



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:32 PM UTC

PDB ID : 2P3F / pdb_00002p3f
Title : Crystal structure of the factor Xa/NAP5 complex
Authors : Rios-Steiner, J.L.; Murakami, M.T.; Tulinsky, A.; Arni, R.K.
Deposited on : 2007-03-08
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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

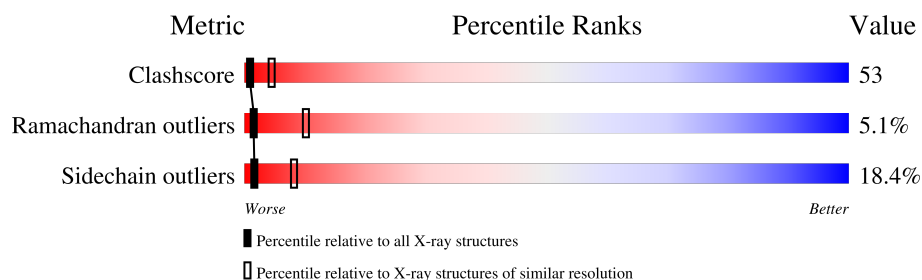
1 Overall quality at a glance

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))
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	H	235	
2	L	54	
3	N	78	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2876 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 Coagulation factor X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	235	Total	C	N	O	S	0	0	0
			1864	1172	327	351	14			

- Molecule 2 is a protein called Coagulation factor X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	51	Total	C	N	O	S	0	0	0
			376	225	64	80	7			

- Molecule 3 is a protein called Anti-coagulant protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	74	Total	C	N	O	S	0	0	0
			583	352	98	123	10			

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 5 is water.

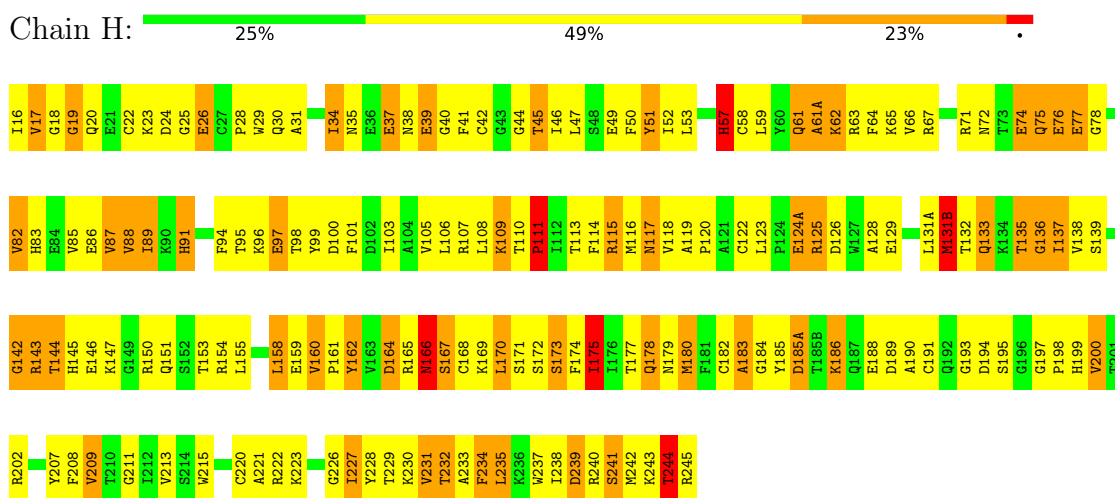
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	33	Total	O	0	0
			33	33		
5	L	9	Total	O	0	0
			9	9		
5	N	10	Total	O	0	0
			10	10		

3 Residue-property plots

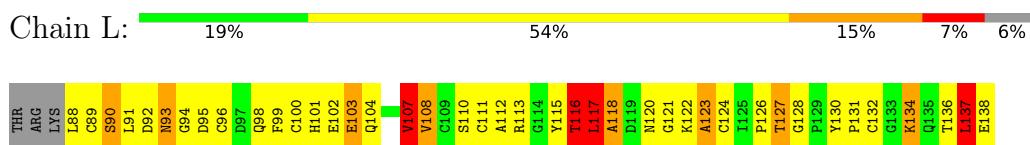
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

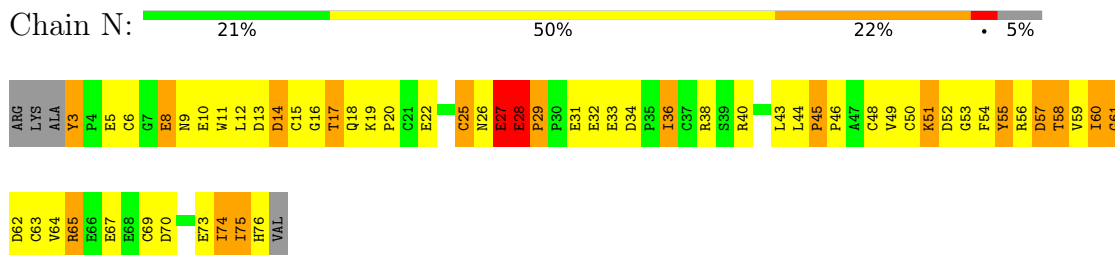
• Molecule 1: Coagulation factor X



• Molecule 2: Coagulation factor X



• Molecule 3: Anti-coagulant protein 5



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	137.17Å 137.17Å 167.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.180 , 0.280	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2876	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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: NA

