



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 11:04 AM UTC

PDB ID : 1C8E / pdb_00001c8e
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

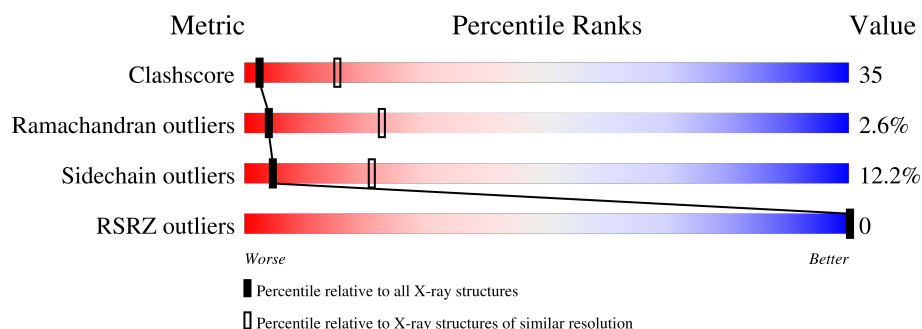
1 Overall quality at a glance

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	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4255 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	534	Total	C	N	O	S	0	0	0
			4255	2714	719	806	16			

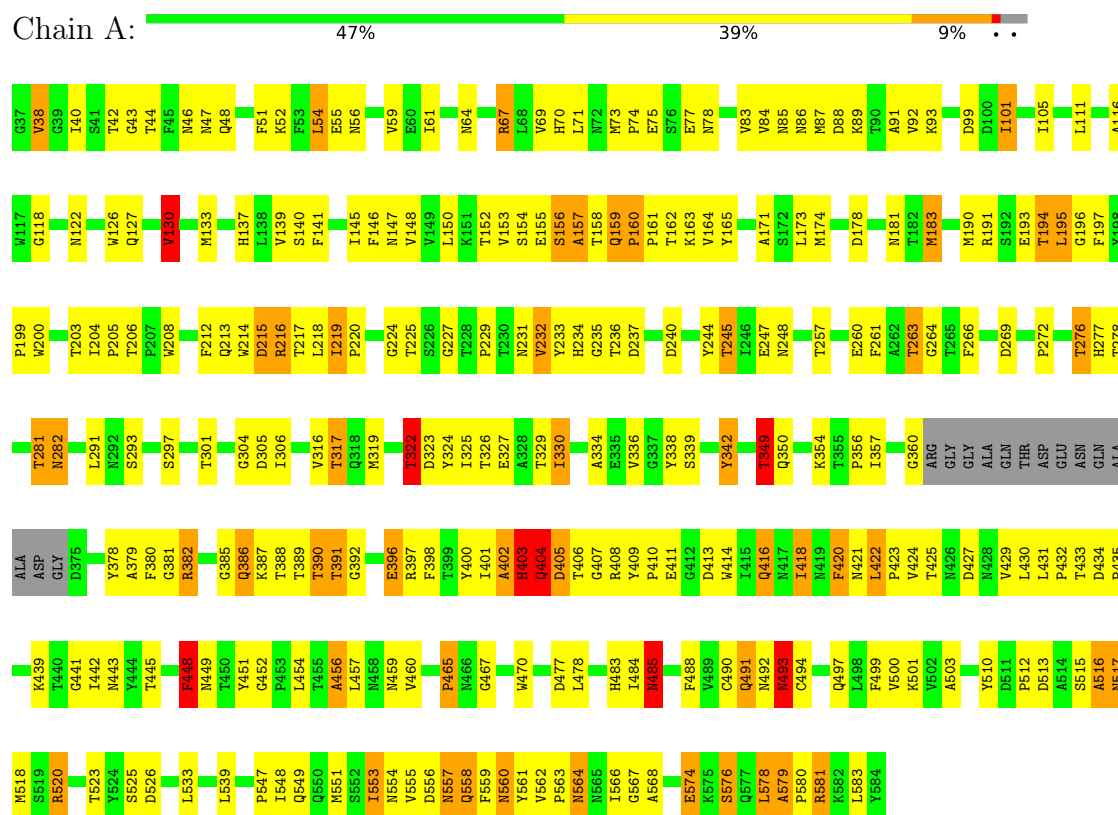
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	GLU	GLN	conflict	UNP P90438
A	484	ILE	VAL	conflict	UNP P90438
A	509	GLN	GLU	conflict	UNP P90438

