



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 07:39 AM UTC

PDB ID : 4HPS / pdb_00004hps
Title : Crystal Structure of a Pyrrolidone-carboxylate peptidase 1 (target ID NYSGRC-012831) from *Xenorhabdus bovienii* SS-2004 in space group P21
Authors : Ghosh, A.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRC)
Deposited on : 2012-10-24
Resolution : 1.55 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

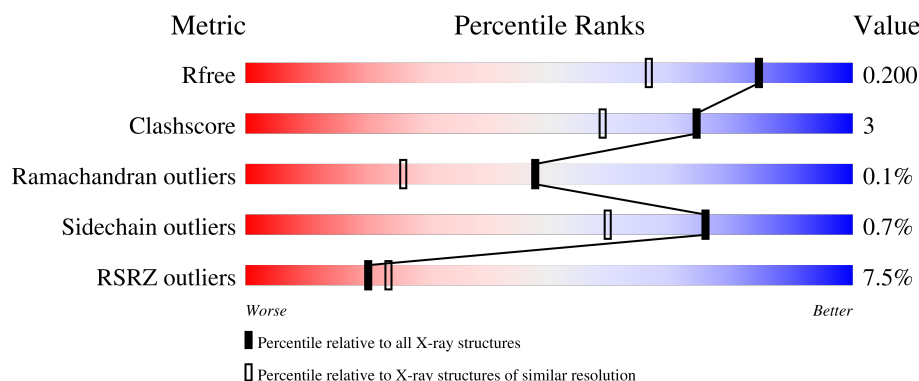
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	228	6% 86% 7% 7%
1	B	228	4% 89% • 8%
1	C	228	11% 82% 8% 10%
1	D	228	6% 83% 6% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7149 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 Pyrrolidone-carboxylate peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	5	0
			1629	1045	268	306	10			
1	B	209	Total	C	N	O	S	0	4	0
			1602	1022	266	304	10			
1	C	205	Total	C	N	O	S	0	1	0
			1554	991	260	294	9			
1	D	205	Total	C	N	O	S	0	2	0
			1562	995	262	296	9			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP D3V0W1
A	-20	HIS	-	expression tag	UNP D3V0W1
A	-19	HIS	-	expression tag	UNP D3V0W1
A	-18	HIS	-	expression tag	UNP D3V0W1
A	-17	HIS	-	expression tag	UNP D3V0W1
A	-16	HIS	-	expression tag	UNP D3V0W1
A	-15	HIS	-	expression tag	UNP D3V0W1
A	-14	SER	-	expression tag	UNP D3V0W1
A	-13	SER	-	expression tag	UNP D3V0W1
A	-12	GLY	-	expression tag	UNP D3V0W1
A	-11	VAL	-	expression tag	UNP D3V0W1
A	-10	ASP	-	expression tag	UNP D3V0W1
A	-9	LEU	-	expression tag	UNP D3V0W1
A	-8	GLY	-	expression tag	UNP D3V0W1
A	-7	THR	-	expression tag	UNP D3V0W1
A	-6	GLU	-	expression tag	UNP D3V0W1
A	-5	ASN	-	expression tag	UNP D3V0W1
A	-4	LEU	-	expression tag	UNP D3V0W1
A	-3	TYR	-	expression tag	UNP D3V0W1
A	-2	PHE	-	expression tag	UNP D3V0W1
A	-1	GLN	-	expression tag	UNP D3V0W1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP D3V0W1
B	-21	MET	-	expression tag	UNP D3V0W1
B	-20	HIS	-	expression tag	UNP D3V0W1
B	-19	HIS	-	expression tag	UNP D3V0W1
B	-18	HIS	-	expression tag	UNP D3V0W1
B	-17	HIS	-	expression tag	UNP D3V0W1
B	-16	HIS	-	expression tag	UNP D3V0W1
B	-15	HIS	-	expression tag	UNP D3V0W1
B	-14	SER	-	expression tag	UNP D3V0W1
B	-13	SER	-	expression tag	UNP D3V0W1
B	-12	GLY	-	expression tag	UNP D3V0W1
B	-11	VAL	-	expression tag	UNP D3V0W1
B	-10	ASP	-	expression tag	UNP D3V0W1
B	-9	LEU	-	expression tag	UNP D3V0W1
B	-8	GLY	-	expression tag	UNP D3V0W1
B	-7	THR	-	expression tag	UNP D3V0W1
B	-6	GLU	-	expression tag	UNP D3V0W1
B	-5	ASN	-	expression tag	UNP D3V0W1
B	-4	LEU	-	expression tag	UNP D3V0W1
B	-3	TYR	-	expression tag	UNP D3V0W1
B	-2	PHE	-	expression tag	UNP D3V0W1
B	-1	GLN	-	expression tag	UNP D3V0W1
B	0	SER	-	expression tag	UNP D3V0W1
C	-21	MET	-	expression tag	UNP D3V0W1
C	-20	HIS	-	expression tag	UNP D3V0W1
C	-19	HIS	-	expression tag	UNP D3V0W1
C	-18	HIS	-	expression tag	UNP D3V0W1
C	-17	HIS	-	expression tag	UNP D3V0W1
C	-16	HIS	-	expression tag	UNP D3V0W1
C	-15	HIS	-	expression tag	UNP D3V0W1
C	-14	SER	-	expression tag	UNP D3V0W1
C	-13	SER	-	expression tag	UNP D3V0W1
C	-12	GLY	-	expression tag	UNP D3V0W1
C	-11	VAL	-	expression tag	UNP D3V0W1
C	-10	ASP	-	expression tag	UNP D3V0W1
C	-9	LEU	-	expression tag	UNP D3V0W1
C	-8	GLY	-	expression tag	UNP D3V0W1
C	-7	THR	-	expression tag	UNP D3V0W1
C	-6	GLU	-	expression tag	UNP D3V0W1
C	-5	ASN	-	expression tag	UNP D3V0W1
C	-4	LEU	-	expression tag	UNP D3V0W1
C	-3	TYR	-	expression tag	UNP D3V0W1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PHE	-	expression tag	UNP D3V0W1
C	-1	GLN	-	expression tag	UNP D3V0W1
C	0	SER	-	expression tag	UNP D3V0W1
D	-21	MET	-	expression tag	UNP D3V0W1
D	-20	HIS	-	expression tag	UNP D3V0W1
D	-19	HIS	-	expression tag	UNP D3V0W1
D	-18	HIS	-	expression tag	UNP D3V0W1
D	-17	HIS	-	expression tag	UNP D3V0W1
D	-16	HIS	-	expression tag	UNP D3V0W1
D	-15	HIS	-	expression tag	UNP D3V0W1
D	-14	SER	-	expression tag	UNP D3V0W1
D	-13	SER	-	expression tag	UNP D3V0W1
D	-12	GLY	-	expression tag	UNP D3V0W1
D	-11	VAL	-	expression tag	UNP D3V0W1
D	-10	ASP	-	expression tag	UNP D3V0W1
D	-9	LEU	-	expression tag	UNP D3V0W1
D	-8	GLY	-	expression tag	UNP D3V0W1
D	-7	THR	-	expression tag	UNP D3V0W1
D	-6	GLU	-	expression tag	UNP D3V0W1
D	-5	ASN	-	expression tag	UNP D3V0W1
D	-4	LEU	-	expression tag	UNP D3V0W1
D	-3	TYR	-	expression tag	UNP D3V0W1
D	-2	PHE	-	expression tag	UNP D3V0W1
D	-1	GLN	-	expression tag	UNP D3V0W1
D	0	SER	-	expression tag	UNP D3V0W1

