



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:45 PM UTC

PDB ID : 2AMF / pdb_00002amf
Title : Crystal structure of 1-Pyrroline-5-Carboxylate Reductase from Human Pathogen Streptococcus Pyogenes
Authors : Nocek, B.; Lezondra, L.; Holzle, D.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2005-08-09
Resolution : 2.20 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
Mogul : 2022.3.0, CSD as543be (2022)
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

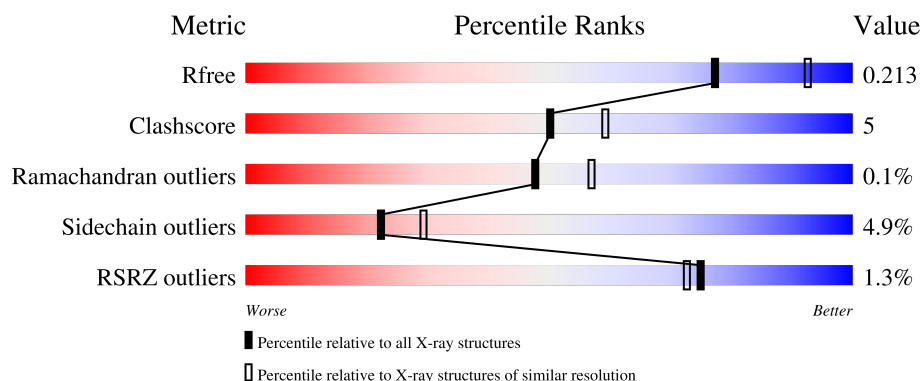
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	259	89% 8% ..
1	B	259	% 89% 10% .
1	C	259	4% 84% 12% ..
1	D	259	% 86% 12% .
1	E	259	% 86% 11% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PRO	A	4243	-	-	X	-
3	PRO	B	4242	-	-	X	-
3	PRO	B	4332	-	-	X	-
3	PRO	C	4241	-	-	X	-
3	PRO	D	4240	-	-	X	-
3	PRO	E	4244	-	-	X	-
3	PRO	E	4334	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10448 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 1-Pyrroline-5-Carboxylate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	5	1	0
			1926	1227	319	372	8			
1	B	257	Total	C	N	O	S	0	0	0
			1921	1224	319	370	8			
1	C	256	Total	C	N	O	S	0	0	0
			1916	1221	318	369	8			
1	D	258	Total	C	N	O	S	0	0	0
			1926	1227	320	371	8			
1	E	259	Total	C	N	O	S	0	0	0
			1935	1231	322	374	8			

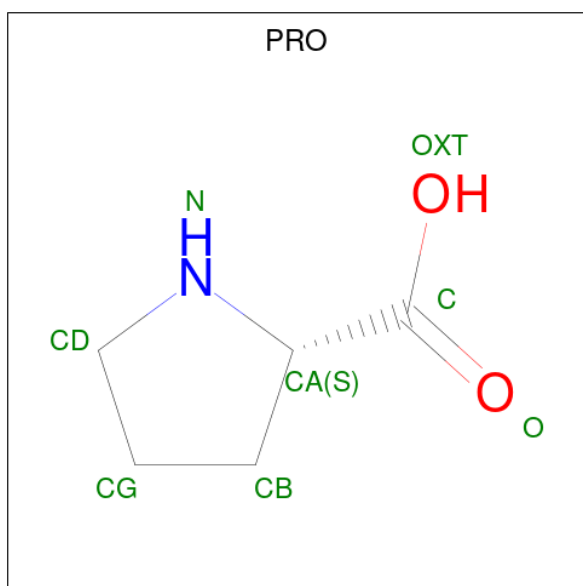
There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	cloning artifact	GB 13621418
A	-1	ASN	-	cloning artifact	GB 13621418
A	0	ALA	-	cloning artifact	GB 13621418
B	-2	SER	-	cloning artifact	GB 13621418
B	-1	ASN	-	cloning artifact	GB 13621418
B	0	ALA	-	cloning artifact	GB 13621418
C	-2	SER	-	cloning artifact	GB 13621418
C	-1	ASN	-	cloning artifact	GB 13621418
C	0	ALA	-	cloning artifact	GB 13621418
D	-2	SER	-	cloning artifact	GB 13621418
D	-1	ASN	-	cloning artifact	GB 13621418
D	0	ALA	-	cloning artifact	GB 13621418
E	-2	SER	-	cloning artifact	GB 13621418
E	-1	ASN	-	cloning artifact	GB 13621418
E	0	ALA	-	cloning artifact	GB 13621418