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	254.15Å 253.96Å 380.29Å 90.00° 92.83° 90.00°	Depositor
Resolution (Å)	9.00 – 3.00 9.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	79.9 (9.00-3.00) 73.6 (9.00-3.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.62 (at 3.01Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.283 , (Not available) 0.254 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.762	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.085 for k,h,-l 0.065 for -k,-h,-l 0.077 for h,-k,-l	Xtriage
F_o, F_c correlation	0.31	EDS
Total number of atoms	4255	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.53% 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	0.60	1/4383 (0.0%)	1.10	32/5996 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	401	ILE	CA-CB	-5.04	1.48	1.54

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	405	ASP	N-CA-C	-10.91	102.18	114.62
1	A	404	GLN	N-CA-C	-10.69	88.02	110.80
1	A	448	PHE	N-CA-C	7.76	121.18	110.24
1	A	555	VAL	N-CA-C	-7.65	102.67	113.07
1	A	322	THR	N-CA-C	7.61	119.77	110.41
1	A	402	ALA	N-CA-C	7.39	123.32	113.72
1	A	160	PRO	N-CA-C	6.82	119.02	110.70
1	A	403	HIS	N-CA-C	6.66	124.99	110.80
1	A	434	ASP	CA-C-N	6.23	126.14	119.85
1	A	434	ASP	C-N-CA	6.23	126.14	119.85
1	A	232	VAL	N-CA-C	6.11	116.42	108.35
1	A	396	GLU	N-CA-C	-6.04	101.05	110.42
1	A	342	TYR	N-CA-C	6.00	119.02	109.24
1	A	323	ASP	N-CA-C	-5.98	104.51	112.94
1	A	130	VAL	N-CA-C	5.96	116.70	110.62
1	A	304	GLY	N-CA-C	-5.94	103.50	112.89
1	A	560	ASN	N-CA-C	-5.79	105.87	113.17
1	A	38	VAL	N-CA-C	5.78	115.97	110.42
1	A	485	ASN	N-CA-C	5.77	120.38	113.23
1	A	40	ILE	N-CA-C	5.72	116.31	107.78
1	A	492	ASN	N-CA-C	5.65	117.11	111.07
1	A	456	ALA	N-CA-C	-5.62	101.71	110.42
1	A	452	GLY	CA-C-N	5.45	126.66	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	452	GLY	C-N-CA	5.45	126.66	119.84
1	A	576	SER	N-CA-C	5.43	120.40	113.55
1	A	219	ILE	N-CA-C	5.37	114.39	108.05
1	A	349	THR	N-CA-C	5.34	122.19	110.80
1	A	78	ASN	N-CA-C	5.32	118.66	110.42
1	A	430	LEU	N-CA-C	-5.29	98.77	108.02
1	A	493	ASN	N-CA-C	5.27	117.48	108.90
1	A	139	VAL	N-CA-C	5.26	120.27	109.34
1	A	574	GLU	N-CA-C	5.07	117.08	109.23

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	4255	0	4072	289	0
All	All	4255	0	4072	289	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 35.