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Cl 2 2	0	0
2	B	5	Total Cl 5 5	0	0
2	C	3	Total Cl 3 3	0	0
2	D	5	Total Cl 5 5	0	0

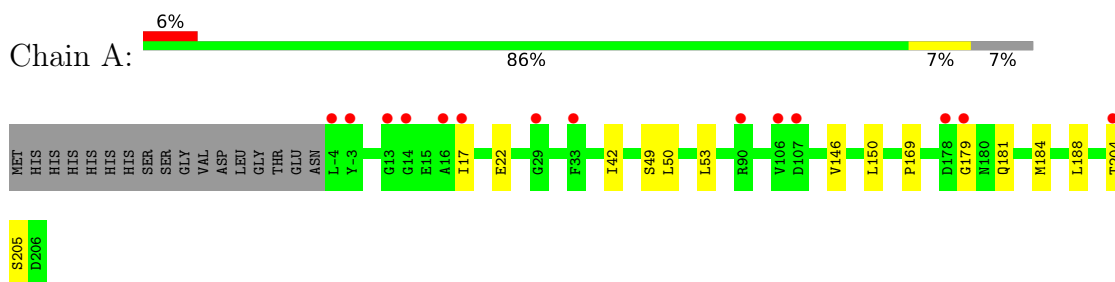
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	202	Total 204	O 204	0	2
3	B	190	Total 190	O 190	0	0
3	C	160	Total 161	O 161	0	1
3	D	230	Total 232	O 232	0	2

