



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:35 AM UTC

PDB ID : 1LVY / pdb_00001lvY
Title : PORCINE ELASTASE
Authors : Schiltz, M.; Prange, T.
Deposited on : 1996-07-20
Resolution : 1.87 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

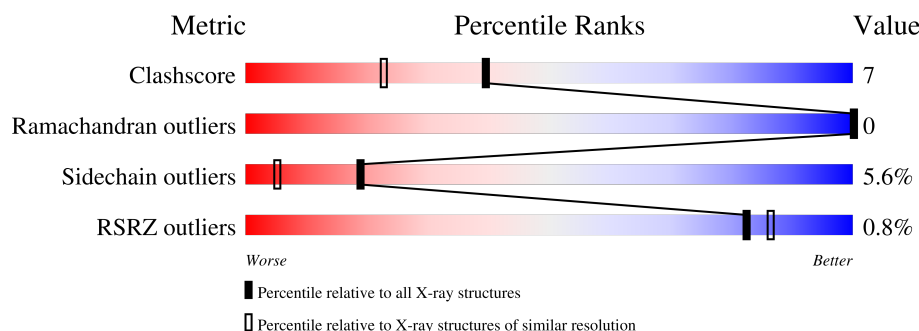
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	240	59% 34% 6%

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	SO4	A	290	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1907 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 ELASTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	240	1822	1135	330	347	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ASN	ASP	conflict	UNP P00772

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

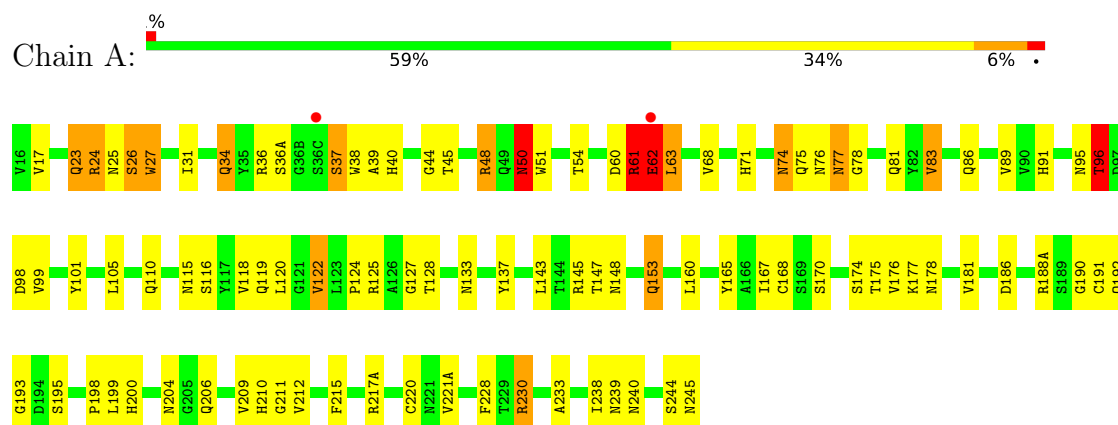
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	79	Total	O	0	0
			79	79		

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: ELASTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.64Å 57.97Å 75.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.87 10.00 – 1.87	Depositor EDS
% Data completeness (in resolution range)	93.0 (10.00-1.87) 91.7 (10.00-1.87)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	21.66 (at 1.88Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.187 , 0.229 0.170 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1907	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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: SO4, 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	1.33	4/1862 (0.2%)	2.66	137/2543 (5.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	44	GLY	C-N	-5.35	1.26	1.33
1	A	211	GLY	N-CA	5.30	1.50	1.45
1	A	228	PHE	N-CA	-5.28	1.39	1.45
1	A	118	VAL	C-O	-5.25	1.18	1.24