All (289) 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:193:GLU:HB3	1:A:206:THR:HG21	1.31	1.11
1:A:418:ILE:HD12	1:A:418:ILE:H	1.16	1.05
1:A:360:GLY:HA3	1:A:403:HIS:NE2	1.73	1.03
1:A:564:ASN:ND2	1:A:568:ALA:H	1.64	0.96
1:A:493:ASN:HD22	1:A:493:ASN:H	1.00	0.95
1:A:157:ALA:HA	1:A:161:PRO:HB2	1.47	0.95
1:A:485:ASN:H	1:A:485:ASN:HD22	1.01	0.93
1:A:245:THR:HG22	1:A:248:ASN:H	1.33	0.92
1:A:159:GLN:HB2	1:A:160:PRO:CD	1.99	0.92
1:A:493:ASN:HD22	1:A:493:ASN:N	1.68	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ASN:HD21	1:A:87:MET:HG3	1.36	0.88
1:A:183:MET:HE2	1:A:244:TYR:HB3	1.53	0.88
1:A:414:TRP:HE1	1:A:416:GLN:HE21	1.22	0.86
1:A:282:ASN:HD21	1:A:336:VAL:H	1.19	0.86
1:A:554:ASN:ND2	1:A:557:ASN:HD21	1.71	0.86
1:A:317:THR:CG2	1:A:319:MET:H	1.90	0.85
1:A:101:ILE:HD11	1:A:233:TYR:HB2	1.59	0.84
1:A:548:ILE:HG22	1:A:549:GLN:H	1.44	0.82
1:A:548:ILE:HG22	1:A:549:GLN:N	1.96	0.81
1:A:156:SER:HB3	1:A:162:THR:HB	1.63	0.80
1:A:317:THR:HG22	1:A:319:MET:H	1.46	0.79
1:A:418:ILE:HD12	1:A:418:ILE:N	1.96	0.79
1:A:557:ASN:H	1:A:557:ASN:ND2	1.79	0.79
1:A:162:THR:HG22	1:A:163:LYS:H	1.48	0.78
1:A:418:ILE:H	1:A:418:ILE:CD1	1.89	0.78
1:A:127:GLN:HB2	1:A:551:MET:HE2	1.64	0.77
1:A:159:GLN:HB2	1:A:160:PRO:HD2	1.65	0.77
1:A:564:ASN:C	1:A:564:ASN:HD22	1.93	0.76
1:A:216:ARG:C	1:A:216:ARG:HD3	2.09	0.76
1:A:485:ASN:HD22	1:A:485:ASN:N	1.81	0.76
1:A:382:ARG:H	1:A:386:GLN:HB3	1.50	0.76
1:A:414:TRP:NE1	1:A:416:GLN:HE21	1.83	0.76
1:A:564:ASN:HD21	1:A:568:ALA:H	1.33	0.75
1:A:101:ILE:CD1	1:A:233:TYR:HB2	2.15	0.75
1:A:158:THR:O	1:A:160:PRO:HD2	1.87	0.75
1:A:339:SER:O	1:A:449:ASN:HA	1.86	0.74
1:A:360:GLY:HA3	1:A:403:HIS:HE2	1.48	0.73
1:A:404:GLN:OE1	1:A:404:GLN:C	2.31	0.73
1:A:557:ASN:ND2	1:A:557:ASN:N	2.35	0.73
1:A:564:ASN:HD22	1:A:567:GLY:H	1.33	0.73
1:A:564:ASN:ND2	1:A:567:GLY:H	1.85	0.73
1:A:42:THR:H	1:A:147:ASN:ND2	1.87	0.72
1:A:564:ASN:ND2	1:A:567:GLY:N	2.37	0.72
1:A:183:MET:HE3	1:A:183:MET:HA	1.71	0.72
1:A:422:LEU:HA	1:A:423:PRO:C	2.14	0.72
1:A:554:ASN:CG	1:A:557:ASN:HD21	1.97	0.72
1:A:360:GLY:HA3	1:A:403:HIS:CD2	2.24	0.71
1:A:316:VAL:O	1:A:330:ILE:HD13	1.90	0.71
1:A:360:GLY:CA	1:A:403:HIS:NE2	2.53	0.71
1:A:485:ASN:H	1:A:485:ASN:ND2	1.81	0.70
1:A:435:PRO:HB3	1:A:439:LYS:O	1.90	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ALA:CA	1:A:161:PRO:HB2	2.21	0.70
1:A:85:ASN:HD22	1:A:86:ASN:N	1.89	0.70
1:A:578:LEU:H	1:A:578:LEU:HD22	1.58	0.69
1:A:99:ASP:OD1	1:A:101:ILE:HG22	1.93	0.68
1:A:391:THR:HG22	1:A:392:GLY:H	1.59	0.68