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	B	1	Total Na 1 1	0	0
2	C	1	Total Na 1 1	0	0
2	D	1	Total Na 1 1	0	0
2	E	1	Total Na 1 1	0	0

- Molecule 3 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 8 5 1 2	0	0
3	A	1	Total C N O 8 5 1 2	0	0
3	B	1	Total C N O 8 5 1 2	0	0
3	B	1	Total C N O 8 5 1 2	0	0
3	C	1	Total C N O 8 5 1 2	0	0
3	C	1	Total C N O 8 5 1 2	0	0
3	D	1	Total C N O 8 5 1 2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			8	5	1	2		
3	E	1	Total	C	N	O	0	0
			8	5	1	2		
3	E	1	Total	C	N	O	0	0
			8	5	1	2		

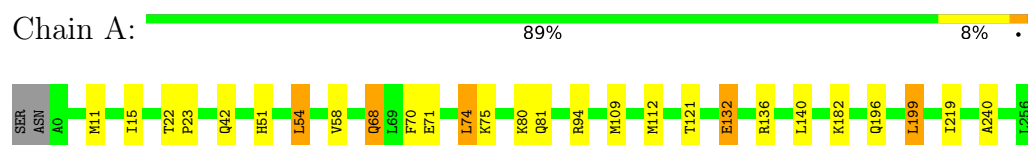
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	162	Total	O	0	0
			162	162		
4	B	133	Total	O	0	0
			133	133		
4	C	113	Total	O	0	0
			113	113		
4	D	158	Total	O	0	0
			158	158		
4	E	173	Total	O	0	0
			173	173		

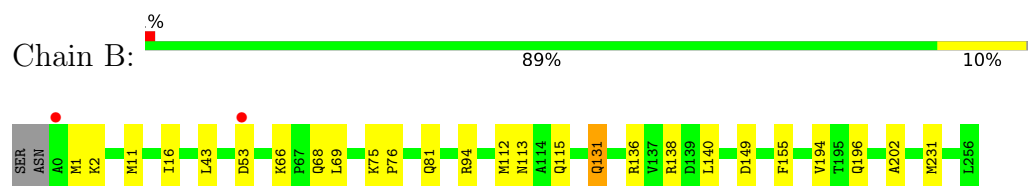
3 Residue-property plots [i](#)

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.

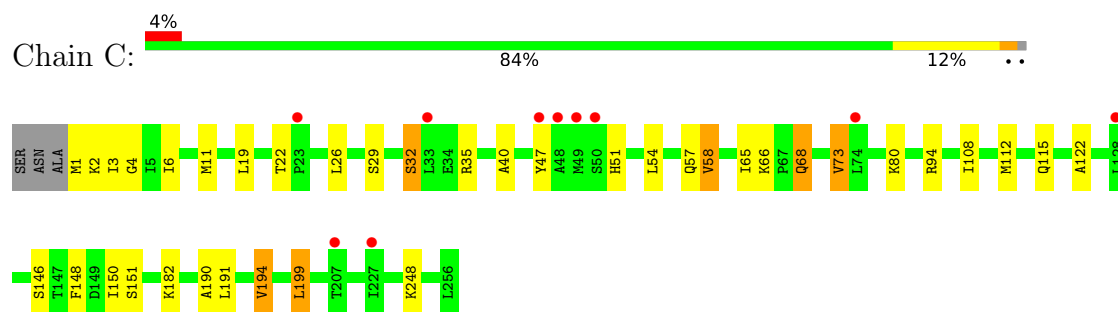
- Molecule 1: 1-Pyrroline-5-Carboxylate reductase