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	H	1.41	9/1902 (0.5%)	1.65	41/2560 (1.6%)
2	L	1.41	2/382 (0.5%)	1.82	10/516 (1.9%)
3	N	1.31	2/596 (0.3%)	1.94	20/808 (2.5%)
All	All	1.39	13/2880 (0.5%)	1.74	71/3884 (1.8%)

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 (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	160	VAL	CA-CB	-7.15	1.49	1.54
1	H	52	ILE	CA-CB	-7.13	1.45	1.54
3	N	69	CYS	CA-C	6.13	1.60	1.53
1	H	119	ALA	CA-CB	-5.64	1.47	1.53
3	N	48	CYS	CA-C	-5.60	1.45	1.52
2	L	127	THR	N-CA	-5.57	1.40	1.46
1	H	200	VAL	CA-CB	-5.55	1.47	1.54
2	L	92	ASP	CA-C	-5.51	1.45	1.53
1	H	39	GLU	N-CA	-5.39	1.39	1.46
1	H	186	LYS	CA-C	-5.33	1.46	1.52
1	H	131(B)	MET	SD-CE	-5.12	1.66	1.79
1	H	183	ALA	CA-CB	-5.01	1.44	1.53
1	H	57	HIS	C-O	-5.00	1.17	1.24

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	28	GLU	CA-C-N	15.82	131.21	119.66
3	N	28	GLU	C-N-CA	15.82	131.21	119.66
2	L	127	THR	N-CA-C	-10.98	100.16	112.57
1	H	26	GLU	N-CA-C	10.90	122.73	111.07
2	L	93	ASN	N-CA-C	-10.80	100.05	113.23
1	H	133	GLN	N-CA-C	-10.36	95.57	110.59
3	N	59	VAL	N-CA-C	9.27	119.14	110.42
2	L	137	LEU	N-CA-C	-9.27	91.05	110.80
3	N	43	LEU	N-CA-C	9.20	124.57	113.16
1	H	234	PHE	N-CA-C	-8.70	98.98	112.99
3	N	60	ILE	N-CA-C	-8.69	94.85	107.98
1	H	74	GLU	N-CA-C	-8.39	103.04	113.20
3	N	59	VAL	CB-CA-C	-8.08	101.45	111.87
1	H	199	HIS	N-CA-C	-8.05	93.93	108.02
3	N	29	PRO	N-CA-C	7.99	118.14	110.47
3	N	70	ASP	N-CA-C	7.85	127.51	110.80
2	L	123	ALA	N-CA-C	7.81	122.46	110.36
1	H	51	TYR	N-CA-C	7.64	121.67	108.76
1	H	123	LEU	CA-C-N	-7.56	110.39	119.84
1	H	123	LEU	C-N-CA	-7.56	110.39	119.84
1	H	76	GLU	N-CA-C	-7.09	99.05	110.32
1	H	185(A)	ASP	N-CA-C	-6.93	103.34	111.03
1	H	173	SER	N-CA-C	-6.86	105.25	112.93
1	H	57	HIS	N-CA-C	6.82	121.05	112.87
3	N	58	THR	CA-C-N	6.73	128.94	120.72
3	N	58	THR	C-N-CA	6.73	128.94	120.72
1	H	160	VAL	CA-C-N	6.59	126.57	119.78
1	H	160	VAL	C-N-CA	6.59	126.57	119.78
1	H	142	GLY	N-CA-C	6.58	119.57	112.33
1	H	175	ILE	CB-CA-C	-6.44	101.09	111.59
2	L	91	LEU	N-CA-C	-6.41	101.10	111.04
1	H	175	ILE	N-CA-C	6.34	117.93	109.37
1	H	179	ASN	N-CA-C	-6.34	105.29	113.16
3	N	50	CYS	N-CA-C	6.25	119.29	110.23
2	L	107	VAL	N-CA-C	-6.03	101.80	109.58
3	N	65	ARG	N-CA-C	-5.97	102.79	110.19
2	L	111	CYS	N-CA-C	5.95	117.82	108.96
2	L	117	LEU	N-CA-C	5.92	118.29	109.59
1	H	124(A)	GLU	N-CA-C	-5.89	99.59	108.96
1	H	144	THR	N-CA-C	5.88	120.07	113.02
3	N	6	CYS	N-CA-C	5.87	118.28	110.53
1	H	19	GLY	N-CA-C	-5.85	99.33	113.18
1	H	34	ILE	N-CA-C	5.82	117.13	108.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	162	TYR	N-CA-C	-5.82	101.01	110.20
1	H	46	ILE	CB-CA-C	-5.78	104.99	111.23
1	H	182	CYS	N-CA-C	5.76	119.20	109.76
3	N	26	ASN	N-CA-C	-5.74	98.56	110.80
3	N	51	LYS	N-CA-C	-5.73	102.96	110.53
1	H	197	GLY	CA-C-N	-5.72	113.30	120.51
1	H	197	GLY	C-N-CA	-5.72	113.30	120.51
3	N	45	PRO	CA-C-N	5.72	126.05	119.93
3	N	45	PRO	C-N-CA	5.72	126.05	119.93
1	H	226	GLY	N-CA-C	-5.72	100.49	112.04
1	H	91	HIS	N-CA-C	-5.67	101.89	110.28
2	L	90	SER	N-CA-C	5.54	122.59	110.80
1	H	244	THR	N-CA-C	5.53	122.59	110.80
2	L	116	THR	N-CA-C	-5.52	99.60	108.55
1	H	109	LYS	N-CA-C	-5.49	104.93	111.03
1	H	226	GLY	CA-C-N	-5.48	115.50	123.06
1	H	226	GLY	C-N-CA	-5.48	115.50	123.06
1	H	136	GLY	CA-C-N	-5.31	116.37	123.17
1	H	136	GLY	C-N-CA	-5.31	116.37	123.17
1	H	166	ASN	N-CA-C	-5.31	105.49	111.28
3	N	61	GLY	CA-C-N	-5.31	113.87	122.36
3	N	61	GLY	C-N-CA	-5.31	113.87	122.36
1	H	75	GLN	N-CA-C	5.30	117.81	108.75
1	H	135	THR	N-CA-C	5.21	115.93	108.74
1	H	139	SER	N-CA-C	5.11	116.83	108.55
1	H	22	CYS	N-CA-C	-5.09	101.67	109.76
1	H	193	GLY	N-CA-C	-5.07	107.99	114.37
3	N	57	ASP	N-CA-C	-5.05	102.43	109.96