1:A:85:ASN:ND2	1:A:87:MET:HG3	2.08	0.68
1:A:194:THR:HG22	1:A:195:LEU:H	1.57	0.68
1:A:319:MET:SD	1:A:329:THR:HG23	2.33	0.68
1:A:85:ASN:HD22	1:A:86:ASN:H	1.43	0.67
1:A:360:GLY:CA	1:A:403:HIS:HE2	2.08	0.67
1:A:379:ALA:HA	1:A:397:ARG:HB3	1.75	0.66
1:A:557:ASN:N	1:A:557:ASN:HD22	1.93	0.66
1:A:554:ASN:HB2	1:A:557:ASN:ND2	2.11	0.66
1:A:157:ALA:HA	1:A:161:PRO:CB	2.25	0.65
1:A:493:ASN:H	1:A:493:ASN:ND2	1.84	0.65
1:A:47:ASN:HD21	1:A:67:ARG:HH21	1.42	0.65
1:A:216:ARG:CZ	1:A:218:LEU:HB2	2.27	0.64
1:A:386:GLN:O	1:A:387:LYS:C	2.40	0.64
1:A:554:ASN:ND2	1:A:557:ASN:ND2	2.45	0.64
1:A:183:MET:HG3	1:A:208:TRP:HH2	1.62	0.64
1:A:338:TYR:CD1	1:A:451:TYR:HB2	2.32	0.64
1:A:263:THR:HG22	1:A:264:GLY:O	1.98	0.63
1:A:130:VAL:HG13	1:A:578:LEU:HD21	1.80	0.63
1:A:422:LEU:N	1:A:422:LEU:HD23	2.14	0.63
1:A:154:SER:HB2	1:A:164:VAL:HB	1.81	0.62
1:A:215:ASP:HB3	1:A:234:HIS:HB2	1.80	0.62
1:A:293:SER:HB3	1:A:305:ASP:HB3	1.81	0.62
1:A:554:ASN:CB	1:A:557:ASN:HD21	2.11	0.62
1:A:557:ASN:HB2	1:A:561:TYR:HE2	1.64	0.62
1:A:174:MET:HE2	1:A:503:ALA:HA	1.80	0.62
1:A:459:ASN:OD1	1:A:460:VAL:N	2.33	0.62
1:A:564:ASN:ND2	1:A:564:ASN:C	2.58	0.61
1:A:510:TYR:HE2	1:A:512:PRO:HG3	1.66	0.61
1:A:99:ASP:CG	1:A:216:ARG:HH12	2.08	0.61
1:A:557:ASN:HB2	1:A:561:TYR:CE2	2.35	0.61
1:A:245:THR:HG21	1:A:248:ASN:OD1	2.01	0.60
1:A:564:ASN:ND2	1:A:566:ILE:H	1.99	0.60
1:A:87:MET:O	1:A:91:ALA:N	2.33	0.60
1:A:69:VAL:CG1	1:A:205:PRO:HD3	2.32	0.60
1:A:183:MET:HG3	1:A:208:TRP:CH2	2.37	0.60
1:A:413:ASP:O	1:A:432:PRO:HD3	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:LEU:HD22	1:A:500:VAL:HG12	1.84	0.59
1:A:326:THR:H	1:A:329:THR:HB	1.67	0.59
1:A:133:MET:SD	1:A:539:LEU:HD23	2.42	0.59
1:A:381:GLY:HA2	1:A:386:GLN:HB3	1.83	0.59
1:A:548:ILE:CG2	1:A:549:GLN:H	2.13	0.58
1:A:245:THR:CG2	1:A:248:ASN:H	2.11	0.58
1:A:431:LEU:C	1:A:433:THR:H	2.09	0.58
1:A:554:ASN:HD22	1:A:557:ASN:HD21	1.50	0.58
1:A:483:HIS:HB3	1:A:485:ASN:ND2	2.18	0.58
1:A:554:ASN:HB2	1:A:557:ASN:HD21	1.67	0.58
1:A:266:PHE:HZ	1:A:493:ASN:O	1.87	0.58
1:A:216:ARG:HD3	1:A:217:THR:N	2.18	0.58
1:A:424:VAL:CG1	1:A:429:VAL:HG21	2.34	0.58
1:A:518:MET:O	1:A:518:MET:HG3	2.03	0.58
1:A:137:HIS:CE1	1:A:272:PRO:HB3	2.38	0.57
1:A:282:ASN:N	1:A:282:ASN:HD22	2.03	0.57
1:A:183:MET:CG	1:A:208:TRP:CH2	2.88	0.57
1:A:386:GLN:HE21	1:A:396:GLU:CB	2.17	0.57
1:A:317:THR:HG23	1:A:319:MET:H	1.68	0.57
1:A:548:ILE:CG2	1:A:549:GLN:N	2.66	0.57
1:A:162:THR:HG22	1:A:163:LYS:N	2.16	0.56
1:A:46:ASN:OD1	1:A:48:GLN:HG3	2.06	0.56
1:A:360:GLY:N	1:A:403:HIS:HE2	2.03	0.56
