
1	B	228/228 (100%)	1.28	62 (27%) 1 1	35, 79, 126, 164	3 (1%)
2	D	213/214 (99%)	-0.09	2 (0%) 81 79	25, 46, 68, 119	0
2	L	214/214 (100%)	-0.09	3 (1%) 73 70	29, 43, 65, 84	0
3	E	216/218 (99%)	-0.09	2 (0%) 81 79	32, 46, 70, 99	0
3	H	215/218 (98%)	-0.11	8 (3%) 45 41	31, 41, 76, 109	0
All	All	1314/1320 (99%)	0.14	78 (5%) 28 24	23, 46, 97, 164	6 (0%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	139	THR	5.8
1	B	69	GLY	5.2
1	B	70	ALA	4.6
3	H	141	GLY	4.3
3	H	137	LYS	4.2
1	B	216	GLY	4.2
1	B	68	LEU	4.2
1	B	214	THR	4.1
1	B	77	GLU	4.0
1	B	202	GLY	3.8
1	B	67	LEU	3.6
1	B	215	SER	3.5
1	B	25	HIS	3.5
1	B	217	SER	3.4
1	B	71	HIS	3.4
1	B	79	SER	3.4
1	B	153	ASP	3.3
1	B	24	ALA	3.2
1	B	158	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	141	TRP	3.2
3	E	72	LEU	3.1
1	B	76	PRO	3.0
1	B	114	LEU	2.9
3	H	135	SER	2.8
1	B	16	ILE	2.8
1	B	61(B)	ALA	2.8
1	B	73	LEU	2.7
1	B	191	CYS	2.7
1	B	66	VAL	2.7
1	A	97	ASP	2.7
1	B	82	LEU	2.7
1	B	219	VAL	2.7
3	E	197	LEU	2.7
1	B	86	LEU	2.6
1	B	83	TYR	2.6
1	B	32	SER	2.6
1	B	113	THR	2.6
3	H	192	VAL	2.6
1	B	144	VAL	2.5
1	B	30	MET	2.5
2	D	1	ASP	2.5
1	B	155	LEU	2.4
3	H	197	LEU	2.4
1	B	129	ARG	2.4
1	B	39	ALA	2.4
1	B	243	ALA	2.4
1	B	150	ARG	2.4
1	B	108	LEU	2.4
1	B	156	GLN	2.3
1	B	78	PRO	2.3
1	B	51	TRP	2.3
1	B	242	LEU	2.3
1	B	85	VAL	2.3
1	B	28	PRO	2.3
1	B	152	PRO	2.3
1	B	140	GLY	2.2
2	D	213	GLU	2.2
1	B	59	LEU	2.2
1	B	106	LEU	2.2
1	B	189	ASP	2.2
1	B	124	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	72	SER	2.2
3	H	140	SER	2.2
1	B	151	ARG	2.2
1	B	118	PRO	2.2
3	H	198	GLY	2.1
2	L	57	GLY	2.1
1	B	143	ILE	2.1
1	B	52	VAL	2.1
1	B	22	ALA	2.1
1	B	119	ALA	2.1
1	B	74	SER	2.1
1	B	57[A]	HIS	2.1
2	L	154	LEU	2.1
2	L	214	CYS	2.1
1	B	120	VAL	2.0
1	B	80	LYS	2.0
1	B	207	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	CL	D	302	1/1	0.96	0.18	63,63,63,63	0
4	CL	D	301	1/1	0.99	0.03	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.