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	130	TYR	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	H	1864	0	1821	215	0
2	L	376	0	336	35	0
3	N	583	0	512	57	0
4	H	1	0	0	0	0
5	H	33	0	0	2	0
5	L	9	0	0	1	0
5	N	10	0	0	0	0
All	All	2876	0	2669	293	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 53.

All (293) 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:H:45:THR:HG23	1:H:198:PRO:HB3	1.40	1.00
1:H:98:THR:HG21	1:H:175:ILE:HD11	1.40	1.00
1:H:227:ILE:C	1:H:227:ILE:HD12	1.92	0.94
1:H:215:TRP:CD1	1:H:227:ILE:HD11	2.04	0.93
2:L:117:LEU:HD23	2:L:123:ALA:O	1.69	0.92
1:H:50:PHE:CZ	1:H:111:PRO:HB3	2.03	0.92
1:H:98:THR:CG2	1:H:175:ILE:HD11	2.05	0.87
3:N:64:VAL:HG23	3:N:65:ARG:O	1.76	0.86
1:H:215:TRP:CE2	1:H:227:ILE:HG12	2.11	0.85
1:H:215:TRP:NE1	1:H:227:ILE:HD11	1.91	0.84
1:H:143:ARG:HA	1:H:150:ARG:O	1.77	0.82
1:H:41:PHE:O	1:H:42:CYS:SG	2.37	0.82
1:H:86:GLU:C	1:H:87:VAL:HG12	2.05	0.82
1:H:86:GLU:HG2	1:H:87:VAL:HG12	1.61	0.81
1:H:230:LYS:HG2	1:H:232:THR:HG23	1.63	0.80
1:H:50:PHE:CE1	1:H:111:PRO:HB3	2.18	0.78
1:H:170:LEU:HD12	1:H:171:SER:N	1.97	0.78
1:H:180:MET:CE	1:H:215:TRP:HE1	1.98	0.76
1:H:35:ASN:ND2	1:H:39:GLU:HB2	2.03	0.74
1:H:45:THR:CG2	1:H:198:PRO:HB3	2.15	0.74
1:H:23:LYS:HB2	1:H:26:GLU:HG3	1.68	0.73
1:H:23:LYS:C	1:H:71:ARG:HH12	1.95	0.73
1:H:164:ASP:CG	1:H:167:SER:HB2	2.14	0.73
1:H:195:SER:HA	1:H:213:VAL:HG12	1.72	0.72
1:H:128:ALA:HA	1:H:131(A):LEU:HB2	1.72	0.72
3:N:3:TYR:CD2	3:N:12:LEU:HD21	2.24	0.71
1:H:113:THR:O	1:H:115:ARG:HG2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:ASN:HD21	1:H:74:GLU:HG2	1.56	0.71
1:H:238:ILE:O	1:H:242:MET:HG3	1.91	0.71
3:N:73:GLU:O	3:N:74:ILE:HD13	1.90	0.71
1:H:153:THR:HG23	1:H:154:ARG:HG2	1.72	0.70
1:H:165:ARG:HG2	1:H:169:LYS:HE2	1.73	0.70
3:N:13:ASP:OD2	3:N:18:GLN:HB2	1.92	0.70
3:N:17:THR:HB	3:N:36:ILE:HD13	1.74	0.70
1:H:116:MET:HE1	2:L:137:LEU:HA	1.73	0.70
1:H:180:MET:HE2	1:H:215:TRP:HE1	1.58	0.69
2:L:136:THR:O	2:L:137:LEU:HB2	1.93	0.69
1:H:51:TYR:CE1	1:H:107:ARG:HB2	2.29	0.68
1:H:209:VAL:HG12	1:H:231:VAL:HG11	1.76	0.68
1:H:147:LYS:HD3	3:N:11:TRP:CE2	2.28	0.68
1:H:116:MET:HE1	2:L:137:LEU:CA	2.23	0.68
1:H:220:CYS:O	1:H:221:ALA:HB3	1.92	0.67
1:H:150:ARG:HH21	3:N:12:LEU:HD23	1.59	0.67
2:L:101:HIS:O	2:L:107:VAL:HA	1.94	0.67
1:H:170:LEU:HD12	1:H:170:LEU:C	2.20	0.67
1:H:113:THR:O	1:H:115:ARG:NH1	2.28	0.67
1:H:72:ASN:HD21	1:H:74:GLU:H	1.41	0.66
1:H:89:ILE:N	1:H:89:ILE:HD12	2.10	0.66
1:H:25:GLY:HA2	2:L:136:THR:OG1	1.96	0.66
1:H:72:ASN:ND2	1:H:74:GLU:H	1.92	0.66
1:H:166:ASN:HA	1:H:169:LYS:HE3	1.77	0.66
1:H:94:PHE:HA	1:H:100:ASP:O	1.95	0.66