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	36	ARG	CD-NE-CZ	18.53	150.34	124.40
1	A	188(A)	ARG	NE-CZ-NH2	-17.18	103.74	119.20
1	A	62	GLU	CB-CA-C	16.01	137.45	111.83
1	A	110	GLN	OE1-CD-NE2	13.52	136.12	122.60
1	A	24	ARG	N-CA-C	12.96	127.00	111.33
1	A	62	GLU	O-C-N	-12.48	105.91	122.38
1	A	48	ARG	CD-NE-CZ	11.86	141.00	124.40
1	A	36	ARG	NH1-CZ-NH2	-11.68	104.11	119.30
1	A	206	GLN	OE1-CD-NE2	11.38	133.98	122.60
1	A	115	ASN	O-C-N	-11.10	110.11	122.88
1	A	91	HIS	CA-CB-CG	-10.98	102.82	113.80
1	A	239	ASN	CA-C-O	-10.67	109.24	120.55
1	A	23	GLN	OE1-CD-NE2	10.52	133.12	122.60
1	A	48	ARG	NE-CZ-NH1	10.49	132.00	121.50
1	A	99	VAL	CA-C-O	10.17	131.45	120.57
1	A	240	ASN	OD1-CG-ND2	-9.84	112.76	122.60
1	A	230	ARG	CA-C-O	9.82	131.70	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217(A)	ARG	NH1-CZ-NH2	9.78	132.02	119.30
1	A	210	HIS	CA-C-N	-9.78	111.28	121.35
1	A	210	HIS	C-N-CA	-9.78	111.28	121.35
1	A	119	GLN	OE1-CD-NE2	-9.59	113.01	122.60
1	A	36	ARG	NE-CZ-NH2	9.50	127.75	119.20
1	A	50	ASN	OD1-CG-ND2	-8.85	113.75	122.60
1	A	145	ARG	NE-CZ-NH2	8.84	127.15	119.20
1	A	192	GLN	CA-C-O	-8.80	111.47	121.15
1	A	78	GLY	O-C-N	-8.74	111.49	122.41
1	A	24	ARG	CG-CD-NE	-8.69	92.88	112.00
1	A	23	GLN	CB-CG-CD	-8.59	98.00	112.60
1	A	230	ARG	NE-CZ-NH1	8.15	129.65	121.50
1	A	188(A)	ARG	NH1-CZ-NH2	8.13	129.87	119.30
1	A	186	ASP	CA-CB-CG	8.13	120.73	112.60
1	A	238	ILE	CA-C-O	8.13	129.72	121.27
1	A	217(A)	ARG	NE-CZ-NH2	-8.07	111.94	119.20
1	A	62	GLU	N-CA-CB	-8.06	98.97	110.58
1	A	245	ASN	CA-CB-CG	7.99	120.59	112.60
1	A	122	VAL	CB-CA-C	7.97	120.79	110.91
1	A	145	ARG	CA-C-O	-7.90	112.47	121.40
1	A	24	ARG	CB-CA-C	-7.89	97.27	110.68
1	A	61	ARG	CD-NE-CZ	7.87	135.42	124.40
1	A	239	ASN	OD1-CG-ND2	-7.83	114.77	122.60
1	A	27	TRP	CA-C-N	7.59	127.77	119.87
1	A	27	TRP	C-N-CA	7.59	127.77	119.87
1	A	95	ASN	CA-C-O	-7.51	112.22	120.33
1	A	98	ASP	CA-CB-CG	-7.48	105.12	112.60
1	A	122	VAL	CA-CB-CG1	7.45	123.06	110.40
1	A	54	THR	CA-C-O	-7.43	113.49	121.14
1	A	133	ASN	CA-C-O	-7.41	112.47	121.28
1	A	193	GLY	N-CA-C	-7.27	106.04	114.69
1	A	204	ASN	OD1-CG-ND2	7.16	129.76	122.60
1	A	191	CYS	O-C-N	-7.08	114.96	123.10
1	A	74	ASN	CA-CB-CG	-6.99	105.61	112.60
1	A	99	VAL	O-C-N	-6.92	111.63	122.70
1	A	170	SER	CA-C-O	6.91	129.88	121.87
1	A	50	ASN	CB-CG-ND2	6.90	126.75	116.40
1	A	230	ARG	O-C-N	-6.78	114.01	122.82
1	A	181	VAL	CA-C-O	-6.75	113.03	120.72
1	A	220	CYS	CA-C-O	-6.74	113.96	120.90
1	A	176	VAL	CG1-CB-CG2	-6.72	96.03	110.80
1	A	36	ARG	NE-CZ-NH1	6.63	128.13	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	GLN	OE1-CD-NE2	6.62	129.22	122.60
1	A	45	THR	O-C-N	-6.53	115.67	123.31
1	A	110	GLN	CG-CD-OE1	-6.52	107.77	120.80
1	A	190	GLY	N-CA-C	-6.50	103.85	112.82
1	A	137	TYR	CA-C-O	-6.49	113.69	120.70
1	A	17	VAL	N-CA-CB	6.39	117.68	110.72
1	A	188(A)	ARG	CD-NE-CZ	6.39	133.34	124.40
1	A	199	LEU	N-CA-C	-6.37	96.72	107.99