1:A:554:ASN:HD22	1:A:557:ASN:ND2	2.04	0.56
1:A:126:TRP:O	1:A:130:VAL:HB	2.05	0.56
1:A:382:ARG:HD2	1:A:388:THR:O	2.06	0.56
1:A:557:ASN:O	1:A:559:PHE:N	2.39	0.55
1:A:42:THR:H	1:A:147:ASN:HD21	1.54	0.55
1:A:157:ALA:C	1:A:161:PRO:HB2	2.32	0.55
1:A:158:THR:O	1:A:160:PRO:CD	2.55	0.55
1:A:183:MET:HE2	1:A:244:TYR:CB	2.32	0.55
1:A:282:ASN:HD22	1:A:282:ASN:H	1.54	0.55
1:A:414:TRP:HE1	1:A:416:GLN:NE2	1.97	0.55
1:A:400:TYR:HE2	1:A:402:ALA:HB2	1.72	0.54
1:A:52:LYS:O	1:A:54:LEU:HD13	2.06	0.54
1:A:155:GLU:O	1:A:157:ALA:N	2.41	0.54
1:A:322:THR:HB	1:A:324:TYR:H	1.71	0.54
1:A:510:TYR:CE2	1:A:512:PRO:HG3	2.42	0.54
1:A:398:PHE:HE2	1:A:400:TYR:HB2	1.73	0.54
1:A:493:ASN:N	1:A:493:ASN:ND2	2.42	0.54
1:A:403:HIS:ND1	1:A:404:GLN:N	2.56	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLN:HG3	1:A:240:ASP:HB2	1.89	0.54
1:A:322:THR:HG21	1:A:420:PHE:HD2	1.72	0.53
1:A:404:GLN:CG	1:A:404:GLN:O	2.56	0.53
1:A:173:LEU:HD11	1:A:500:VAL:CG1	2.38	0.53
1:A:322:THR:HG21	1:A:420:PHE:CD2	2.44	0.53
1:A:43:GLY:HA3	1:A:146:PHE:CD2	2.44	0.52
1:A:278:THR:HG22	1:A:581:ARG:HG2	1.90	0.52
1:A:424:VAL:HG13	1:A:429:VAL:HG21	1.91	0.52
1:A:583:LEU:C	1:A:583:LEU:HD23	2.35	0.52
1:A:515:SER:O	1:A:516:ALA:C	2.53	0.52
1:A:405:ASP:OD1	1:A:406:THR:N	2.43	0.52
1:A:562:VAL:HG13	1:A:563:PRO:HD2	1.90	0.52
1:A:547:PRO:C	1:A:548:ILE:HG13	2.35	0.52
1:A:77:GLU:OE2	1:A:520:ARG:NH1	2.43	0.52
1:A:153:VAL:HG11	1:A:163:LYS:HE2	1.91	0.52
1:A:385:GLY:O	1:A:386:GLN:O	2.27	0.52
1:A:386:GLN:HE21	1:A:396:GLU:HB2	1.75	0.51
1:A:553:ILE:HA	1:A:557:ASN:OD1	2.10	0.51
1:A:159:GLN:HB2	1:A:160:PRO:HD3	1.91	0.51
1:A:557:ASN:O	1:A:558:GLN:C	2.53	0.51
1:A:578:LEU:HD23	1:A:578:LEU:O	2.09	0.51
1:A:101:ILE:HD11	1:A:233:TYR:CD2	2.45	0.51
1:A:101:ILE:HD11	1:A:233:TYR:HD2	1.75	0.51
1:A:153:VAL:HG22	1:A:165:TYR:HD2	1.76	0.51
1:A:378:TYR:O	1:A:397:ARG:HA	2.10	0.51
1:A:158:THR:O	1:A:161:PRO:HA	2.10	0.51
1:A:213:GLN:HG3	1:A:240:ASP:CB	2.41	0.51
1:A:404:GLN:C	1:A:404:GLN:CD	2.75	0.51
1:A:153:VAL:HG22	1:A:165:TYR:CD2	2.46	0.51
1:A:409:TYR:CE1	1:A:411:GLU:HB2	2.45	0.51
1:A:71:LEU:HD22	1:A:500:VAL:CG1	2.41	0.51
1:A:160:PRO:HG2	1:A:161:PRO:C	2.35	0.51
1:A:48:GLN:O	1:A:64:ASN:HB2	2.10	0.50
1:A:93:LYS:HE2	1:A:229:PRO:HD3	1.94	0.50
1:A:173:LEU:HD11	1:A:500:VAL:HG13	1.92	0.50
1:A:282:ASN:ND2	1:A:336:VAL:H	1.99	0.50
1:A:470:TRP:HA	1:A:488:PHE:O	2.11	0.50
1:A:578:LEU:O	1:A:579:ALA:HB2	2.11	0.50
1:A:203:THR:O	1:A:204:ILE:HG23	2.12	0.50
1:A:276:THR:HG22	1:A:579:ALA:O	2.11	0.50