1:H:35:ASN:HD21	1:H:39:GLU:HB2	1.61	0.65
3:N:44:LEU:HB3	3:N:45:PRO:HD2	1.78	0.65
1:H:135:THR:HG22	1:H:161:PRO:HA	1.79	0.64
1:H:62:LYS:H	1:H:62:LYS:HD2	1.63	0.64
1:H:72:ASN:HD21	1:H:74:GLU:N	1.96	0.64
1:H:86:GLU:HB2	1:H:109:LYS:HG2	1.80	0.64
3:N:13:ASP:O	3:N:46:PRO:HA	1.97	0.64
1:H:184:GLY:HA3	5:H:256:HOH:O	1.96	0.63
3:N:55:TYR:CD1	3:N:55:TYR:N	2.65	0.63
1:H:240:ARG:HA	1:H:243:LYS:HE2	1.80	0.63
1:H:174:PHE:CD1	3:N:38:ARG:CZ	2.81	0.63
1:H:215:TRP:NE1	1:H:227:ILE:CD1	2.60	0.63
3:N:12:LEU:HD11	3:N:46:PRO:HB2	1.81	0.63
1:H:24:ASP:HA	1:H:71:ARG:NH1	2.13	0.63
1:H:230:LYS:CG	1:H:232:THR:HG23	2.29	0.63
1:H:85:VAL:HG11	1:H:88:VAL:HG12	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:ASN:ND2	1:H:74:GLU:N	2.47	0.62
3:N:8:GLU:O	3:N:9:ASN:HB2	2.00	0.62
1:H:115:ARG:HG2	1:H:115:ARG:HH11	1.64	0.62
1:H:19:GLY:C	1:H:20:GLN:HG2	2.24	0.62
1:H:103:ILE:HD13	1:H:234:PHE:CB	2.30	0.62
1:H:95:THR:O	1:H:98:THR:N	2.30	0.61
1:H:165:ARG:O	1:H:168:CYS:HB3	2.00	0.61
2:L:136:THR:O	2:L:137:LEU:CB	2.49	0.61
3:N:60:ILE:O	3:N:62:ASP:N	2.33	0.61
3:N:3:TYR:CE2	3:N:12:LEU:HD21	2.35	0.61
2:L:113:ARG:HD3	5:L:147:HOH:O	2.00	0.60
3:N:9:ASN:ND2	3:N:54:PHE:CE2	2.70	0.60
2:L:116:THR:HB	2:L:127:THR:CG2	2.32	0.60
2:L:99:PHE:HB3	2:L:101:HIS:CE1	2.37	0.60
1:H:96:LYS:HB3	1:H:97:GLU:OE1	2.02	0.59
3:N:25:CYS:SG	3:N:57:ASP:HA	2.43	0.59
1:H:178:GLN:O	1:H:230:LYS:NZ	2.27	0.59
2:L:115:TYR:OH	2:L:134:LYS:HE2	2.03	0.59
1:H:231:VAL:C	1:H:233:ALA:H	2.10	0.59
1:H:202:ARG:HB2	1:H:207:TYR:CE1	2.38	0.59
2:L:116:THR:HB	2:L:127:THR:HG21	1.83	0.59
3:N:14:ASP:HA	3:N:46:PRO:HB3	1.84	0.58
2:L:120:ASN:C	2:L:120:ASN:OD1	2.46	0.58
1:H:107:ARG:NH1	1:H:108:LEU:O	2.36	0.58
1:H:151:GLN:HG2	3:N:14:ASP:OD2	2.02	0.58
1:H:232:THR:HA	1:H:235:LEU:HD22	1.84	0.58
1:H:94:PHE:CE1	1:H:99:TYR:HA	2.39	0.58
1:H:243:LYS:O	1:H:245:ARG:N	2.37	0.58
2:L:98:GLN:OE1	2:L:112:ALA:N	2.34	0.58
1:H:34:ILE:HD13	1:H:67:ARG:NH1	2.19	0.58
1:H:59:LEU:CD2	1:H:64:PHE:CZ	2.87	0.57
1:H:17:VAL:O	1:H:188:GLU:HA	2.04	0.57
3:N:55:TYR:HD1	3:N:55:TYR:H	1.52	0.57
3:N:25:CYS:O	3:N:27:GLU:N	2.37	0.57
1:H:91:HIS:HB2	1:H:103:ILE:HG23	1.86	0.57
1:H:28:PRO:HG2	1:H:29:TRP:CE3	2.40	0.56
1:H:98:THR:CB	1:H:175:ILE:HD11	2.35	0.56
1:H:239:ASP:O	1:H:240:ARG:C	2.49	0.56
1:H:59:LEU:HD21	1:H:64:PHE:CZ	2.40	0.56
2:L:88:LEU:HA	2:L:102:GLU:OE2	2.05	0.56
2:L:89:CYS:N	2:L:102:GLU:OE2	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:83:HIS:HB3	1:H:108:LEU:HD22	1.86	0.56
1:H:124(A):GLU:OE1	1:H:126:ASP:HB2	2.06	0.56
1:H:170:LEU:C	1:H:170:LEU:CD1	2.80	0.55
1:H:145:HIS:CE1	1:H:147:LYS:H	2.24	0.55