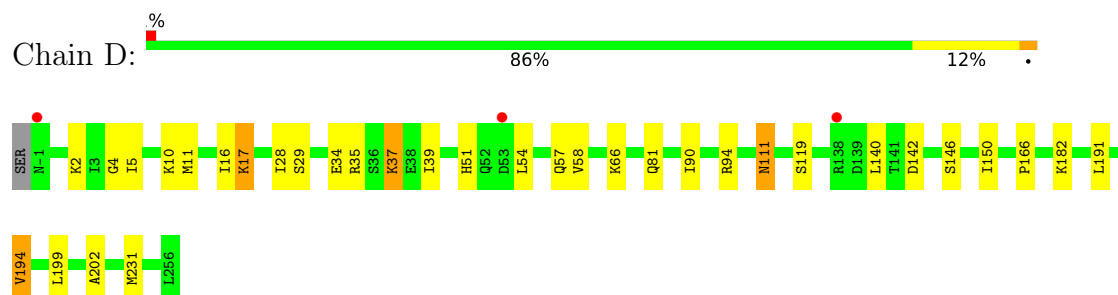
- Molecule 1: 1-Pyrroline-5-Carboxylate reductase



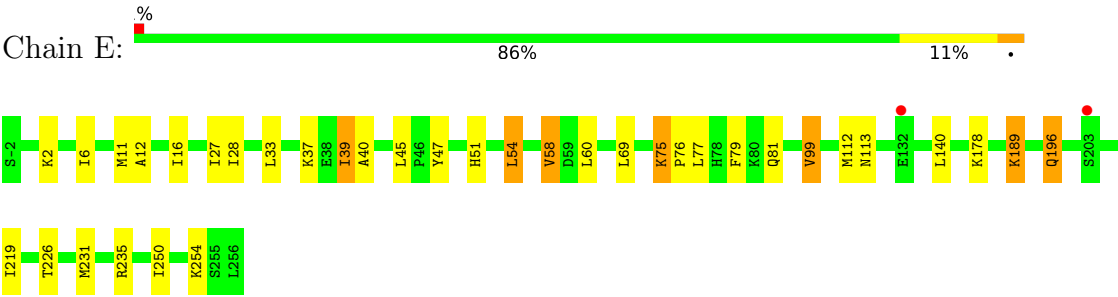
- Molecule 1: 1-Pyrroline-5-Carboxylate reductase



- Molecule 1: 1-Pyrroline-5-Carboxylate reductase



- Molecule 1: 1-Pyrroline-5-Carboxylate reductase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	171.82Å 109.96Å 84.16Å 90.00° 95.38° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.20) 99.1 (50.00-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.173 , 0.215 0.172 , 0.213	Depositor DCC
R_{free} test set	3930 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10448	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.83% 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: 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	A	0.71	0/1955	0.94	0/2644
1	B	0.72	0/1947	0.89	1/2633 (0.0%)
1	C	0.67	0/1942	0.93	2/2626 (0.1%)
1	D	0.74	1/1952 (0.1%)	0.90	0/2640
1	E	0.73	0/1961	0.95	2/2652 (0.1%)
All	All	0.71	1/9757 (0.0%)	0.92	5/13195 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	194	VAL	CA-CB	5.26	1.61	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	22	THR	CA-C-N	-6.35	114.35	120.83
1	C	22	THR	C-N-CA	-6.35	114.35	120.83
1	B	155	PHE	N-CA-C	5.07	116.80	111.28
1	E	75	LYS	CA-C-N	5.06	124.72	119.56
1	E	75	LYS	C-N-CA	5.06	124.72	119.56

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	1926	0	2018	19	0
1	B	1921	0	2014	13	0
1	C	1916	0	2009	27	0
1	D	1926	0	2016	21	0
1	E	1935	0	2025	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	16	0	14	4	0
3	B	16	0	14	8	0
3	C	16	0	14	4	0
3	D	16	0	14	5	0
3	E	16	0	14	7	0
4	A	162	0	0	2	0
4	B	133	0	0	4	0
4	C	113	0	0	1	0
4	D	158	0	0	1	0
4	E	173	0	0	4	0
All	All	10448	0	10152	106	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 5.

