



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:28 AM UTC

PDB ID : 2QQL / pdb_00002qql
Title : Neuropilin-2 a1a2b1b2 Domains in Complex with a Semaphorin-Blocking Fab
Authors : Appleton, B.A.; Wiesmann, C.
Deposited on : 2007-07-26
Resolution : 3.10 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

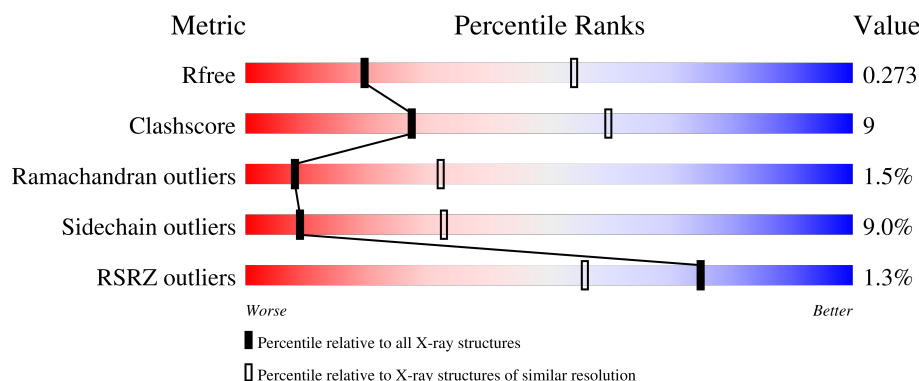
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	579	% 73% 20% ...
2	H	231	3% 73% 20% ..
3	L	214	% 72% 24% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7740 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 Neuropilin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	554	Total	C	N	O	S	0	0	0
			4416	2804	764	826	22			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	596	HIS	-	expression tag	UNP O60462
A	597	HIS	-	expression tag	UNP O60462
A	598	HIS	-	expression tag	UNP O60462
A	599	HIS	-	expression tag	UNP O60462
A	600	HIS	-	expression tag	UNP O60462
A	601	HIS	-	expression tag	UNP O60462

- Molecule 2 is a protein called Antibody Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	222	Total	C	N	O	S	0	0	0
			1682	1064	284	327	7			

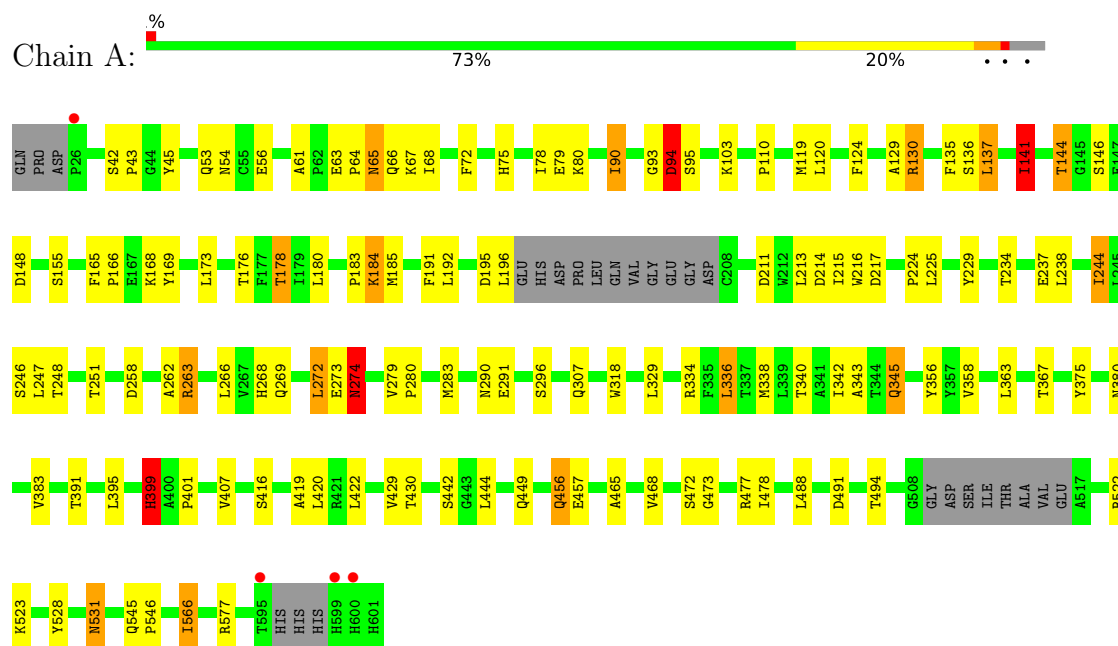
- Molecule 3 is a protein called Antibody Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1642	1031	272	333	6			