1	A	175	THR	O-C-N	6.36	130.09	122.27
1	A	178	ASN	OD1-CG-ND2	6.36	128.96	122.60
1	A	195	SER	CB-CA-C	-6.34	99.49	109.70
1	A	221(A)	VAL	CA-C-O	-6.32	113.66	120.36
1	A	174	SER	CA-CB-OG	-6.27	98.57	111.10
1	A	198	PRO	N-CA-C	6.19	120.98	111.57
1	A	239	ASN	CB-CG-ND2	6.19	125.68	116.40
1	A	143	LEU	CA-C-O	6.08	127.88	121.19
1	A	71	HIS	CA-CB-CG	-6.07	107.73	113.80
1	A	188(A)	ARG	CA-CB-CG	6.05	126.21	114.10
1	A	48	ARG	O-C-N	-6.03	116.38	123.25
1	A	38	TRP	CA-C-O	-6.00	114.23	120.70
1	A	153	GLN	OE1-CD-NE2	5.96	128.56	122.60
1	A	48	ARG	NE-CZ-NH2	-5.96	113.84	119.20
1	A	192	GLN	CB-CG-CD	5.91	122.65	112.60
1	A	167	ILE	CB-CA-C	-5.87	104.33	112.02
1	A	89	VAL	CA-C-O	5.85	126.91	120.48
1	A	212	VAL	N-CA-C	-5.85	99.21	107.75
1	A	192	GLN	OE1-CD-NE2	-5.82	116.78	122.60
1	A	177	LYS	O-C-N	-5.82	114.88	122.97
1	A	25	ASN	CB-CG-OD1	5.80	132.40	120.80
1	A	34	GLN	OE1-CD-NE2	5.80	128.40	122.60
1	A	238	ILE	O-C-N	-5.76	116.18	121.94
1	A	51	TRP	N-CA-CB	5.75	120.47	110.81
1	A	37	SER	CB-CA-C	5.74	123.17	111.11
1	A	165	TYR	N-CA-C	5.73	117.20	111.07
1	A	244	SER	O-C-N	-5.69	115.48	122.25
1	A	200	HIS	CA-CB-CG	5.68	119.48	113.80
1	A	83	VAL	CA-C-O	-5.68	114.31	120.67
1	A	148	ASN	CA-CB-CG	-5.66	106.94	112.60
1	A	76	ASN	CA-C-O	5.64	127.04	120.49
1	A	48	ARG	CA-C-O	-5.63	115.25	121.33
1	A	160	LEU	N-CA-CB	-5.54	103.39	111.20
1	A	245	ASN	CB-CG-ND2	5.54	124.71	116.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	TRP	N-CA-CB	-5.49	102.32	110.99
1	A	83	VAL	CB-CA-C	-5.48	102.06	110.50
1	A	206	GLN	N-CA-CB	-5.48	101.09	111.00
1	A	217(A)	ARG	NE-CZ-NH1	-5.46	116.05	121.50
1	A	147	THR	O-C-N	-5.43	116.21	122.95
1	A	96	THR	CA-CB-CG2	-5.41	101.31	110.50
1	A	178	ASN	CA-CB-CG	-5.39	107.21	112.60
1	A	118	VAL	N-CA-C	5.37	116.16	106.61
1	A	233	ALA	CA-C-O	-5.35	112.82	119.18
1	A	128	THR	CA-CB-CG2	-5.34	101.42	110.50
1	A	239	ASN	O-C-N	5.33	127.76	122.12
1	A	24	ARG	O-C-N	-5.31	116.49	122.12
1	A	175	THR	CA-CB-OG1	-5.31	101.64	109.60
1	A	168	CYS	N-CA-C	5.30	117.05	111.28
1	A	39	ALA	CA-C-O	-5.29	115.13	121.11
1	A	101	TYR	CA-CB-CG	-5.27	104.42	113.90
1	A	120	LEU	O-C-N	-5.26	116.80	123.01
1	A	174	SER	N-CA-C	5.24	119.30	113.01
1	A	71	HIS	ND1-CE1-NE2	-5.22	103.18	108.40
1	A	77	ASN	CB-CG-ND2	5.19	124.19	116.40
1	A	77	ASN	N-CA-C	-5.19	107.00	113.38
1	A	78	GLY	CA-C-N	5.18	130.37	122.23
1	A	78	GLY	C-N-CA	5.18	130.37	122.23
1	A	81	GLN	N-CA-CB	5.18	119.77	110.80
1	A	192	GLN	O-C-N	5.18	129.29	122.97
1	A	188(A)	ARG	CG-CD-NE	-5.16	100.66	112.00
1	A	101	TYR	CB-CA-C	-5.15	103.37	111.51
1	A	83	VAL	N-CA-C	5.15	116.13	108.46
1	A	211	GLY	CA-C-O	-5.15	116.12	121.63
1	A	86	GLN	CB-CG-CD	-5.14	103.87	112.60
1	A	78	GLY	CA-C-O	5.13	125.38	119.13
1	A	230	ARG	CD-NE-CZ	5.08	131.51	124.40
1	A	105	LEU	O-C-N	-5.05	117.33	123.29
1	A	215	PHE	CA-CB-CG	5.04	118.84	113.80
1	A	36(A)	SER	CA-CB-OG	5.02	121.15	111.10
1	A	200	HIS	O-C-N	5.00	128.92	123.22