All (106) 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)
3:E:4244:PRO:OXT	4:E:4426:HOH:O	1.80	0.98
3:B:4242:PRO:HA	3:B:4332:PRO:N	1.82	0.94
3:E:4244:PRO:HA	3:E:4334:PRO:N	1.81	0.94
3:C:4241:PRO:HA	3:C:4331:PRO:N	1.92	0.84
3:E:4244:PRO:HA	3:E:4334:PRO:CD	2.11	0.81
3:D:4240:PRO:HA	3:D:4330:PRO:N	1.97	0.80
3:B:4242:PRO:HB2	1:C:11:MET:HB2	1.69	0.75
1:B:202:ALA:HB3	1:C:199:LEU:HD13	1.72	0.72
3:C:4241:PRO:HA	3:C:4331:PRO:CD	2.19	0.72
1:A:112:MET:HE2	3:D:4240:PRO:HD2	1.70	0.72
3:A:4243:PRO:HA	3:A:4333:PRO:N	2.05	0.70
1:E:11:MET:HB2	3:E:4244:PRO:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4:GLY:HA3	1:D:54:LEU:HD11	1.75	0.67
1:C:148:PHE:HB3	1:C:150:ILE:HD11	1.79	0.64
1:A:94:ARG:HD3	4:A:4488:HOH:O	1.97	0.63
3:B:4242:PRO:HA	3:B:4332:PRO:CD	2.28	0.63
3:D:4240:PRO:HA	3:D:4330:PRO:CD	2.28	0.63
3:E:4244:PRO:HA	3:E:4334:PRO:HD3	1.81	0.63
1:D:111:ASN:C	1:D:111:ASN:HD22	2.07	0.63
1:C:1:MET:HE3	1:C:3:ILE:HD11	1.82	0.62
1:B:112:MET:O	1:B:115:GLN:HG2	1.99	0.62
1:E:113:ASN:ND2	4:E:4403:HOH:O	2.32	0.61
1:D:182:LYS:HD2	1:E:231:MET:HG3	1.84	0.59
3:A:4243:PRO:HA	3:A:4333:PRO:CA	2.32	0.59
1:A:196:GLN:HE22	1:D:146:SER:HB2	1.68	0.58
3:A:4243:PRO:HB2	1:D:11:MET:HB2	1.85	0.58
1:B:11:MET:HB2	3:C:4241:PRO:HB2	1.85	0.58
1:E:112:MET:HE3	3:E:4244:PRO:HD2	1.85	0.58
1:E:189:LYS:HA	1:E:189:LYS:HE3	1.86	0.58
1:C:148:PHE:CB	1:C:150:ILE:HD11	2.33	0.58
1:B:202:ALA:CB	1:C:199:LEU:HD13	2.33	0.58
1:C:40:ALA:HB2	1:C:47:TYR:HB3	1.85	0.57
1:E:75:LYS:N	1:E:76:PRO:HD2	2.18	0.57
3:B:4242:PRO:HA	3:B:4332:PRO:CA	2.34	0.57
1:B:1:MET:HE1	1:B:136:ARG:HG2	1.87	0.57
1:C:4:GLY:N	1:C:58:VAL:HG21	2.20	0.56
3:C:4241:PRO:HA	3:C:4331:PRO:HD3	1.87	0.56
1:D:111:ASN:HD21	1:D:119:SER:HA	1.70	0.56
1:D:34:GLU:HG3	1:D:37:LYS:HE2	1.87	0.55
1:C:148:PHE:CB	1:C:150:ILE:CD1	2.86	0.54
1:C:32:SER:H	1:C:35:ARG:HB2	1.73	0.53
1:A:11:MET:HB2	3:D:4240:PRO:HB2	1.91	0.53
1:A:71:GLU:HG3	1:A:75:LYS:CE	2.39	0.52
1:B:94:ARG:HD3	4:B:4429:HOH:O	2.08	0.52
1:B:149:ASP:HB2	4:B:4451:HOH:O	2.08	0.52
3:A:4243:PRO:HA	3:A:4333:PRO:CD	2.39	0.52
1:C:148:PHE:HB3	1:C:150:ILE:CD1	2.40	0.52
1:E:40:ALA:HB1	1:E:45:LEU:O	2.09	0.52
1:A:70:PHE:O	1:A:74:LEU:HB2	2.10	0.52
1:A:199:LEU:HD12	1:D:199:LEU:HD12	1.91	0.52
3:B:4242:PRO:HB2	1:C:11:MET:CB	2.40	0.51
1:B:113:ASN:ND2	4:B:4384:HOH:O	2.43	0.50
1:C:190:ALA:O	1:C:194:VAL:HG13	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:219:ILE:HG22	1:E:226:THR:HG21	1.93	0.50
1:A:71:GLU:HG3	1:A:75:LYS:HE2	1.93	0.50
1:D:90:ILE:HG23	1:D:94:ARG:HD2	1.93	0.49
