



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:34 AM UTC

PDB ID : 1C8G / pdb_00001c8g
Title : FELINE PANLEUKOPENIA VIRUS EMPTY CAPSID STRUCTURE
Authors : Rossmann, M.G.; Simpson, A.A.
Deposited on : 2000-05-05
Resolution : 3.00 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

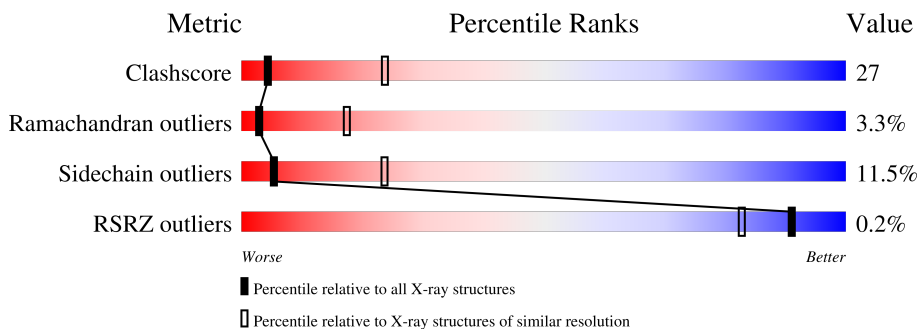
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	548	62% 28% 9% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4352 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 FELINE PANLEUKOPENIA VIRUS CAPSID.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4350	2766	739	829	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	ILE	THR	conflict	UNP P24840
A	104	GLU	GLN	conflict	UNP P24840
A	232	VAL	ILE	conflict	UNP P24840
A	484	ILE	VAL	conflict	UNP P24840
A	550	GLN	GLU	conflict	UNP P24840
A	572	VAL	LEU	conflict	UNP P24840

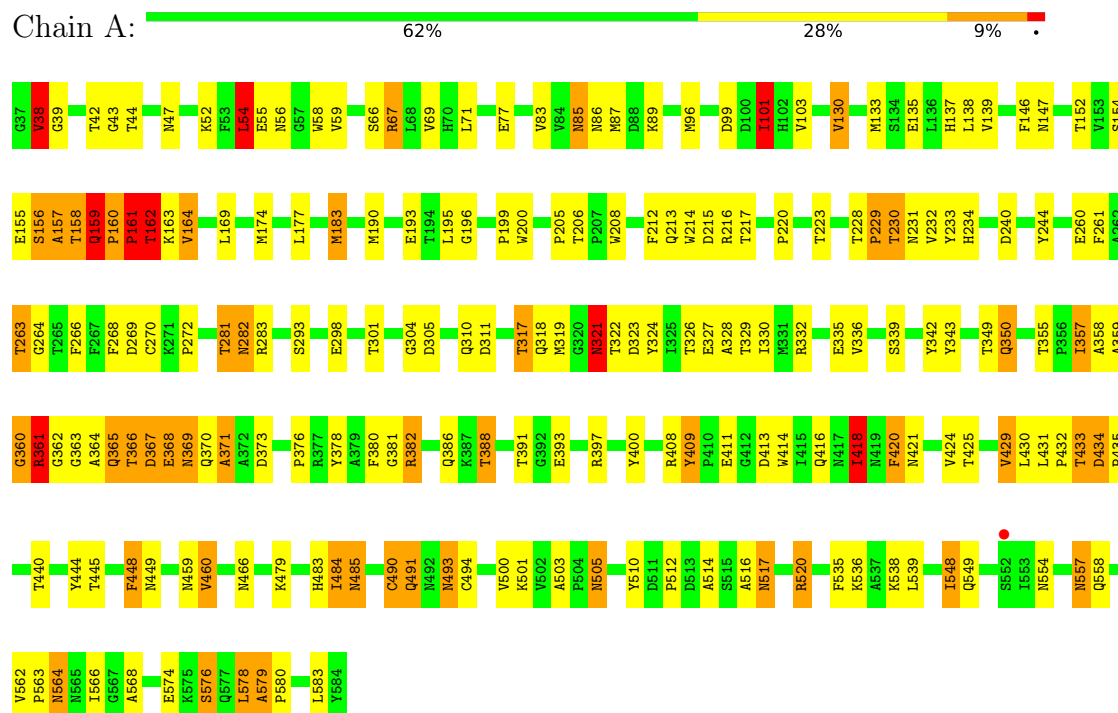
- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