1:H:215:TRP:CE2	1:H:227:ILE:CG1	2.87	0.55
1:H:232:THR:O	1:H:232:THR:OG1	2.24	0.54
1:H:59:LEU:HD22	1:H:64:PHE:CE1	2.43	0.54
1:H:165:ARG:HG2	1:H:169:LYS:CE	2.37	0.54
1:H:41:PHE:HE1	1:H:58:CYS:O	1.91	0.54
1:H:164:ASP:OD2	1:H:167:SER:HB2	2.06	0.54
2:L:115:TYR:CZ	2:L:131:PRO:HB2	2.42	0.54
1:H:53:LEU:HD21	1:H:231:VAL:HG21	1.88	0.54
1:H:131(B):MET:HE3	1:H:162:TYR:CE1	2.42	0.54
2:L:89:CYS:SG	2:L:101:HIS:N	2.81	0.54
1:H:86:GLU:HB2	1:H:109:LYS:HA	1.90	0.54
1:H:173:SER:C	1:H:174:PHE:CD2	2.86	0.54
1:H:131(B):MET:SD	1:H:232:THR:HG21	2.47	0.54
1:H:23:LYS:O	1:H:26:GLU:HB2	2.07	0.54
3:N:27:GLU:O	3:N:28:GLU:HB2	2.08	0.54
1:H:72:ASN:ND2	1:H:72:ASN:C	2.65	0.53
1:H:91:HIS:HA	1:H:237:TRP:CZ2	2.43	0.53
3:N:55:TYR:N	3:N:55:TYR:HD1	2.06	0.53
1:H:160:VAL:HG23	1:H:160:VAL:O	2.07	0.53
1:H:177:THR:O	1:H:180:MET:HG2	2.08	0.53
3:N:10:GLU:OE2	3:N:56:ARG:NH2	2.39	0.53
1:H:88:VAL:C	1:H:89:ILE:HD12	2.33	0.53
1:H:136:GLY:C	1:H:137:ILE:HG12	2.32	0.53
1:H:145:HIS:O	1:H:146:GLU:C	2.48	0.53
2:L:115:TYR:CE1	2:L:134:LYS:HE2	2.44	0.53
3:N:17:THR:HB	3:N:36:ILE:CD1	2.38	0.53
1:H:183:ALA:HB3	1:H:228:TYR:CE2	2.43	0.53
1:H:241:SER:O	1:H:244:THR:HG23	2.09	0.53
2:L:103:GLU:HB2	2:L:108:VAL:HG11	1.90	0.53
3:N:56:ARG:NH2	3:N:63:CYS:SG	2.82	0.53
1:H:94:PHE:CG	1:H:95:THR:N	2.77	0.53
1:H:117:ASN:C	1:H:118:VAL:CG2	2.81	0.53
1:H:72:ASN:HD22	1:H:75:GLN:H	1.56	0.53
1:H:86:GLU:CG	1:H:87:VAL:HG12	2.35	0.52
1:H:147:LYS:HE2	3:N:52:ASP:OD1	2.08	0.52
1:H:215:TRP:CZ2	1:H:227:ILE:HG12	2.43	0.52
3:N:13:ASP:C	3:N:15:CYS:H	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:ASN:ND2	1:H:75:GLN:N	2.57	0.52
1:H:105:VAL:HG12	1:H:106:LEU:N	2.23	0.52
2:L:117:LEU:O	2:L:118:ALA:C	2.52	0.52
1:H:94:PHE:HA	1:H:101:PHE:HB2	1.92	0.52
3:N:73:GLU:HG3	3:N:74:ILE:N	2.25	0.52
1:H:61:GLN:O	1:H:61(A):ALA:HB3	2.09	0.52
1:H:165:ARG:HH22	1:H:177:THR:C	2.18	0.52
2:L:99:PHE:HB3	2:L:101:HIS:HE1	1.75	0.52
1:H:114:PHE:HA	1:H:118:VAL:O	2.10	0.51
1:H:150:ARG:NH1	5:H:257:HOH:O	2.43	0.51
1:H:207:TYR:CD2	1:H:207:TYR:N	2.78	0.51
1:H:72:ASN:ND2	1:H:75:GLN:H	2.10	0.51
3:N:51:LYS:HB2	3:N:54:PHE:CD1	2.46	0.51
1:H:116:MET:O	1:H:117:ASN:HB2	2.11	0.50
1:H:185(A):ASP:C	1:H:185(A):ASP:OD1	2.53	0.50
1:H:115:ARG:HG3	1:H:118:VAL:HB	1.92	0.50
3:N:9:ASN:O	3:N:51:LYS:HG3	2.12	0.50
1:H:95:THR:O	1:H:99:TYR:N	2.42	0.50
1:H:50:PHE:CZ	1:H:111:PRO:CB	2.89	0.50
1:H:103:ILE:HD13	1:H:234:PHE:HB2	1.94	0.50
2:L:100:CYS:O	2:L:101:HIS:CD2	2.65	0.50
1:H:50:PHE:CE2	1:H:111:PRO:HB3	2.46	0.49
1:H:166:ASN:HA	1:H:169:LYS:CE	2.41	0.49
1:H:131(A):LEU:C	1:H:132:THR:H	2.19	0.49
1:H:35:ASN:OD1	1:H:38:ASN:N	2.46	0.49