1:D:35:ARG:O	1:D:39:ILE:HG12	2.14	0.48
1:D:5:ILE:HD13	1:D:16:ILE:HD11	1.95	0.48
1:E:37:LYS:HG2	1:E:47:TYR:CZ	2.49	0.48
1:B:196:GLN:HE22	1:C:146:SER:HB2	1.79	0.47
1:C:108:ILE:HA	1:C:122:ALA:O	2.15	0.47
1:E:79:PHE:CD1	1:E:99:VAL:HG22	2.50	0.47
1:C:148:PHE:HB2	1:C:150:ILE:CD1	2.45	0.47
1:C:6:ILE:HG23	1:C:51:HIS:CD2	2.49	0.46
1:A:112:MET:CE	3:D:4240:PRO:HD2	2.43	0.46
1:B:75:LYS:N	1:B:76:PRO:HD2	2.30	0.46
1:C:29:SER:OG	1:C:51:HIS:HD2	1.99	0.45
1:C:248:LYS:HE3	4:C:4339:HOH:O	2.17	0.44
3:E:4244:PRO:CA	3:E:4334:PRO:N	2.69	0.44
1:B:138:ARG:HD2	4:B:4450:HOH:O	2.16	0.44
3:B:4242:PRO:CA	3:B:4332:PRO:N	2.69	0.44
1:D:29:SER:OG	1:D:51:HIS:HD2	2.01	0.44
1:A:68:GLN:NE2	1:A:68:GLN:H	2.15	0.44
1:E:12:ALA:O	1:E:16:ILE:HG12	2.17	0.44
1:E:196:GLN:HG2	4:E:4338:HOH:O	2.16	0.44
3:B:4242:PRO:HD2	1:C:112:MET:HE3	2.00	0.44
1:C:65:ILE:HD13	1:C:73:VAL:CG2	2.48	0.43
1:D:142:ASP:O	4:D:4456:HOH:O	2.21	0.43
1:A:22:THR:HB	1:A:23:PRO:HD2	1.99	0.43
1:C:2:LYS:HD2	1:C:57:GLN:O	2.19	0.43
1:A:42:GLN:NE2	4:A:4409:HOH:O	2.52	0.42
1:A:199:LEU:HD13	1:D:202:ALA:HB3	2.01	0.42
1:D:2:LYS:NZ	1:D:57:GLN:HE21	2.17	0.42
1:B:66:LYS:HE3	1:B:68:GLN:HB2	2.01	0.42
1:C:112:MET:O	1:C:115:GLN:HG3	2.19	0.42
1:A:219:ILE:HD13	1:D:166:PRO:HB2	2.01	0.42
1:E:28:ILE:HD13	1:E:39:ILE:HD11	2.02	0.42
1:A:132:GLU:O	1:A:136:ARG:HG3	2.20	0.42
1:A:182:LYS:HD2	1:B:231:MET:HG3	2.00	0.42
1:C:66:LYS:HB3	1:C:68:GLN:HE21	1.84	0.42
1:E:178:LYS:NZ	4:E:4368:HOH:O	2.49	0.42
1:E:27:ILE:HG23	1:E:54:LEU:HD22	2.02	0.42
1:C:182:LYS:HD2	1:D:231:MET:HG3	2.01	0.41
1:D:4:GLY:CA	1:D:54:LEU:HD11	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:LYS:H	1:D:17:LYS:HG2	1.66	0.41
1:D:111:ASN:ND2	1:D:119:SER:HA	2.34	0.41
1:A:109:MET:O	1:A:121:THR:HA	2.20	0.41
1:C:150:ILE:HG22	1:C:151:SER:O	2.19	0.41
1:D:28:ILE:C	1:D:28:ILE:HD12	2.45	0.41
1:A:240:ALA:CB	1:E:235:ARG:HA	2.51	0.41
3:B:4242:PRO:HD2	1:C:112:MET:CE	2.51	0.41
1:E:250:ILE:HG22	1:E:254:LYS:HE2	2.03	0.41
1:E:33:LEU:O	1:E:37:LYS:HG3	2.21	0.41
1:E:6:ILE:HG23	1:E:51:HIS:CE1	2.56	0.40
1:A:51:HIS:O	1:A:54:LEU:HB3	2.20	0.40
1:E:58:VAL:HG13	1:E:60:LEU:H	1.85	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	256/259 (99%)	253 (99%)	3 (1%)	0	100	100
1	B	255/259 (98%)	249 (98%)	5 (2%)	1 (0%)	30	34
1	C	254/259 (98%)	244 (96%)	10 (4%)	0	100	100
1	D	256/259 (99%)	252 (98%)	4 (2%)	0	100	100
1	E	257/259 (99%)	252 (98%)	5 (2%)	0	100	100
All	All	1278/1295 (99%)	1250 (98%)	27 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	131	GLN