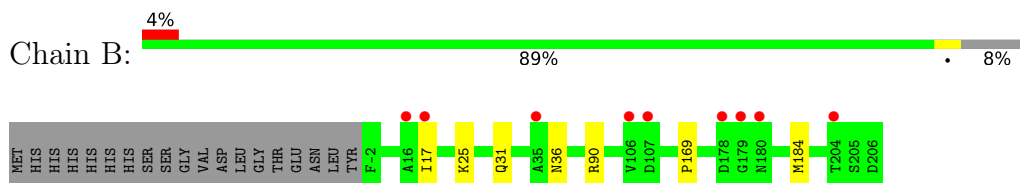
3 Residue-property plots

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.

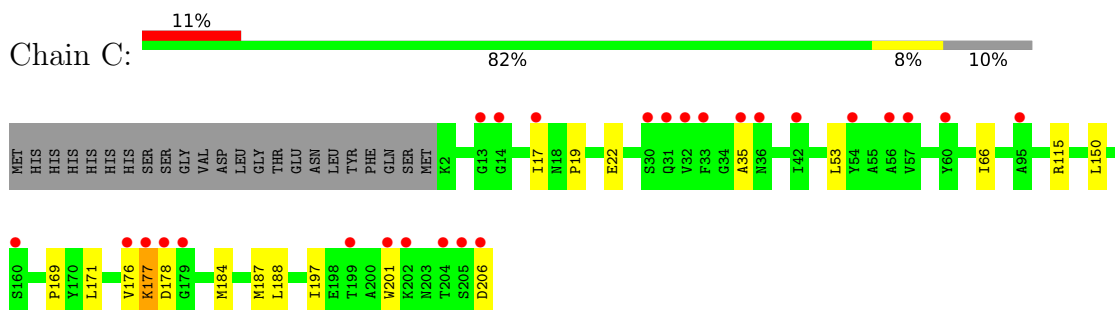
- Molecule 1: Pyrrolidone-carboxylate peptidase



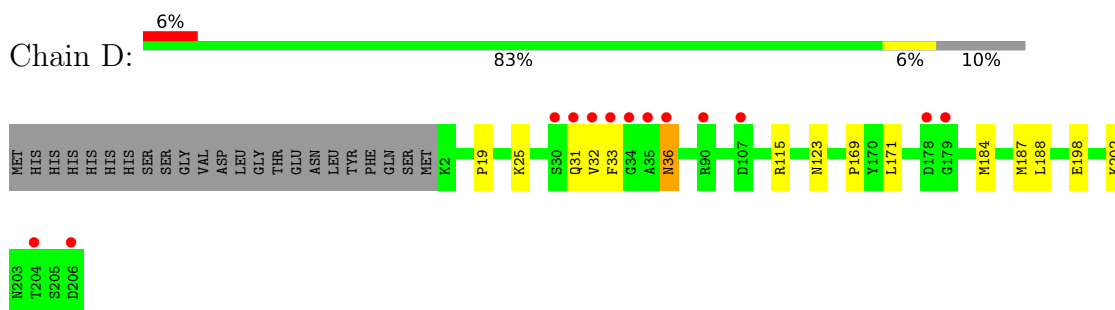
- Molecule 1: Pyrrolidone-carboxylate peptidase



- Molecule 1: Pyrrolidone-carboxylate peptidase



- Molecule 1: Pyrrolidone-carboxylate peptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.06Å 73.34Å 80.54Å 90.00° 111.96° 90.00°	Depositor
Resolution (Å)	39.76 – 1.55 39.76 – 1.55	Depositor EDS
% Data completeness (in resolution range)	96.0 (39.76-1.55) 96.1 (39.76-1.55)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 1.55Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.173 , 0.200 0.174 , 0.200	Depositor DCC
R_{free} test set	5788 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.008 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7149	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.6853e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/1680	0.72	0/2295
1	B	0.41	0/1649	0.76	0/2253
1	C	0.40	0/1591	0.74	0/2174
1	D	0.41	0/1599	0.72	0/2185
All	All	0.41	0/6519	0.73	0/8907

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1629	0	1645	10	0
1	B	1602	0	1608	4	0
1	C	1554	0	1557	11	0
1	D	1562	0	1562	11	0
2	A	2	0	0	0	0
2	B	5	0	0	2	0
2	C	3	0	0	1	0
2	D	5	0	0	1	0
3	A	204	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	190	0	0	2	0
3	C	161	0	0	3	0
3	D	232	0	0	3	0
All	All	7149	0	6372	39	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 3.