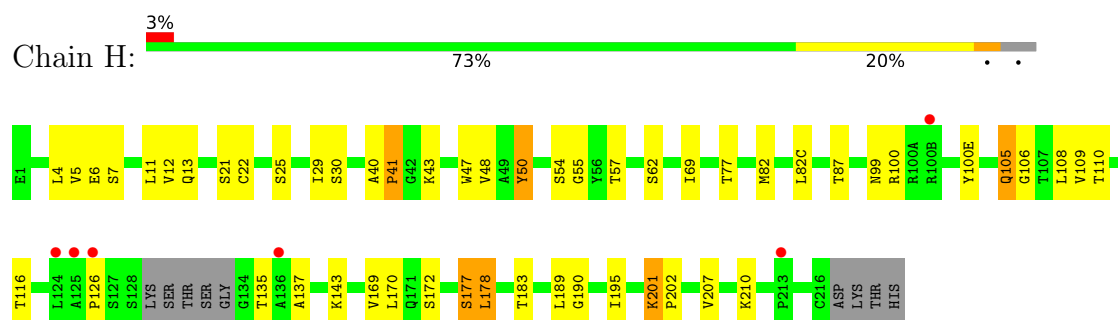
3 Residue-property plots

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.

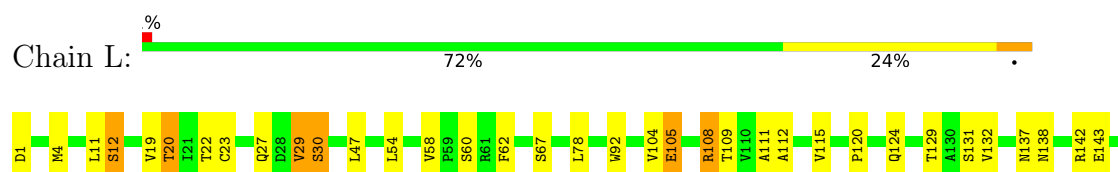
• Molecule 1: Neuropilin-2

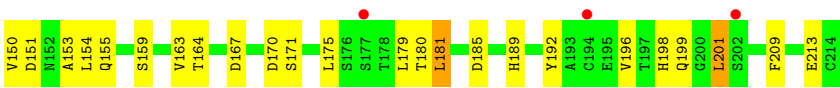


• Molecule 2: Antibody Heavy Chain



• Molecule 3: Antibody Light Chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	121.41Å 121.41Å 202.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.10 30.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-3.10) 99.5 (30.00-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 3.12Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.188 , 0.232 (Not available) , 0.273	Depositor DCC
R_{free} test set	1611 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	92.5	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 104.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7740	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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

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	0.65	1/4540 (0.0%)	0.84	3/6162 (0.0%)
2	H	0.63	0/1724	0.83	1/2349 (0.0%)
3	L	0.64	0/1679	0.82	0/2281
All	All	0.64	1/7943 (0.0%)	0.83	4/10792 (0.0%)

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	141	ILE	CA-CB	5.01	1.59	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	29	ILE	CB-CA-C	-6.35	103.46	112.22
1	A	478	ILE	N-CA-C	-5.51	102.10	107.55
1	A	42	SER	CA-C-N	5.47	126.68	119.84
1	A	42	SER	C-N-CA	5.47	126.68	119.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	PRO	Peptide

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	4416	0	4250	79	0
2	H	1682	0	1635	26	0
3	L	1642	0	1591	36	0
All	All	7740	0	7476	138	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 9.