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	213/214 (100%)	203 (95%)	10 (5%)	23	31
1	B	212/214 (99%)	203 (96%)	9 (4%)	26	36
1	C	212/214 (99%)	200 (94%)	12 (6%)	18	23
1	D	212/214 (99%)	201 (95%)	11 (5%)	21	26
1	E	214/214 (100%)	203 (95%)	11 (5%)	21	27
All	All	1063/1070 (99%)	1010 (95%)	53 (5%)	22	28

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ILE
1	A	54	LEU
1	A	58	VAL
1	A	68	GLN
1	A	74	LEU
1	A	80	LYS
1	A	81	GLN
1	A	132	GLU
1	A	140	LEU
1	A	199	LEU
1	B	2	LYS
1	B	16	ILE
1	B	43	LEU
1	B	53	ASP
1	B	69	LEU
1	B	81	GLN
1	B	131	GLN
1	B	140	LEU
1	B	194	VAL
1	C	19	LEU
1	C	26	LEU
1	C	32	SER
1	C	54	LEU

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Mol	Chain	Res	Type
1	C	58	VAL
1	C	68	GLN
1	C	73	VAL
1	C	80	LYS
1	C	94	ARG
1	C	191	LEU
1	C	194	VAL
1	C	199	LEU
1	D	10	LYS
1	D	17	LYS
1	D	37	LYS
1	D	58	VAL
1	D	66	LYS
1	D	81	GLN
1	D	111	ASN
1	D	140	LEU
1	D	150	ILE
1	D	191	LEU
1	D	194	VAL
1	E	2	LYS
1	E	39	ILE
1	E	54	LEU
1	E	58	VAL
1	E	69	LEU
1	E	77	LEU
1	E	81	GLN
1	E	99	VAL
1	E	140	LEU
1	E	189	LYS
1	E	196	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	101	GLN
1	A	196	GLN
1	A	204	ASN
1	A	210	GLN
1	B	113	ASN
1	B	118	GLN
1	B	131	GLN