All (39) 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:D:31:GLN:HE22	1:D:36:ASN:HB3	1.53	0.74
1:A:184[B]:MET:HG3	1:A:188:LEU:HD23	1.74	0.68
2:B:302:CL:CL	3:B:509:HOH:O	2.51	0.65
1:C:66:ILE:HD12	1:C:197:ILE:HG12	1.83	0.59
1:C:184[B]:MET:HG3	1:C:188:LEU:HD23	1.85	0.58
1:C:177:LYS:HG3	3:C:481:HOH:O	2.02	0.58
1:D:169:PRO:HG2	1:D:184[A]:MET:HB2	1.88	0.56
1:D:184[B]:MET:HG3	1:D:188:LEU:HD23	1.89	0.55
2:D:302:CL:CL	2:D:303:CL:CL	3.01	0.53
1:C:19:PRO:HB3	1:C:171:LEU:HG	1.90	0.52
1:A:17:ILE:HD11	1:A:22:GLU:HG3	1.91	0.52
1:B:90:ARG:HG2	2:B:301:CL:CL	2.46	0.51
1:D:25:LYS:NZ	3:D:626:HOH:O	2.40	0.51
1:A:42[B]:ILE:HD11	1:A:49:SER:HB2	1.92	0.51
1:D:33:PHE:CE2	1:D:202:LYS:HD3	2.46	0.51
1:A:169:PRO:HG2	1:A:184[A]:MET:HB2	1.94	0.50
1:C:17:ILE:HD11	1:C:22:GLU:HG3	1.92	0.50
1:D:19:PRO:HB3	1:D:171:LEU:HG	1.94	0.50
1:D:123[B]:ASN:ND2	3:D:471:HOH:O	2.42	0.50
1:D:115:ARG:NH1	3:D:595:HOH:O	2.42	0.49
2:C:301:CL:CL	2:C:303:CL:CL	3.05	0.48
1:C:169:PRO:HG2	1:C:184[A]:MET:HB2	1.97	0.47
1:D:31:GLN:NE2	1:D:36:ASN:HB3	2.25	0.47
1:B:25:LYS:NZ	3:B:560:HOH:O	2.49	0.46
1:C:115:ARG:NH1	3:C:453:HOH:O	2.49	0.46
1:C:176:VAL:O	1:C:178:ASP:N	2.49	0.46
1:A:17:ILE:HG22	3:A:563:HOH:O	2.16	0.46
1:D:187:MET:HE3	1:D:187:MET:HB2	1.88	0.45
1:B:169:PRO:HG2	1:B:184[A]:MET:HB2	1.99	0.45
1:A:50:LEU:HD21	1:A:146:VAL:HA	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:LEU:HD21	1:C:150:LEU:HB2	1.99	0.44
1:C:187:MET:HB2	1:C:187:MET:HE3	1.80	0.44
1:A:53:LEU:HD21	1:A:150:LEU:HB2	2.01	0.43
1:A:42[B]:ILE:HD11	1:A:146:VAL:HG21	2.01	0.42
1:A:179:GLY:O	1:A:181:GLN:NE2	2.53	0.42
1:B:31:GLN:HG2	1:B:36:ASN:OD1	2.21	0.41
1:D:32:VAL:HG13	1:D:198:GLU:HG2	2.03	0.41
1:C:35:ALA:HB2	1:C:201:TRP:CZ2	2.56	0.40
1:A:184[A]:MET:HG2	3:C:405:HOH: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	214/228 (94%)	208 (97%)	6 (3%)	0	100	100
1	B	211/228 (92%)	206 (98%)	5 (2%)	0	100	100
1	C	204/228 (90%)	199 (98%)	4 (2%)	1 (0%)	24	8
1	D	205/228 (90%)	198 (97%)	7 (3%)	0	100	100
All	All	834/912 (91%)	811 (97%)	22 (3%)	1 (0%)	48	26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	177	LYS