All (138) 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)
1:A:180:LEU:HD23	1:A:244:ILE:HG22	1.57	0.86
1:A:244:ILE:HD12	1:A:444:LEU:HD11	1.62	0.80
2:H:137:ALA:HB2	2:H:183:THR:HG22	1.64	0.77
1:A:68:ILE:CG2	1:A:120:LEU:HD12	2.15	0.77
1:A:68:ILE:HG22	1:A:120:LEU:HD12	1.68	0.74
1:A:343:ALA:HB2	1:A:395:LEU:HD12	1.73	0.70
2:H:11:LEU:HD23	2:H:12:VAL:N	2.07	0.70
3:L:54:LEU:HD11	3:L:62:PHE:O	1.91	0.70
1:A:61:ALA:HB1	1:A:66:GLN:HE21	1.57	0.70
3:L:159:SER:HB3	3:L:179:LEU:HD12	1.73	0.69
1:A:244:ILE:HD13	1:A:244:ILE:N	2.07	0.69
2:H:50:TYR:C	2:H:69:ILE:HD13	2.18	0.69
1:A:274:ASN:C	1:A:274:ASN:HD22	1.99	0.68
1:A:90:ILE:N	1:A:90:ILE:HD12	2.08	0.68
1:A:456:GLN:HA	1:A:477:ARG:HA	1.77	0.67
1:A:528:TYR:CD2	1:A:566:ILE:HD12	2.30	0.66
1:A:215:ILE:HG12	1:A:247:LEU:HD22	1.78	0.65
1:A:290:ASN:HD22	1:A:307:GLN:CG	2.09	0.65
3:L:29:VAL:CG1	3:L:29:VAL:O	2.46	0.63
2:H:183:THR:HG21	3:L:137:ASN:HD22	1.63	0.63
1:A:367:THR:HB	1:A:468:VAL:HG22	1.81	0.62
3:L:108:ARG:NH1	3:L:111:ALA:HB2	2.15	0.62
1:A:90:ILE:HD12	1:A:90:ILE:H	1.64	0.60
1:A:180:LEU:CD2	1:A:244:ILE:HG22	2.30	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:ASN:HD22	1:A:307:GLN:HG3	1.65	0.60
2:H:178:LEU:C	2:H:178:LEU:HD12	2.28	0.59
2:H:189:LEU:HD13	2:H:190:GLY:N	2.18	0.58
3:L:112:ALA:HB1	3:L:201:LEU:CD1	2.34	0.58
1:A:336:LEU:CD1	1:A:468:VAL:HG21	2.34	0.57
3:L:30:SER:HB2	3:L:92:TRP:CZ3	2.39	0.57
2:H:99:ASN:C	2:H:100:ARG:HG3	2.29	0.57
3:L:29:VAL:O	3:L:29:VAL:HG13	2.05	0.57
3:L:120:PRO:HD3	3:L:132:VAL:HG22	1.86	0.56
1:A:279:VAL:HG13	1:A:280:PRO:HD2	1.87	0.56
2:H:12:VAL:HG11	2:H:82(C):LEU:HD13	1.88	0.56
3:L:4:MET:HE3	3:L:23:CYS:SG	2.46	0.55
3:L:115:VAL:HG21	3:L:196:VAL:HG21	1.88	0.55
1:A:93:GLY:O	1:A:119:MET:HB2	2.06	0.54
3:L:180:THR:O	3:L:181:LEU:HD12	2.07	0.54
2:H:143:LYS:HA	2:H:177:SER:HB2	1.90	0.54
1:A:336:LEU:HD11	1:A:468:VAL:HG21	1.91	0.53
3:L:150:VAL:HG13	3:L:192:TYR:CE2	2.43	0.53
2:H:22:CYS:O	2:H:77:THR:HG23	2.08	0.53
1:A:211:ASP:OD1	1:A:251:THR:HA	2.09	0.52
1:A:244:ILE:HD13	1:A:244:ILE:H	1.75	0.52
1:A:79:GLU:OE2	1:A:130:ARG:HB3	2.09	0.52
1:A:342:ILE:HD11	1:A:363:LEU:HD22	1.90	0.52