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: FELINE PANLEUKOPENIA VIRUS CAPSID



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	266.17Å 250.12Å 379.10Å 90.00° 94.11° 90.00°	Depositor
Resolution (Å)	9.00 – 3.00 9.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	55.3 (9.00-3.00) 30.8 (9.00-3.01)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.87 (at 2.99Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.245 , (Not available) 0.229 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	1.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.15	EDS
Total number of atoms	4352	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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:
CA

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	0.60	0/4479	1.11	41/6128 (0.7%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	THR	N-CA-C	-12.39	98.96	113.21
1	A	162	THR	N-CA-C	9.50	122.67	109.18
1	A	369	ASN	N-CA-C	-8.67	101.07	112.34
1	A	139	VAL	N-CA-C	8.55	119.52	111.48
1	A	270	CYS	N-CA-C	7.11	118.55	108.74
1	A	342	TYR	N-CA-C	7.02	120.38	109.07
1	A	493	ASN	N-CA-C	6.79	119.76	108.96
1	A	38	VAL	N-CA-C	6.51	116.66	110.53
1	A	343	TYR	N-CA-C	-6.50	102.26	111.56
1	A	448	PHE	N-CA-C	6.28	119.09	110.24
1	A	228	THR	CA-C-N	6.24	127.64	119.84
1	A	228	THR	C-N-CA	6.24	127.64	119.84
1	A	298	GLU	N-CA-C	-6.18	101.94	110.35
1	A	321	ASN	N-CA-C	5.91	120.06	112.26
1	A	342	TYR	CA-C-N	5.77	130.85	122.36
1	A	342	TYR	C-N-CA	5.77	130.85	122.36
1	A	101	ILE	N-CA-C	5.71	117.08	109.37
1	A	349	THR	N-CA-C	5.54	119.66	113.01
1	A	418	ILE	CB-CA-C	-5.47	104.06	112.05
1	A	409	TYR	CA-C-N	5.45	126.65	119.84
1	A	409	TYR	C-N-CA	5.45	126.65	119.84
1	A	466	ASN	N-CA-C	5.42	119.62	112.89
1	A	310	GLN	N-CA-C	5.42	118.68	111.75
1	A	304	GLY	N-CA-C	-5.36	104.42	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	434	ASP	CA-C-N	5.22	125.20	120.03
1	A	434	ASP	C-N-CA	5.22	125.20	120.03
1	A	444	TYR	N-CA-C	-5.21	105.67	112.23
1	A	430	LEU	N-CA-C	-5.21	98.91	108.02
1	A	517	ASN	N-CA-C	-5.14	99.85	110.80
1	A	361	ARG	N-CA-C	5.12	121.72	110.80
1	A	576	SER	N-CA-C	5.12	119.52	113.12
1	A	355	THR	CA-C-N	5.07	124.97	119.85
1	A	355	THR	C-N-CA	5.07	124.97	119.85
1	A	360	GLY	CA-C-O	-5.05	117.18	121.78
1	A	169	LEU	N-CA-C	5.03	118.19	111.75
1	A	268	PHE	N-CA-C	5.03	117.17	110.53
1	A	332	ARG	CA-C-N	5.03	124.47	119.24
1	A	332	ARG	C-N-CA	5.03	124.47	119.24
1	A	514	ALA	N-CA-C	5.00	117.65	109.59
1	A	160	PRO	N-CA-C	5.00	116.80	110.70
1	A	350	GLN	N-CA-C	5.00	118.46	111.56

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	A	4350	0	4153	228	0
2	A	2	0	0	0	0
All	All	4352	0	4153	228	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 27.