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Mol	Chain	Res	Type
1	B	134	GLN
1	B	196	GLN
1	C	51	HIS
1	C	68	GLN
1	C	101	GLN
1	C	113	ASN
1	C	115	GLN
1	C	118	GLN
1	C	204	ASN
1	D	21	GLN
1	D	51	HIS
1	D	57	GLN
1	D	111	ASN
1	D	115	GLN
1	D	131	GLN
1	D	196	GLN
1	D	204	ASN
1	E	113	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 15 ligands modelled in this entry, 5 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	PRO	A	4243	-	8,8,8	1.10	0	10,10,10	1.74	3 (30%)
3	PRO	B	4332	-	8,8,8	0.66	0	10,10,10	1.32	2 (20%)
3	PRO	E	4244	-	8,8,8	1.07	1 (12%)	10,10,10	1.80	3 (30%)
3	PRO	C	4241	-	8,8,8	1.22	1 (12%)	10,10,10	1.72	2 (20%)
3	PRO	A	4333	-	8,8,8	0.75	0	10,10,10	1.22	2 (20%)
3	PRO	E	4334	-	8,8,8	0.93	1 (12%)	10,10,10	1.11	0
3	PRO	D	4240	-	8,8,8	1.10	1 (12%)	10,10,10	1.48	2 (20%)
3	PRO	B	4242	-	8,8,8	1.03	0	10,10,10	1.59	3 (30%)
3	PRO	C	4331	-	8,8,8	0.70	0	10,10,10	1.17	1 (10%)
3	PRO	D	4330	-	8,8,8	0.83	0	10,10,10	1.29	2 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PRO	A	4243	-	-	3/4/11/11	0/1/1/1
3	PRO	B	4332	-	-	2/4/11/11	0/1/1/1
3	PRO	E	4244	-	-	4/4/11/11	0/1/1/1
3	PRO	C	4241	-	-	4/4/11/11	0/1/1/1
3	PRO	A	4333	-	-	0/4/11/11	0/1/1/1
3	PRO	E	4334	-	-	0/4/11/11	0/1/1/1
3	PRO	D	4240	-	-	4/4/11/11	0/1/1/1
3	PRO	B	4242	-	-	2/4/11/11	0/1/1/1
3	PRO	C	4331	-	-	0/4/11/11	0/1/1/1
3	PRO	D	4330	-	-	0/4/11/11	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	4240	PRO	OXT-C	-2.42	1.22	1.30
3	C	4241	PRO	OXT-C	-2.34	1.23	1.30
3	E	4334	PRO	OXT-C	-2.23	1.23	1.30
3	E	4244	PRO	OXT-C	-2.21	1.23	1.30

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4244	PRO	OXT-C-O	-3.71	115.65	124.08
3	C	4241	PRO	OXT-C-O	-3.60	115.92	124.08
3	E	4244	PRO	C-CA-N	3.15	119.13	106.84
3	A	4243	PRO	OXT-C-O	-3.08	117.09	124.08
3	D	4240	PRO	OXT-C-O	-2.94	117.42	124.08
3	B	4242	PRO	OXT-C-O	-2.90	117.51	124.08
3	C	4241	PRO	C-CA-N	2.89	118.12	106.84
3	A	4243	PRO	C-CA-N	2.76	117.59	106.84
3	B	4242	PRO	C-CA-N	2.75	117.58	106.84
3	A	4243	PRO	OXT-C-CA	2.72	122.71	113.51
3	D	4240	PRO	C-CA-N	2.63	117.11	106.84
3	B	4332	PRO	CD-N-CA	2.26	113.06	107.22
3	E	4244	PRO	OXT-C-CA	2.26	121.14	113.51
3	B	4332	PRO	OXT-C-CA	2.21	120.97	113.51
3	B	4242	PRO	OXT-C-CA	2.20	120.94	113.51
3	C	4331	PRO	CD-N-CA	2.16	112.81	107.22
3	D	4330	PRO	CD-N-CA	2.15	112.77	107.22
3	D	4330	PRO	OXT-C-CA	2.14	120.74	113.51
3	A	4333	PRO	CD-N-CA	2.13	112.71	107.22
3	A	4333	PRO	OXT-C-CA	2.00	120.28	113.51