1:A:183:MET:HA	1:A:183:MET:CE	2.41	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:TYR:CE1	1:A:235:GLY:HA2	2.47	0.50
1:A:301:THR:O	1:A:301:THR:HG22	2.12	0.50
1:A:118:GLY:HA3	1:A:197:PHE:CE2	2.47	0.49
1:A:150:LEU:HD23	1:A:525:SER:HB2	1.94	0.49
1:A:217:THR:CB	1:A:234:HIS:HE1	2.26	0.49
1:A:548:ILE:HG21	1:A:580:PRO:HD2	1.94	0.49
1:A:407:GLY:O	1:A:408:ARG:HD3	2.13	0.49
1:A:431:LEU:C	1:A:433:THR:N	2.70	0.49
1:A:578:LEU:H	1:A:578:LEU:CD2	2.25	0.49
1:A:199:PRO:HD2	1:A:200:TRP:CZ3	2.48	0.49
1:A:425:THR:HG22	1:A:427:ASP:H	1.78	0.49
1:A:101:ILE:HD13	1:A:216:ARG:HG3	1.94	0.48
1:A:148:VAL:O	1:A:257:THR:HG23	2.13	0.48
1:A:382:ARG:N	1:A:386:GLN:HB3	2.24	0.48
1:A:403:HIS:HE1	1:A:407:GLY:CA	2.27	0.48
1:A:43:GLY:HA3	1:A:146:PHE:CG	2.49	0.48
1:A:183:MET:HE3	1:A:183:MET:CA	2.41	0.48
1:A:554:ASN:HB2	1:A:556:ASP:H	1.80	0.47
1:A:178:ASP:OD2	1:A:181:ASN:HA	2.14	0.47
1:A:224:GLY:O	1:A:225:THR:C	2.57	0.47
1:A:281:THR:O	1:A:282:ASN:C	2.58	0.47
1:A:400:TYR:CE2	1:A:402:ALA:HB2	2.49	0.47
1:A:403:HIS:HE1	1:A:407:GLY:N	2.13	0.47
1:A:424:VAL:HG22	1:A:429:VAL:HG23	1.96	0.47
1:A:141:PHE:HB2	1:A:533:LEU:HD12	1.95	0.47
1:A:183:MET:HG2	1:A:208:TRP:CH2	2.49	0.47
1:A:564:ASN:ND2	1:A:568:ALA:N	2.46	0.47
1:A:212:PHE:O	1:A:214:TRP:HE3	1.97	0.47
1:A:325:ILE:HG23	1:A:330:ILE:HG12	1.96	0.47
1:A:74:PRO:O	1:A:520:ARG:NH2	2.32	0.47
1:A:54:LEU:CD1	1:A:54:LEU:N	2.77	0.47
1:A:145:ILE:O	1:A:260:GLU:HG2	2.15	0.47
1:A:156:SER:CB	1:A:162:THR:HB	2.39	0.47
1:A:217:THR:HB	1:A:234:HIS:HE1	1.79	0.47
1:A:325:ILE:CG2	1:A:330:ILE:HG12	2.45	0.47
1:A:566:ILE:HG22	1:A:566:ILE:O	2.13	0.47
1:A:477:ASP:C	1:A:478:LEU:HD23	2.41	0.46
1:A:356:PRO:O	1:A:357:ILE:HD13	2.16	0.46
1:A:174:MET:HE3	1:A:501:LYS:HD3	1.98	0.46
1:A:156:SER:O	1:A:162:THR:N	2.49	0.46
1:A:564:ASN:HD21	1:A:567:GLY:N	2.11	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:HIS:CD2	1:A:526:ASP:OD1	2.69	0.46
1:A:424:VAL:CG2	1:A:429:VAL:CG2	2.94	0.46
1:A:84:VAL:O	1:A:101:ILE:HA	2.15	0.45
1:A:422:LEU:HD23	1:A:422:LEU:H	1.82	0.45
1:A:517:ASN:O	1:A:518:MET:C	2.58	0.45
1:A:116:ALA:HA	1:A:467:GLY:O	2.16	0.45
1:A:92:VAL:O	1:A:93:LYS:C	2.60	0.45
1:A:554:ASN:H	1:A:557:ASN:CG	2.24	0.45
1:A:410:PRO:HA	1:A:413:ASP:OD2	2.17	0.45
1:A:431:LEU:HB3	1:A:432:PRO:HD2	1.98	0.45
1:A:564:ASN:ND2	1:A:566:ILE:N	2.64	0.45
1:A:564:ASN:OD1	1:A:568:ALA:HB3	2.17	0.45
1:A:158:THR:O	1:A:158:THR:HG23	2.16	0.45
1:A:231:ASN:OD1	1:A:231:ASN:C	2.58	0.45
1:A:237:ASP:OD1	1:A:237:ASP:C	2.59	0.45
1:A:386:GLN:HB2	1:A:396:GLU:CB	2.47	0.45
1:A:150:LEU:CD2	1:A:525:SER:HB2	2.47	0.45