All (228) 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:157:ALA:C	1:A:161:PRO:HB2	1.72	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:VAL:HG13	1:A:578:LEU:HD21	1.41	1.00
1:A:326:THR:HG22	1:A:328:ALA:H	1.27	0.99
1:A:156:SER:HB3	1:A:162:THR:HB	1.40	0.99
1:A:361:ARG:HD3	1:A:362:GLY:H	1.26	0.97
1:A:155:GLU:HG3	1:A:157:ALA:HB2	1.44	0.96
1:A:414:TRP:HE1	1:A:416:GLN:HE21	1.10	0.95
1:A:193:GLU:HB3	1:A:206:THR:HG21	1.49	0.95
1:A:485:ASN:H	1:A:485:ASN:HD22	1.17	0.92
1:A:216:ARG:HD3	1:A:217:THR:N	1.84	0.92
1:A:554:ASN:H	1:A:557:ASN:HD21	1.18	0.91
1:A:360:GLY:O	1:A:361:ARG:HB2	1.69	0.91
1:A:154:SER:OG	1:A:164:VAL:HB	1.71	0.90
1:A:158:THR:O	1:A:161:PRO:HA	1.73	0.88
1:A:365:GLN:C	1:A:367:ASP:H	1.77	0.87
1:A:156:SER:CB	1:A:162:THR:HB	2.03	0.87
1:A:459:ASN:ND2	1:A:460:VAL:H	1.74	0.84
1:A:491:GLN:HE21	1:A:491:GLN:C	1.85	0.84
1:A:85:ASN:C	1:A:85:ASN:HD22	1.84	0.83
1:A:564:ASN:ND2	1:A:568:ALA:H	1.77	0.83
1:A:361:ARG:HD3	1:A:362:GLY:N	1.94	0.82
1:A:156:SER:O	1:A:158:THR:HG22	1.81	0.81
1:A:281:THR:HG22	1:A:283:ARG:H	1.45	0.80
1:A:293:SER:HB3	1:A:305:ASP:HB3	1.64	0.80
1:A:557:ASN:HD22	1:A:558:GLN:N	1.81	0.79
1:A:554:ASN:H	1:A:557:ASN:ND2	1.82	0.76
1:A:557:ASN:HD22	1:A:557:ASN:C	1.93	0.76
1:A:157:ALA:CA	1:A:161:PRO:HB2	2.15	0.75
1:A:156:SER:O	1:A:158:THR:N	2.17	0.74
1:A:317:THR:CG2	1:A:319:MET:H	2.00	0.74
1:A:263:THR:HG22	1:A:264:GLY:O	1.87	0.73
1:A:366:THR:N	1:A:370:GLN:OE1	2.21	0.73
1:A:564:ASN:HD21	1:A:568:ALA:H	1.37	0.72
1:A:155:GLU:C	1:A:157:ALA:H	1.98	0.72
1:A:155:GLU:CG	1:A:157:ALA:HB2	2.18	0.72
1:A:159:GLN:HB2	1:A:160:PRO:CD	2.20	0.72
1:A:414:TRP:HE1	1:A:416:GLN:NE2	1.87	0.71
1:A:158:THR:N	1:A:161:PRO:HB2	2.05	0.71
1:A:365:GLN:HA	1:A:370:GLN:OE1	1.91	0.70
1:A:361:ARG:CD	1:A:362:GLY:H	2.04	0.70
1:A:578:LEU:CD2	1:A:578:LEU:H	2.05	0.70
1:A:368:GLU:HG2	1:A:369:ASN:N	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ASN:HD22	1:A:321:ASN:H	1.39	0.70
1:A:366:THR:C	1:A:370:GLN:HB2	2.17	0.70
1:A:367:ASP:HA	1:A:370:GLN:HB3	1.74	0.70
1:A:368:GLU:HG2	1:A:369:ASN:HD22	1.56	0.69
1:A:368:GLU:C	1:A:370:GLN:N	2.47	0.69
1:A:99:ASP:CG	1:A:216:ARG:HH12	1.99	0.69
1:A:52:LYS:O	1:A:54:LEU:HD13	1.93	0.69
1:A:162:THR:HG22	1:A:163:LYS:H	1.59	0.68
1:A:431:LEU:C	1:A:433:THR:H	2.03	0.66
1:A:85:ASN:ND2	1:A:87:MET:H	1.93	0.66
1:A:157:ALA:HA	1:A:161:PRO:HB2	1.76	0.66
1:A:301:THR:O	1:A:301:THR:HG22	1.94	0.66
1:A:155:GLU:HG3	1:A:157:ALA:CB	2.23	0.66
1:A:158:THR:O	1:A:160:PRO:HD2	1.96	0.66