3:L:192:TYR:HB2	3:L:209:PHE:CE2	2.45	0.52
1:A:68:ILE:HG21	1:A:120:LEU:HD12	1.91	0.52
1:A:244:ILE:HD11	1:A:442:SER:CB	2.40	0.52
3:L:20:THR:O	3:L:20:THR:HG22	2.09	0.51
1:A:268:HIS:C	1:A:269:GLN:HE21	2.18	0.51
3:L:153:ALA:O	3:L:155:GLN:N	2.44	0.51
1:A:168:LYS:NZ	1:A:258:ASP:OD1	2.30	0.50
1:A:215:ILE:HD12	1:A:229:TYR:CE1	2.47	0.50
2:H:6:GLU:HA	2:H:21:SER:O	2.10	0.50
1:A:78:ILE:HD13	1:A:124:PHE:HE1	1.76	0.50
2:H:137:ALA:CB	2:H:183:THR:HG22	2.39	0.50
1:A:216:TRP:CH2	1:A:225:LEU:HD13	2.47	0.50
1:A:178:THR:HB	1:A:246:SER:HB3	1.93	0.50
1:A:272:LEU:N	1:A:272:LEU:HD23	2.27	0.49
1:A:185:MET:HE3	1:A:266:LEU:HB3	1.95	0.48
1:A:244:ILE:HD11	1:A:442:SER:HB2	1.95	0.48
1:A:528:TYR:CE2	1:A:566:ILE:HD12	2.48	0.48
2:H:4:LEU:HD22	2:H:22:CYS:SG	2.53	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:195:ILE:HG22	2:H:210:LYS:HA	1.95	0.48
1:A:215:ILE:HD12	1:A:229:TYR:HE1	1.78	0.48
1:A:531:ASN:HD22	1:A:531:ASN:N	2.12	0.48
2:H:105:GLN:NE2	2:H:106:GLY:O	2.47	0.48
3:L:163:VAL:HG22	3:L:175:LEU:HD12	1.96	0.48
1:A:356:TYR:HB2	1:A:419:ALA:HB2	1.94	0.47
1:A:75:HIS:CE1	2:H:100(E):TYR:CE2	3.02	0.47
3:L:115:VAL:CG2	3:L:196:VAL:HG21	2.44	0.47
2:H:40:ALA:O	2:H:41:PRO:C	2.58	0.47
2:H:87:THR:HG23	2:H:110:THR:HA	1.96	0.47
1:A:237:GLU:O	1:A:238:LEU:HD23	2.14	0.47
1:A:363:LEU:HD11	1:A:407:VAL:HG13	1.97	0.47
3:L:19:VAL:HG21	3:L:78:LEU:HD22	1.96	0.47
3:L:150:VAL:HG22	3:L:192:TYR:CD2	2.51	0.46
3:L:170:ASP:OD1	3:L:170:ASP:C	2.58	0.46
1:A:195:ASP:C	1:A:196:LEU:HD23	2.39	0.46
1:A:274:ASN:C	1:A:274:ASN:ND2	2.71	0.46
2:H:47:TRP:HZ2	2:H:50:TYR:CD2	2.33	0.46
1:A:215:ILE:HG12	1:A:247:LEU:CD2	2.45	0.46
1:A:283:MET:HE2	1:A:422:LEU:HD23	1.96	0.46
3:L:47:LEU:HA	3:L:58:VAL:HG21	1.98	0.46
1:A:375:TYR:HE2	1:A:399:HIS:CD2	2.34	0.45
1:A:137:LEU:CD2	1:A:137:LEU:C	2.90	0.45
1:A:180:LEU:HD23	1:A:244:ILE:CG2	2.39	0.45
2:H:47:TRP:CZ2	2:H:50:TYR:CD2	3.05	0.45
1:A:165:PHE:CG	1:A:166:PRO:HA	2.52	0.44
1:A:340:THR:HG22	1:A:401:PRO:HB3	1.98	0.44
1:A:192:LEU:HD22	1:A:263:ARG:NH2	2.33	0.44
1:A:345:GLN:NE2	1:A:391:THR:O	2.51	0.43
1:A:244:ILE:N	1:A:244:ILE:CD1	2.78	0.43