1:H:143:ARG:HD3	1:H:145:HIS:O	2.13	0.49
1:H:24:ASP:CA	1:H:71:ARG:NH1	2.76	0.49
1:H:83:HIS:CB	1:H:108:LEU:HD22	2.43	0.49
1:H:95:THR:HG22	1:H:98:THR:H	1.77	0.49
1:H:97:GLU:CD	1:H:97:GLU:H	2.21	0.49
1:H:94:PHE:HE1	1:H:99:TYR:HA	1.76	0.49
1:H:117:ASN:C	1:H:118:VAL:HG23	2.38	0.49
1:H:158:LEU:HD22	1:H:160:VAL:CG1	2.42	0.49
3:N:13:ASP:O	3:N:15:CYS:N	2.46	0.49
1:H:124(A):GLU:O	1:H:125:ARG:C	2.55	0.48
1:H:165:ARG:O	1:H:168:CYS:N	2.47	0.48
1:H:237:TRP:O	1:H:241:SER:HB3	2.14	0.48
3:N:75:ILE:HG22	3:N:76:HIS:N	2.27	0.48
1:H:105:VAL:HG23	1:H:237:TRP:HZ3	1.79	0.48
3:N:16:GLY:C	3:N:18:GLN:H	2.20	0.48
1:H:131(A):LEU:HD12	1:H:131(A):LEU:HA	1.63	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:10:GLU:HG2	3:N:63:CYS:SG	2.54	0.48
1:H:174:PHE:CE1	3:N:38:ARG:CZ	2.96	0.47
1:H:143:ARG:HA	1:H:151:GLN:HA	1.96	0.47
1:H:131(A):LEU:O	1:H:133:GLN:HB2	2.14	0.47
1:H:142:GLY:HA3	1:H:194:ASP:OD2	2.14	0.47
1:H:220:CYS:O	1:H:221:ALA:CB	2.58	0.47
2:L:93:ASN:O	2:L:100:CYS:HB2	2.13	0.47
3:N:40:ARG:HH11	3:N:40:ARG:HG2	1.80	0.47
1:H:23:LYS:C	1:H:71:ARG:NH1	2.70	0.47
1:H:151:GLN:NE2	3:N:15:CYS:SG	2.87	0.47
1:H:180:MET:HE1	1:H:215:TRP:HE1	1.73	0.47
3:N:9:ASN:C	3:N:51:LYS:HG3	2.40	0.47
1:H:16:ILE:O	1:H:144:THR:HA	2.15	0.47
1:H:122:CYS:SG	2:L:132:CYS:O	2.72	0.47
1:H:75:GLN:HB3	1:H:77:GLU:OE2	2.15	0.47
1:H:125:ARG:NH1	1:H:129:GLU:OE1	2.48	0.47
3:N:36:ILE:HD13	3:N:36:ILE:O	2.15	0.46
1:H:173:SER:O	1:H:174:PHE:CD2	2.68	0.46
3:N:53:GLY:O	3:N:54:PHE:CG	2.68	0.46
3:N:16:GLY:O	3:N:18:GLN:N	2.48	0.46
1:H:72:ASN:HD22	1:H:75:GLN:N	2.13	0.46
1:H:135:THR:HG22	1:H:161:PRO:CA	2.46	0.46
1:H:227:ILE:HD12	1:H:227:ILE:O	2.15	0.46
2:L:115:TYR:HB3	2:L:124:CYS:HB3	1.97	0.45
1:H:37:GLU:O	1:H:38:ASN:HB2	2.15	0.45
1:H:158:LEU:HD23	1:H:159:GLU:N	2.32	0.45
1:H:103:ILE:HG21	1:H:234:PHE:CD2	2.51	0.45
1:H:158:LEU:HD22	1:H:160:VAL:HG13	1.99	0.45
1:H:65:LYS:HB3	1:H:82:VAL:HG12	1.99	0.45
1:H:72:ASN:ND2	1:H:74:GLU:HG2	2.29	0.45
1:H:76:GLU:O	1:H:77:GLU:HB3	2.17	0.45
1:H:35:ASN:OD1	1:H:39:GLU:N	2.26	0.45
1:H:96:LYS:HB3	1:H:96:LYS:HE2	1.82	0.44
1:H:175:ILE:H	1:H:175:ILE:HG12	1.57	0.44
3:N:19:LYS:O	3:N:20:PRO:C	2.54	0.44
1:H:59:LEU:CD2	1:H:64:PHE:CE1	3.00	0.44
1:H:83:HIS:CB	1:H:108:LEU:HD13	2.48	0.44
3:N:31:GLU:HA	3:N:31:GLU:OE1	2.16	0.44
1:H:34:ILE:HG22	1:H:40:GLY:HA2	2.00	0.44
1:H:96:LYS:HE2	1:H:97:GLU:OE1	2.17	0.44
1:H:191:CYS:O	1:H:194:ASP:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:30:GLN:HG2	1:H:155:LEU:CD1	2.48	0.44
1:H:209:VAL:HG12	1:H:209:VAL:O	2.15	0.44
1:H:24:ASP:N	1:H:71:ARG:NH1	2.65	0.44
3:N:16:GLY:C	3:N:18:GLN:N	2.76	0.44