1:A:578:LEU:H	1:A:578:LEU:HD23	1.60	0.66
1:A:564:ASN:ND2	1:A:566:ILE:H	1.94	0.65
1:A:216:ARG:HD3	1:A:216:ARG:C	2.22	0.65
1:A:420:PHE:O	1:A:421:ASN:HB2	1.95	0.65
1:A:282:ASN:HD21	1:A:336:VAL:H	1.42	0.64
1:A:357:ILE:HD13	1:A:358:ALA:H	1.60	0.64
1:A:459:ASN:ND2	1:A:460:VAL:N	2.46	0.64
1:A:322:THR:HG21	1:A:420:PHE:HD2	1.63	0.64
1:A:367:ASP:N	1:A:370:GLN:HB2	2.13	0.63
1:A:155:GLU:OE2	1:A:155:GLU:HA	1.97	0.63
1:A:42:THR:H	1:A:147:ASN:ND2	1.97	0.63
1:A:269:ASP:OD1	1:A:490:CYS:HB3	2.00	0.62
1:A:367:ASP:HA	1:A:370:GLN:CB	2.29	0.62
1:A:156:SER:HB2	1:A:164:VAL:CG2	2.29	0.62
1:A:564:ASN:C	1:A:564:ASN:HD22	2.06	0.62
1:A:85:ASN:C	1:A:85:ASN:ND2	2.57	0.62
1:A:317:THR:HG22	1:A:319:MET:H	1.63	0.62
1:A:554:ASN:N	1:A:557:ASN:HD21	1.95	0.61
1:A:137:HIS:CE1	1:A:272:PRO:HB3	2.35	0.61
1:A:424:VAL:HG22	1:A:429:VAL:HG22	1.81	0.61
1:A:362:GLY:HA3	1:A:370:GLN:NE2	2.16	0.60
1:A:562:VAL:HG13	1:A:563:PRO:HD2	1.83	0.60
1:A:322:THR:HG21	1:A:420:PHE:CD2	2.36	0.60
1:A:382:ARG:HH11	1:A:382:ARG:HG2	1.66	0.60
1:A:159:GLN:C	1:A:161:PRO:HA	2.27	0.60
1:A:54:LEU:CD1	1:A:54:LEU:N	2.65	0.59
1:A:578:LEU:O	1:A:579:ALA:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:THR:O	1:A:160:PRO:CD	2.49	0.59
1:A:47:ASN:HD21	1:A:67:ARG:HH21	1.49	0.59
1:A:357:ILE:HD13	1:A:358:ALA:N	2.18	0.59
1:A:365:GLN:C	1:A:367:ASP:N	2.51	0.59
1:A:548:ILE:HG12	1:A:580:PRO:HD2	1.85	0.59
1:A:54:LEU:HD13	1:A:54:LEU:N	2.19	0.58
1:A:282:ASN:ND2	1:A:336:VAL:H	2.00	0.58
1:A:459:ASN:HD22	1:A:460:VAL:H	1.50	0.58
1:A:213:GLN:HG3	1:A:240:ASP:CB	2.34	0.57
1:A:510:TYR:CE2	1:A:512:PRO:HG3	2.39	0.57
1:A:260:GLU:HG2	1:A:261:PHE:N	2.19	0.57
1:A:160:PRO:N	1:A:161:PRO:HA	2.19	0.57
1:A:193:GLU:CB	1:A:206:THR:HG21	2.30	0.57
1:A:367:ASP:O	1:A:368:GLU:HB3	2.04	0.57
1:A:317:THR:HG23	1:A:319:MET:H	1.70	0.56
1:A:160:PRO:HG2	1:A:161:PRO:C	2.30	0.56
1:A:174:MET:HE2	1:A:503:ALA:HA	1.87	0.56
1:A:158:THR:C	1:A:161:PRO:HA	2.31	0.56
1:A:358:ALA:O	1:A:359:ALA:HB3	2.05	0.56
1:A:413:ASP:O	1:A:432:PRO:HD3	2.05	0.56
1:A:157:ALA:HA	1:A:161:PRO:CB	2.36	0.56
1:A:160:PRO:HB2	1:A:161:PRO:O	2.06	0.56
1:A:382:ARG:HG3	1:A:388:THR:HA	1.87	0.55
1:A:159:GLN:CB	1:A:160:PRO:CD	2.85	0.55
1:A:491:GLN:HE21	1:A:491:GLN:CA	2.20	0.55
1:A:101:ILE:CD1	1:A:233:TYR:HB2	2.37	0.55
1:A:485:ASN:HD22	1:A:485:ASN:N	1.93	0.54
1:A:368:GLU:C	1:A:370:GLN:H	2.16	0.54
1:A:578:LEU:O	1:A:579:ALA:CB	2.56	0.54
1:A:156:SER:N	1:A:162:THR:O	2.41	0.54
1:A:156:SER:O	1:A:162:THR:N	2.40	0.53
1:A:557:ASN:ND2	1:A:557:ASN:C	2.65	0.53