1:A:336:LEU:HD13	1:A:468:VAL:HG21	2.00	0.43
1:A:465:ALA:HB1	1:A:488:LEU:HD21	1.99	0.43
2:H:178:LEU:C	2:H:178:LEU:CD1	2.91	0.43
1:A:291:GLU:OE1	1:A:334:ARG:NH2	2.52	0.43
3:L:167:ASP:O	3:L:171:SER:HA	2.18	0.43
1:A:72:PHE:CG	1:A:110:PRO:HD2	2.53	0.43
1:A:545:GLN:O	1:A:546:PRO:C	2.60	0.43
3:L:12:SER:HA	3:L:105:GLU:O	2.18	0.43
2:H:195:ILE:HG22	2:H:210:LYS:CB	2.49	0.43
1:A:472:SER:OG	1:A:473:GLY:N	2.52	0.43
2:H:55:GLY:O	2:H:57:THR:HG23	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:GLN:HB3	1:A:491:ASP:O	2.19	0.43
1:A:180:LEU:CD2	1:A:244:ILE:CG2	2.97	0.42
1:A:217:ASP:HB3	1:A:224:PRO:HD2	2.01	0.42
3:L:124:GLN:HG2	3:L:129:THR:O	2.18	0.42
1:A:318:TRP:CG	1:A:329:LEU:HD13	2.54	0.42
1:A:358:VAL:HG23	1:A:419:ALA:O	2.19	0.42
3:L:54:LEU:HD21	3:L:60:SER:HA	2.02	0.42
1:A:246:SER:C	1:A:247:LEU:HD23	2.44	0.42
2:H:201:LYS:N	2:H:202:PRO:CD	2.82	0.42
3:L:181:LEU:HD23	3:L:185:ASP:CB	2.50	0.42
1:A:141:ILE:C	1:A:141:ILE:HD12	2.45	0.42
1:A:522:ARG:O	1:A:523:LYS:HG2	2.20	0.42
3:L:11:LEU:HD11	3:L:104:VAL:HG13	2.01	0.42
1:A:135:PHE:CD1	1:A:135:PHE:C	2.98	0.42
3:L:151:ASP:OD2	3:L:189:HIS:ND1	2.49	0.42
3:L:47:LEU:HD22	3:L:58:VAL:HG13	2.02	0.41
1:A:94:ASP:O	1:A:95:SER:CB	2.69	0.41
1:A:148:ASP:OD1	1:A:148:ASP:C	2.62	0.41
1:A:358:VAL:HG21	1:A:420:LEU:HD13	2.01	0.41
1:A:531:ASN:N	1:A:531:ASN:ND2	2.67	0.41
2:H:82:MET:HE1	2:H:109:VAL:HG21	2.03	0.41
3:L:124:GLN:HE22	3:L:131:SER:HB2	1.85	0.41
3:L:198:HIS:O	3:L:199:GLN:C	2.63	0.41
1:A:191:PHE:CD2	1:A:262:ALA:HB2	2.56	0.41
1:A:213:LEU:HD23	1:A:213:LEU:C	2.46	0.41
3:L:47:LEU:HD22	3:L:58:VAL:CG1	2.50	0.41
1:A:169:TYR:CD1	1:A:173:LEU:HD21	2.56	0.40
1:A:144:THR:CG2	1:A:146:SER:H	2.34	0.40
1:A:183:PRO:O	1:A:184:LYS:CB	2.70	0.40
2:H:183:THR:HG21	3:L:137:ASN:ND2	2.35	0.40
3:L:11:LEU:CD1	3:L:104:VAL:HG13	2.51	0.40
3:L:175:LEU:C	3:L:175:LEU:HD23	2.47	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	546/579 (94%)	495 (91%)	42 (8%)	9 (2%)	7	30
2	H	218/231 (94%)	204 (94%)	12 (6%)	2 (1%)	14	44
3	L	212/214 (99%)	193 (91%)	15 (7%)	4 (2%)	6	27
All	All	976/1024 (95%)	892 (91%)	69 (7%)	15 (2%)	8	32