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	1822	0	1759	24	0
2	A	1	0	0	0	0
3	A	5	0	0	2	0
4	A	79	0	0	6	0
All	All	1907	0	1759	24	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 7.

All (24) 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:61:ARG:HB3	1:A:63:LEU:HD22	1.61	0.81
1:A:62:GLU:CB	4:A:473:HOH:O	2.27	0.81
1:A:50:ASN:HD22	1:A:50:ASN:H	1.30	0.80
1:A:62:GLU:HG3	4:A:473:HOH:O	1.84	0.76
1:A:61:ARG:CB	1:A:63:LEU:HD22	2.22	0.68
1:A:74:ASN:OD1	1:A:153:GLN:HG2	1.92	0.68
1:A:62:GLU:HB2	4:A:473:HOH:O	1.91	0.68
1:A:62:GLU:O	1:A:62:GLU:OE2	2.15	0.65
1:A:60:ASP:OD2	1:A:96:THR:HG23	2.03	0.59
1:A:34:GLN:HG2	1:A:40:HIS:HA	1.90	0.53
1:A:62:GLU:HG3	4:A:478:HOH:O	2.09	0.52
1:A:50:ASN:HD22	1:A:50:ASN:N	2.06	0.49
1:A:31:ILE:HG22	1:A:68:VAL:HG12	1.94	0.49
1:A:26:SER:HB3	1:A:27:TRP:CD1	2.48	0.48
1:A:24:ARG:HH12	1:A:77:ASN:ND2	2.11	0.48
1:A:230:ARG:NH1	3:A:290:SO4:O2	2.25	0.48
1:A:62:GLU:CG	4:A:473:HOH:O	2.41	0.46
1:A:23:GLN:O	1:A:26:SER:HB2	2.18	0.44
1:A:62:GLU:CG	4:A:478:HOH:O	2.65	0.43
1:A:48:ARG:HD3	1:A:48:ARG:HA	1.80	0.43
1:A:124:PRO:HD3	1:A:209:VAL:O	2.18	0.43
1:A:61:ARG:HB3	1:A:63:LEU:CD2	2.40	0.43
1:A:127:GLY:HA2	3:A:290:SO4:O2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ASN:H	1:A:50:ASN:ND2	2.05	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	238/240 (99%)	233 (98%)	5 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	198/198 (100%)	187 (94%)	11 (6%)	19	5

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	SER
1	A	37	SER
1	A	50	ASN
1	A	61	ARG
1	A	62	GLU

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Mol	Chain	Res	Type
1	A	63	LEU
1	A	83	VAL
1	A	96	THR
1	A	116	SER
1	A	122	VAL
1	A	125	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	204	ASN
1	A	239	ASN
1	A	240	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	SO4	A	290	-	4,4,4	0.87	0	6,6,6	0.93	0

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	290	SO4	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 [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	240/240 (100%)	-0.54	2 (0%) 82 86	4, 12, 31, 50	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	62	GLU	4.3
1	A	36(C)	SER	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(Å ²)	Q<0.9
3	SO4	A	290	5/5	0.93	0.13	44,47,48,51	0
2	CA	A	280	1/1	0.98	0.05	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.