1:A:158:THR:C	1:A:159:GLN:HG2	2.33	0.53
1:A:156:SER:HB3	1:A:162:THR:C	2.33	0.53
1:A:429:VAL:HB	1:A:431:LEU:CD1	2.39	0.53
1:A:183:MET:HE3	1:A:183:MET:HA	1.90	0.53
1:A:564:ASN:ND2	1:A:564:ASN:C	2.67	0.53
1:A:157:ALA:HA	1:A:161:PRO:CG	2.38	0.53
1:A:130:VAL:HG13	1:A:578:LEU:CD2	2.29	0.52
1:A:336:VAL:O	1:A:408:ARG:NH2	2.42	0.52
1:A:376:PRO:HG2	1:A:400:TYR:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:GLU:O	1:A:369:ASN:C	2.53	0.52
1:A:156:SER:OG	1:A:162:THR:HB	2.10	0.51
1:A:69:VAL:CG1	1:A:205:PRO:HD3	2.39	0.51
1:A:282:ASN:HD21	1:A:335:GLU:HA	1.75	0.51
1:A:58:TRP:CE2	1:A:538:LYS:HD3	2.46	0.51
1:A:174:MET:HE3	1:A:501:LYS:HD3	1.92	0.51
1:A:155:GLU:C	1:A:157:ALA:N	2.65	0.50
1:A:213:GLN:HG3	1:A:240:ASP:HB2	1.93	0.50
1:A:159:GLN:CB	1:A:160:PRO:HD2	2.40	0.50
1:A:358:ALA:HA	1:A:484:ILE:HD11	1.94	0.50
1:A:326:THR:CG2	1:A:327:GLU:N	2.74	0.50
1:A:42:THR:H	1:A:147:ASN:HD21	1.60	0.49
1:A:321:ASN:HD22	1:A:321:ASN:N	2.02	0.49
1:A:71:LEU:CD2	1:A:500:VAL:HG12	2.43	0.49
1:A:566:ILE:HG22	1:A:566:ILE:O	2.11	0.49
1:A:212:PHE:O	1:A:214:TRP:HE3	1.96	0.49
1:A:339:SER:O	1:A:449:ASN:HA	2.13	0.49
1:A:183:MET:HE3	1:A:183:MET:CA	2.43	0.48
1:A:133:MET:SD	1:A:539:LEU:HD23	2.53	0.48
1:A:156:SER:HB3	1:A:163:LYS:N	2.29	0.48
1:A:183:MET:HA	1:A:183:MET:CE	2.43	0.48
1:A:429:VAL:HB	1:A:431:LEU:HD12	1.94	0.48
1:A:505:ASN:O	1:A:520:ARG:HB2	2.12	0.48
1:A:159:GLN:O	1:A:160:PRO:C	2.56	0.48
1:A:365:GLN:HB3	1:A:367:ASP:HB2	1.95	0.48
1:A:130:VAL:CG2	1:A:576:SER:HA	2.43	0.48
1:A:85:ASN:HD22	1:A:86:ASN:N	2.11	0.47
1:A:213:GLN:HG3	1:A:240:ASP:HB3	1.96	0.47
1:A:156:SER:HB3	1:A:162:THR:CB	2.28	0.47
1:A:217:THR:OG1	1:A:234:HIS:HE1	1.97	0.47
1:A:138:LEU:HD13	1:A:535:PHE:CE1	2.50	0.47
1:A:578:LEU:CD2	1:A:578:LEU:N	2.74	0.47
1:A:137:HIS:HB2	1:A:536:LYS:HB3	1.96	0.47
1:A:156:SER:HB2	1:A:164:VAL:HG22	1.96	0.47
1:A:269:ASP:OD1	1:A:269:ASP:N	2.48	0.47
1:A:367:ASP:CA	1:A:370:GLN:CB	2.92	0.47
1:A:321:ASN:H	1:A:321:ASN:ND2	2.08	0.47
1:A:324:TYR:O	1:A:329:THR:HG21	2.15	0.47
1:A:183:MET:HG3	1:A:208:TRP:HH2	1.80	0.46
1:A:85:ASN:HD22	1:A:87:MET:H	1.60	0.46
1:A:157:ALA:HA	1:A:161:PRO:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:GLN:CG	1:A:160:PRO:HD2	2.46	0.46
1:A:424:VAL:HG21	1:A:429:VAL:HG13	1.96	0.46
1:A:485:ASN:H	1:A:485:ASN:ND2	1.98	0.46
1:A:135:GLU:HG2	1:A:538:LYS:HB3	1.98	0.46
1:A:326:THR:HG22	1:A:327:GLU:N	2.31	0.45
1:A:281:THR:CG2	1:A:282:ASN:N	2.79	0.45
1:A:409:TYR:CZ	1:A:411:GLU:HB2	2.52	0.45