1:A:410:PRO:HD2	1:A:411:GLU:OE1	2.17	0.45
1:A:549:GLN:CD	1:A:578:LEU:HB2	2.41	0.45
1:A:334:ALA:HB1	1:A:454:LEU:O	2.18	0.44
1:A:404:GLN:O	1:A:404:GLN:HG3	2.16	0.44
1:A:583:LEU:HD23	1:A:583:LEU:O	2.17	0.44
1:A:160:PRO:HG2	1:A:161:PRO:HA	1.99	0.44
1:A:445:THR:HA	1:A:448:PHE:HB2	2.00	0.44
1:A:122:ASN:OD1	1:A:122:ASN:C	2.59	0.44
1:A:73:MET:HB2	1:A:523:THR:O	2.17	0.44
1:A:118:GLY:CA	1:A:465:PRO:HB2	2.47	0.44
1:A:420:PHE:O	1:A:421:ASN:HB2	2.18	0.44
1:A:483:HIS:HB3	1:A:485:ASN:HD21	1.81	0.43
1:A:500:VAL:HG12	1:A:501:LYS:N	2.32	0.43
1:A:150:LEU:HD13	1:A:171:ALA:C	2.43	0.43
1:A:277:HIS:O	1:A:580:PRO:HA	2.19	0.43
1:A:70:HIS:O	1:A:204:ILE:HG22	2.19	0.43
1:A:326:THR:HG22	1:A:327:GLU:N	2.33	0.43
1:A:203:THR:C	1:A:204:ILE:HG23	2.44	0.43
1:A:70:HIS:HD2	1:A:526:ASP:OD1	2.01	0.43
1:A:557:ASN:O	1:A:560:ASN:N	2.52	0.43
1:A:322:THR:CG2	1:A:420:PHE:HD2	2.32	0.42
1:A:554:ASN:CB	1:A:557:ASN:ND2	2.77	0.42
1:A:183:MET:CE	1:A:244:TYR:HB3	2.38	0.42
1:A:130:VAL:HG13	1:A:578:LEU:CD2	2.47	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ALA:C	1:A:161:PRO:CB	2.92	0.42
1:A:127:GLN:HB2	1:A:551:MET:CE	2.44	0.42
1:A:215:ASP:N	1:A:235:GLY:O	2.44	0.42
1:A:456:ALA:O	1:A:457:LEU:HB2	2.20	0.42
1:A:55:GLU:O	1:A:56:ASN:HB2	2.19	0.42
1:A:219:ILE:HA	1:A:220:PRO:HD3	1.82	0.42
1:A:277:HIS:O	1:A:581:ARG:N	2.52	0.42
1:A:55:GLU:HA	1:A:55:GLU:OE1	2.19	0.42
1:A:385:GLY:O	1:A:386:GLN:C	2.62	0.42
1:A:261:PHE:CD1	1:A:261:PHE:C	2.98	0.42
1:A:87:MET:O	1:A:88:ASP:C	2.63	0.41
1:A:269:ASP:CG	1:A:493:ASN:ND2	2.78	0.41
1:A:420:PHE:HB3	1:A:421:ASN:H	1.72	0.41
1:A:83:VAL:HG12	1:A:84:VAL:N	2.36	0.41
1:A:291:LEU:HA	1:A:306:ILE:HA	2.02	0.41
1:A:130:VAL:HG22	1:A:576:SER:O	2.20	0.41
1:A:199:PRO:HD2	1:A:200:TRP:CE3	2.55	0.41
1:A:212:PHE:HE1	1:A:236:THR:HG21	1.85	0.41
1:A:380:PHE:CD1	1:A:380:PHE:N	2.89	0.41
1:A:386:GLN:HE21	1:A:386:GLN:HB2	1.68	0.41
1:A:387:LYS:O	1:A:390:THR:HB	2.21	0.41
1:A:389:THR:CG2	1:A:568:ALA:HB2	2.51	0.41
1:A:140:SER:HA	1:A:266:PHE:O	2.21	0.41
1:A:51:PHE:CD2	1:A:61:ILE:HG12	2.56	0.40
1:A:441:GLY:O	1:A:442:ILE:HD13	2.21	0.40
1:A:93:LYS:HE2	1:A:227:GLY:O	2.21	0.40
1:A:245:THR:HG23	1:A:247:GLU:OE1	2.20	0.40
1:A:386:GLN:NE2	1:A:396:GLU:N	2.69	0.40
1:A:562:VAL:CG1	1:A:563:PRO:HD2	2.51	0.40
1:A:578:LEU:CD2	1:A:578:LEU:N	2.83	0.40
1:A:203:THR:O	1:A:204:ILE:CG2	2.70	0.40
1:A:414:TRP:CD1	1:A:414:TRP:C	2.99	0.40
1:A:497:GLN:HB2	1:A:499:PHE:CZ	2.56	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	530/548 (97%)	477 (90%)	39 (7%)	14 (3%)	4	23