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	130	ARG
1	A	399	HIS
3	L	154	LEU
1	A	94	ASP
1	A	129	ALA
1	A	274	ASN
2	H	126	PRO
3	L	67	SER
3	L	138	ASN
1	A	80	LYS
3	L	213	GLU
1	A	43	PRO
2	H	41	PRO
1	A	45	TYR

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	481/502 (96%)	440 (92%)	41 (8%)	10	35
2	H	185/193 (96%)	164 (89%)	21 (11%)	5	23
3	L	186/186 (100%)	171 (92%)	15 (8%)	11	36

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	852/881 (97%)	775 (91%)	77 (9%)	9 33

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	54	ASN
1	A	56	GLU
1	A	63	GLU
1	A	65	ASN
1	A	67	LYS
1	A	90	ILE
1	A	94	ASP
1	A	103	LYS
1	A	136	SER
1	A	137	LEU
1	A	141	ILE
1	A	144	THR
1	A	155	SER
1	A	176	THR
1	A	178	THR
1	A	184	LYS
1	A	214	ASP
1	A	234	THR
1	A	244	ILE
1	A	248	THR
1	A	263	ARG
1	A	272	LEU
1	A	273	GLU
1	A	274	ASN
1	A	296	SER
1	A	336	LEU
1	A	338	MET
1	A	345	GLN
1	A	380	ASN
1	A	383	VAL
1	A	399	HIS
1	A	416	SER
1	A	429	VAL
1	A	430	THR
1	A	456	GLN
1	A	457	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	494	THR
1	A	531	ASN
1	A	566	ILE
1	A	577	ARG
2	H	5	VAL
2	H	7	SER
2	H	13	GLN
2	H	25	SER
2	H	30	SER
2	H	43	LYS
2	H	48	VAL
2	H	50	TYR
2	H	54	SER
2	H	62	SER
2	H	105	GLN
2	H	108	LEU
2	H	116	THR
2	H	135	THR
2	H	169	VAL
2	H	170	LEU
2	H	172	SER
2	H	177	SER
2	H	178	LEU
2	H	201	LYS
2	H	207	VAL
3	L	1	ASP
3	L	12	SER
3	L	20	THR
3	L	22	THR
3	L	27	GLN
3	L	29	VAL
3	L	30	SER
3	L	105	GLU
3	L	108	ARG
3	L	109	THR
3	L	142	ARG
3	L	143	GLU
3	L	164	THR
3	L	181	LEU
3	L	201	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	65	ASN
1	A	66	GLN
1	A	131	GLN
1	A	268	HIS
1	A	269	GLN
1	A	274	ASN
1	A	290	ASN
1	A	312	HIS
1	A	321	ASN
1	A	387	ASN
1	A	399	HIS
1	A	531	ASN
2	H	99	ASN
2	H	105	GLN
2	H	155	ASN
2	H	192	GLN
3	L	3	GLN
3	L	124	GLN
3	L	138	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 ⓘ

There are no ligands in this entry.

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 [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	554/579 (95%)	0.05	4 (0%) 84 68	87, 110, 126, 169	0
2	H	222/231 (96%)	0.42	6 (2%) 56 35	99, 113, 123, 140	0
3	L	214/214 (100%)	0.21	3 (1%) 73 53	90, 112, 122, 134	0
All	All	990/1024 (96%)	0.17	13 (1%) 75 56	87, 111, 125, 169	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	194	CYS	3.1
1	A	595	THR	2.8
1	A	600	HIS	2.7
3	L	202	SER	2.6
2	H	136	ALA	2.4
2	H	125	ALA	2.4
3	L	177	SER	2.4
2	H	124	LEU	2.3
1	A	26	PRO	2.3
1	A	599	HIS	2.3
2	H	100(B)	ARG	2.1
2	H	213	PRO	2.1
2	H	126	PRO	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.