1:A:431:LEU:C	1:A:433:THR:N	2.70	0.45
1:A:130:VAL:HG21	1:A:576:SER:HA	1.97	0.45
1:A:159:GLN:C	1:A:161:PRO:CA	2.89	0.45
1:A:183:MET:HE2	1:A:244:TYR:HB3	1.99	0.45
1:A:301:THR:O	1:A:301:THR:CG2	2.62	0.45
1:A:96:MET:HE3	1:A:220:PRO:HB2	1.99	0.45
1:A:411:GLU:OE1	1:A:411:GLU:N	2.41	0.45
1:A:505:ASN:HD22	1:A:505:ASN:HA	1.57	0.45
1:A:71:LEU:HD22	1:A:500:VAL:HG12	1.98	0.45
1:A:83:VAL:HG22	1:A:103:VAL:HG22	1.99	0.45
1:A:381:GLY:HA2	1:A:386:GLN:HE21	1.82	0.45
1:A:155:GLU:O	1:A:157:ALA:N	2.47	0.44
1:A:424:VAL:CG2	1:A:429:VAL:HG22	2.48	0.44
1:A:536:LYS:HE3	1:A:536:LYS:HB2	1.73	0.44
1:A:47:ASN:ND2	1:A:66:SER:H	2.15	0.44
1:A:55:GLU:O	1:A:56:ASN:HB2	2.16	0.44
1:A:483:HIS:HB3	1:A:485:ASN:ND2	2.32	0.44
1:A:77:GLU:OE2	1:A:520:ARG:NH1	2.51	0.44
1:A:96:MET:HG2	1:A:220:PRO:HA	2.00	0.44
1:A:445:THR:HA	1:A:448:PHE:HB2	1.99	0.44
1:A:159:GLN:HG2	1:A:160:PRO:HD2	2.00	0.44
1:A:215:ASP:HB2	1:A:234:HIS:HB2	2.00	0.44
1:A:367:ASP:CA	1:A:370:GLN:HB2	2.48	0.44
1:A:382:ARG:HG2	1:A:382:ARG:NH1	2.31	0.43
1:A:434:ASP:HA	1:A:435:PRO:HD3	1.85	0.43
1:A:157:ALA:C	1:A:161:PRO:CB	2.66	0.43
1:A:418:ILE:C	1:A:420:PHE:N	2.77	0.43
1:A:583:LEU:C	1:A:583:LEU:HD23	2.44	0.43
1:A:87:MET:HG2	1:A:231:ASN:ND2	2.34	0.43
1:A:157:ALA:HA	1:A:162:THR:H	1.83	0.43
1:A:362:GLY:CA	1:A:370:GLN:NE2	2.82	0.43
1:A:380:PHE:CD1	1:A:380:PHE:N	2.87	0.42
1:A:38:VAL:CG2	1:A:39:GLY:N	2.82	0.42
1:A:43:GLY:HA3	1:A:146:PHE:CD2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:PRO:HD2	1:A:200:TRP:CZ3	2.54	0.42
1:A:548:ILE:HG23	1:A:549:GLN:N	2.34	0.42
1:A:130:VAL:CG1	1:A:578:LEU:HD21	2.29	0.42
1:A:281:THR:HG22	1:A:282:ASN:N	2.35	0.42
1:A:67:ARG:NH1	1:A:196:GLY:O	2.50	0.42
1:A:190:MET:O	1:A:190:MET:HG2	2.19	0.42
1:A:366:THR:O	1:A:367:ASP:O	2.38	0.42
1:A:368:GLU:O	1:A:371:ALA:N	2.53	0.42
1:A:378:TYR:O	1:A:397:ARG:HA	2.20	0.42
1:A:566:ILE:O	1:A:566:ILE:CG2	2.67	0.41
1:A:154:SER:O	1:A:164:VAL:N	2.46	0.41
1:A:266:PHE:HZ	1:A:493:ASN:C	2.28	0.41
1:A:326:THR:H	1:A:329:THR:HB	1.85	0.41
1:A:360:GLY:O	1:A:361:ARG:CB	2.53	0.41
1:A:369:ASN:N	1:A:369:ASN:HD22	2.16	0.41
1:A:317:THR:CG2	1:A:318:GLN:N	2.82	0.41
1:A:562:VAL:CG1	1:A:563:PRO:HD2	2.49	0.41
1:A:578:LEU:HD23	1:A:578:LEU:N	2.31	0.41
1:A:183:MET:CG	1:A:208:TRP:CH2	3.04	0.41
1:A:158:THR:HG23	1:A:162:THR:OG1	2.21	0.40
1:A:418:ILE:C	1:A:420:PHE:H	2.28	0.40
1:A:311:ASP:HA	1:A:323:ASP:O	2.22	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	A	546/548 (100%)	498 (91%)	30 (6%)	18 (3%)	3 17