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	GLN
1	A	386	GLN
1	A	404	GLN
1	A	516	ALA
1	A	517	ASN
1	A	558	GLN
1	A	156	SER
1	A	349	THR
1	A	157	ALA
1	A	382	ARG
1	A	491	GLN
1	A	579	ALA
1	A	403	HIS
1	A	196	GLY

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	469/477 (98%)	412 (88%)	57 (12%)	5	21

All (57) 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	75	GLU
1	A	89	LYS
1	A	101	ILE
1	A	105	ILE
1	A	111	LEU
1	A	130	VAL
1	A	152	THR
1	A	183	MET
1	A	190	MET
1	A	191	ARG
1	A	194	THR
1	A	195	LEU
1	A	215	ASP
1	A	216	ARG
1	A	232	VAL
1	A	245	THR
1	A	263	THR
1	A	276	THR
1	A	281	THR
1	A	282	ASN
1	A	297	SER
1	A	317	THR
1	A	322	THR
1	A	330	ILE
1	A	342	TYR
1	A	349	THR
1	A	350	GLN
1	A	354	LYS
1	A	390	THR
1	A	391	THR
1	A	404	GLN
1	A	416	GLN
1	A	418	ILE
1	A	420	PHE
1	A	422	LEU
1	A	443	ASN
1	A	448	PHE
1	A	465	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	484	ILE
1	A	485	ASN
1	A	490	CYS
1	A	491	GLN
1	A	493	ASN
1	A	494	CYS
1	A	513	ASP
1	A	520	ARG
1	A	553	ILE
1	A	557	ASN
1	A	564	ASN
1	A	574	GLU
1	A	578	LEU
1	A	581	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	64	ASN
1	A	70	HIS
1	A	85	ASN
1	A	147	ASN
1	A	166	ASN
1	A	180	ASN
1	A	234	HIS
1	A	282	ASN
1	A	292	ASN
1	A	310	GLN
1	A	350	GLN
1	A	383	GLN
1	A	384	HIS
1	A	386	GLN
1	A	416	GLN
1	A	419	ASN
1	A	443	ASN
1	A	466	ASN
1	A	468	GLN
1	A	485	ASN
1	A	491	GLN
1	A	493	ASN
1	A	497	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	543	HIS
1	A	546	ASN
1	A	549	GLN
1	A	554	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 ⓘ

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	534/548 (97%)	-0.26	0 100 100	13, 30, 59, 100	0

There are no RSRZ outliers to report.

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.