3:N:19:LYS:N	3:N:20:PRO:HD2	2.33	0.44
1:H:94:PHE:CD1	1:H:95:THR:N	2.84	0.43
1:H:66:VAL:O	1:H:83:HIS:N	2.39	0.43
2:L:94:GLY:C	2:L:96:CYS:H	2.26	0.43
2:L:103:GLU:O	2:L:104:GLN:C	2.62	0.43
1:H:89:ILE:N	1:H:89:ILE:CD1	2.77	0.43
1:H:231:VAL:O	1:H:231:VAL:HG13	2.18	0.43
2:L:117:LEU:O	2:L:118:ALA:O	2.36	0.43
1:H:113:THR:O	1:H:113:THR:HG22	2.19	0.43
3:N:55:TYR:O	3:N:63:CYS:HA	2.18	0.43
1:H:174:PHE:CE1	3:N:38:ARG:NH2	2.87	0.43
1:H:189:ASP:OD2	1:H:190:ALA:N	2.51	0.43
1:H:173:SER:O	1:H:174:PHE:CG	2.72	0.43
1:H:24:ASP:N	1:H:71:ARG:HH12	2.17	0.42
2:L:121:GLY:C	2:L:122:LYS:HD3	2.44	0.42
3:N:28:GLU:N	3:N:29:PRO:HD3	2.34	0.42
2:L:115:TYR:CZ	2:L:134:LYS:HE2	2.54	0.42
2:L:103:GLU:HB2	2:L:108:VAL:CG1	2.49	0.42
1:H:31:ALA:N	1:H:44:GLY:O	2.52	0.42
1:H:88:VAL:O	1:H:88:VAL:CG2	2.65	0.42
1:H:91:HIS:HA	1:H:237:TRP:HZ2	1.82	0.42
1:H:138:VAL:HG12	1:H:158:LEU:HB3	2.02	0.42
1:H:164:ASP:OD1	1:H:167:SER:HB2	2.19	0.41
1:H:165:ARG:O	1:H:166:ASN:C	2.63	0.41
3:N:53:GLY:O	3:N:54:PHE:CD1	2.73	0.41
1:H:122:CYS:O	1:H:208:PHE:HA	2.20	0.41
1:H:125:ARG:O	1:H:128:ALA:HB3	2.20	0.41
2:L:89:CYS:O	2:L:94:GLY:N	2.53	0.41
1:H:50:PHE:CG	1:H:107:ARG:NH2	2.88	0.41
3:N:40:ARG:HG2	3:N:40:ARG:NH1	2.36	0.41
1:H:35:ASN:OD1	1:H:35:ASN:C	2.62	0.41
1:H:25:GLY:CA	1:H:116:MET:HE3	2.51	0.41
1:H:185:TYR:CG	1:H:186:LYS:HB3	2.56	0.41
3:N:33:GLU:O	3:N:34:ASP:C	2.63	0.41
1:H:50:PHE:HD2	1:H:108:LEU:O	2.04	0.41
1:H:57:HIS:CD2	1:H:57:HIS:C	2.97	0.41
1:H:150:ARG:HH21	3:N:12:LEU:CD2	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:126:PRO:C	2:L:128:GLY:H	2.27	0.41
1:H:24:ASP:OD1	1:H:117:ASN:ND2	2.53	0.41
1:H:75:GLN:HG2	1:H:76:GLU:O	2.21	0.41
1:H:41:PHE:CE1	1:H:58:CYS:O	2.72	0.41
1:H:143:ARG:HA	1:H:150:ARG:C	2.45	0.41
1:H:165:ARG:CG	1:H:169:LYS:HE2	2.47	0.41
1:H:195:SER:HA	1:H:213:VAL:O	2.20	0.41
3:N:22:GLU:CD	3:N:56:ARG:HE	2.29	0.41
3:N:13:ASP:C	3:N:15:CYS:N	2.79	0.41
1:H:17:VAL:HG13	1:H:144:THR:O	2.21	0.40
1:H:63:ARG:HB2	1:H:63:ARG:CZ	2.51	0.40
1:H:200:VAL:O	1:H:200:VAL:HG23	2.20	0.40
1:H:211:GLY:HA2	1:H:229:THR:O	2.20	0.40
1:H:166:ASN:O	1:H:167:SER:C	2.63	0.40
1:H:174:PHE:CD1	3:N:38:ARG:NH2	2.89	0.40
1:H:222:ARG:NH2	1:H:222:ARG:HG3	2.36	0.40
2:L:117:LEU:C	2:L:118:ALA:O	2.64	0.40
1:H:47:LEU:HD11	1:H:53:LEU:HB2	2.03	0.40
1:H:116:MET:O	1:H:117:ASN:CB	2.70	0.40
3:N:56:ARG:HA	3:N:62:ASP:O	2.21	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	H	233/235 (99%)	194 (83%)	32 (14%)	7 (3%)	3	19
2	L	49/54 (91%)	39 (80%)	6 (12%)	4 (8%)	0	4
3	N	72/78 (92%)	55 (76%)	10 (14%)	7 (10%)	0	3
All	All	354/367 (96%)	288 (81%)	48 (14%)	18 (5%)	1	10