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	157	ALA
1	A	159	GLN
1	A	230	THR
1	A	361	ARG
1	A	367	ASP
1	A	371	ALA
1	A	373	ASP
1	A	516	ALA
1	A	517	ASN
1	A	579	ALA
1	A	54	LEU
1	A	363	GLY
1	A	365	GLN
1	A	364	ALA
1	A	368	GLU
1	A	229	PRO
1	A	156	SER
1	A	161	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	477/477 (100%)	422 (88%)	55 (12%)	5 24

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	VAL
1	A	44	THR
1	A	54	LEU
1	A	59	VAL
1	A	67	ARG
1	A	85	ASN
1	A	89	LYS
1	A	101	ILE
1	A	130	VAL

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Mol	Chain	Res	Type
1	A	152	THR
1	A	158	THR
1	A	159	GLN
1	A	161	PRO
1	A	162	THR
1	A	164	VAL
1	A	177	LEU
1	A	183	MET
1	A	195	LEU
1	A	223	THR
1	A	229	PRO
1	A	230	THR
1	A	232	VAL
1	A	263	THR
1	A	281	THR
1	A	282	ASN
1	A	317	THR
1	A	321	ASN
1	A	330	ILE
1	A	350	GLN
1	A	357	ILE
1	A	361	ARG
1	A	382	ARG
1	A	388	THR
1	A	391	THR
1	A	393	GLU
1	A	418	ILE
1	A	420	PHE
1	A	425	THR
1	A	429	VAL
1	A	433	THR
1	A	440	THR
1	A	460	VAL
1	A	479	LYS
1	A	484	ILE
1	A	485	ASN
1	A	490	CYS
1	A	491	GLN
1	A	494	CYS
1	A	505	ASN
1	A	520	ARG
1	A	548	ILE

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Mol	Chain	Res	Type
1	A	557	ASN
1	A	564	ASN
1	A	574	GLU
1	A	578	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	70	HIS
1	A	85	ASN
1	A	147	ASN
1	A	180	ASN
1	A	181	ASN
1	A	234	HIS
1	A	282	ASN
1	A	302	ASN
1	A	310	GLN
1	A	321	ASN
1	A	369	ASN
1	A	383	GLN
1	A	386	GLN
1	A	403	HIS
1	A	404	GLN
1	A	416	GLN
1	A	459	ASN
1	A	466	ASN
1	A	468	GLN
1	A	485	ASN
1	A	491	GLN
1	A	505	ASN
1	A	546	ASN
1	A	557	ASN
1	A	560	ASN
1	A	564	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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	548/548 (100%)	-0.64	1 (0%) 91 83	2, 8, 33, 54	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	552	SER	2.7

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(Å ²)	Q<0.9
2	CA	A	585	1/1	0.92	0.14	9,9,9,9	0
2	CA	A	586	1/1	0.94	0.13	9,9,9,9	0

6.5 Other polymers [i](#)

There are no such residues in this entry.