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	4241	PRO	O-C-CA-CB
3	C	4241	PRO	OXT-C-CA-CB
3	E	4244	PRO	O-C-CA-N
3	E	4244	PRO	OXT-C-CA-N
3	E	4244	PRO	O-C-CA-CB
3	E	4244	PRO	OXT-C-CA-CB
3	C	4241	PRO	O-C-CA-N
3	C	4241	PRO	OXT-C-CA-N
3	D	4240	PRO	OXT-C-CA-N
3	D	4240	PRO	O-C-CA-CB
3	D	4240	PRO	OXT-C-CA-CB
3	B	4242	PRO	O-C-CA-CB
3	A	4243	PRO	O-C-CA-CB
3	A	4243	PRO	OXT-C-CA-CB
3	B	4242	PRO	OXT-C-CA-CB
3	B	4332	PRO	OXT-C-CA-CB

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Mol	Chain	Res	Type	Atoms
3	D	4240	PRO	O-C-CA-N
3	A	4243	PRO	O-C-CA-N
3	B	4332	PRO	O-C-CA-CB

There are no ring outliers.

10 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	4243	PRO	4	0
3	B	4332	PRO	4	0
3	E	4244	PRO	7	0
3	C	4241	PRO	4	0
3	A	4333	PRO	3	0
3	E	4334	PRO	4	0
3	D	4240	PRO	5	0
3	B	4242	PRO	8	0
3	C	4331	PRO	3	0
3	D	4330	PRO	2	0

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	257/259 (99%)	-0.25	0 100 100	15, 33, 51, 58	1 (0%)
1	B	257/259 (99%)	-0.19	2 (0%) 82 80	22, 33, 51, 58	1 (0%)
1	C	256/259 (98%)	0.53	10 (3%) 43 40	22, 33, 51, 59	0
1	D	258/259 (99%)	-0.10	3 (1%) 76 74	22, 33, 53, 59	2 (0%)
1	E	259/259 (100%)	-0.22	2 (0%) 82 80	20, 32, 51, 59	2 (0%)
All	All	1287/1295 (99%)	-0.05	17 (1%) 75 73	15, 33, 52, 59	6 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	132	GLU	5.6
1	D	138	ARG	4.8
1	C	23	PRO	3.7
1	B	53	ASP	3.4
1	C	33	LEU	3.4
1	C	50	SER	2.8
1	D	53	ASP	2.5
1	D	-1	ASN	2.3
1	C	47	TYR	2.3
1	E	203	SER	2.3
1	C	74	LEU	2.2
1	C	48	ALA	2.2
1	C	49	MET	2.1
1	C	128	LEU	2.0
1	C	227	ILE	2.0
1	C	207	THR	2.0
1	B	0	ALA	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
3	PRO	B	4242	8/8	0.64	0.25	64,65,65,65	0
3	PRO	A	4243	8/8	0.68	0.22	55,56,56,56	0
3	PRO	E	4244	8/8	0.73	0.19	51,52,52,53	0
3	PRO	C	4241	8/8	0.75	0.18	51,51,52,52	0
3	PRO	D	4240	8/8	0.77	0.20	55,55,56,56	0
3	PRO	A	4333	8/8	0.93	0.11	34,35,35,35	0
2	NA	C	852	1/1	0.94	0.07	38,38,38,38	0
2	NA	D	853	1/1	0.95	0.12	33,33,33,33	0
2	NA	A	850	1/1	0.95	0.07	33,33,33,33	0
3	PRO	B	4332	8/8	0.95	0.13	32,32,33,33	0
3	PRO	D	4330	8/8	0.96	0.11	26,28,28,28	0
3	PRO	C	4331	8/8	0.96	0.11	31,31,32,32	0
3	PRO	E	4334	8/8	0.97	0.08	26,26,27,27	0
2	NA	B	851	1/1	0.98	0.07	35,35,35,35	0
2	NA	E	854	1/1	0.98	0.04	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.