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	244	THR
2	L	137	LEU
3	N	27	GLU
1	H	77	GLU
1	H	78	GLY
2	L	90	SER
3	N	14	ASP
3	N	17	THR
3	N	25	CYS
3	N	67	GLU
1	H	131(B)	MET
2	L	95	ASP
3	N	61	GLY
1	H	61(A)	ALA
2	L	118	ALA
1	H	18	GLY
1	H	111	PRO
3	N	28	GLU

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	H	200/200 (100%)	163 (82%)	37 (18%)	1	8
2	L	43/46 (94%)	35 (81%)	8 (19%)	1	8
3	N	67/70 (96%)	55 (82%)	12 (18%)	2	9
All	All	310/316 (98%)	253 (82%)	57 (18%)	1	8

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	17	VAL
1	H	37	GLU
1	H	45	THR

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Mol	Chain	Res	Type
1	H	49	GLU
1	H	57	HIS
1	H	61	GLN
1	H	62	LYS
1	H	82	VAL
1	H	87	VAL
1	H	88	VAL
1	H	89	ILE
1	H	97	GLU
1	H	110	THR
1	H	111	PRO
1	H	115	ARG
1	H	117	ASN
1	H	120	PRO
1	H	125	ARG
1	H	137	ILE
1	H	143	ARG
1	H	158	LEU
1	H	164	ASP
1	H	166	ASN
1	H	167	SER
1	H	170	LEU
1	H	172	SER
1	H	175	ILE
1	H	178	GLN
1	H	180	MET
1	H	209	VAL
1	H	223	LYS
1	H	227	ILE
1	H	231	VAL
1	H	232	THR
1	H	235	LEU
1	H	239	ASP
1	H	241	SER
2	L	103	GLU
2	L	107	VAL
2	L	108	VAL
2	L	110	SER
2	L	116	THR
2	L	117	LEU
2	L	134	LYS
2	L	138	GLU

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Mol	Chain	Res	Type
3	N	3	TYR
3	N	5	GLU
3	N	8	GLU
3	N	27	GLU
3	N	28	GLU
3	N	32	GLU
3	N	36	ILE
3	N	49	VAL
3	N	55	TYR
3	N	58	THR
3	N	74	ILE
3	N	75	ILE

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

Mol	Chain	Res	Type
1	H	30	GLN
1	H	72	ASN
1	H	75	GLN
1	H	117	ASN
1	H	178	GLN
2	L	101	HIS
3	N	26	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.