5.3.2 Protein sidechains [i](#)

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	180/190 (95%)	178 (99%)	2 (1%)	65	43
1	B	177/190 (93%)	176 (99%)	1 (1%)	78	64
1	C	170/190 (90%)	169 (99%)	1 (1%)	78	64
1	D	171/190 (90%)	170 (99%)	1 (1%)	78	64
All	All	698/760 (92%)	693 (99%)	5 (1%)	76	59

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	204	THR
1	A	205	SER
1	B	17	ILE
1	C	206	ASP
1	D	36	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	41	GLN
1	B	157	ASN
1	C	97	ASN
1	D	31	GLN
1	D	181	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 15 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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	211/228 (92%)	0.36	14 (6%) 24 29	11, 24, 53, 77	5 (2%)
1	B	209/228 (91%)	0.30	9 (4%) 40 48	12, 24, 50, 64	4 (1%)
1	C	205/228 (89%)	0.91	26 (12%) 8 9	13, 36, 68, 89	1 (0%)
1	D	205/228 (89%)	0.29	13 (6%) 26 31	11, 24, 47, 72	2 (0%)
All	All	830/912 (91%)	0.47	62 (7%) 20 23	11, 26, 56, 89	12 (1%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-4	LEU	5.2
1	C	204	THR	4.6
1	C	32	VAL	4.5
1	A	204	THR	4.3
1	C	33	PHE	4.2
1	C	177	LYS	4.1
1	C	35	ALA	4.1
1	C	205	SER	4.1
1	C	31	GLN	3.9
1	C	178	ASP	3.9
1	D	33	PHE	3.9
1	B	179	GLY	3.8
1	A	14	GLY	3.8
1	C	206	ASP	3.8
1	A	33	PHE	3.7
1	B	17	ILE	3.7
1	D	178	ASP	3.7
1	C	42	ILE	3.7
1	C	179	GLY	3.7
1	B	107	ASP	3.5
1	D	34	GLY	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	201	TRP	3.5
1	D	179	GLY	3.4
1	A	179	GLY	3.3
1	D	204	THR	3.3
1	A	-3	TYR	3.2
1	C	56	ALA	3.0
1	B	16	ALA	3.0
1	B	178	ASP	3.0
1	C	36	ASN	3.0
1	C	95	ALA	2.8
1	C	30	SER	2.8
1	C	60	TYR	2.8
1	A	178	ASP	2.6
1	C	176	VAL	2.6
1	A	17	ILE	2.6
1	A	107	ASP	2.5
1	A	13	GLY	2.5
1	B	180	ASN	2.5
1	C	160	SER	2.5
1	D	32	VAL	2.5
1	B	35	ALA	2.4
1	D	90	ARG	2.4
1	C	57	VAL	2.4
1	C	54	TYR	2.3
1	A	106	VAL	2.3
1	D	36	ASN	2.3
1	B	204	THR	2.3
1	C	14	GLY	2.3
1	A	16	ALA	2.2
1	A	90	ARG	2.2
1	D	107	ASP	2.2
1	D	31	GLN	2.2
1	A	29	GLY	2.1
1	C	13	GLY	2.1
1	C	17	ILE	2.1
1	C	202	LYS	2.1
1	C	199	THR	2.1
1	D	30	SER	2.1
1	B	106	VAL	2.0
1	D	35	ALA	2.0
1	D	206	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	C	303	1/1	0.90	0.25	54,54,54,54	0
2	CL	D	301	1/1	0.92	0.18	57,57,57,57	0
2	CL	A	301	1/1	0.93	0.26	71,71,71,71	0
2	CL	B	301	1/1	0.93	0.24	57,57,57,57	0
2	CL	D	304	1/1	0.93	0.15	51,51,51,51	0
2	CL	D	303	1/1	0.94	0.26	52,52,52,52	0
2	CL	B	302	1/1	0.94	0.16	54,54,54,54	0
2	CL	C	301	1/1	0.95	0.10	32,32,32,32	1
2	CL	B	303	1/1	0.96	0.11	48,48,48,48	0
2	CL	D	302	1/1	0.97	0.07	27,27,27,27	1
2	CL	B	304	1/1	0.98	0.08	24,24,24,24	0
2	CL	D	305	1/1	0.98	0.09	25,25,25,25	0
2	CL	B	305	1/1	0.99	0.03	28,28,28,28	1
2	CL	A	302	1/1	0.99	0.06	26,26,26,26	0
2	CL	C	302	1/1	0.99	0.08	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.