



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:50 AM UTC

PDB ID : 2TGP / pdb_00002tgp
Title : THE GEOMETRY OF THE REACTIVE SITE AND OF THE PEPTIDE GROUPS IN TRYPSIN, TRYPSINOGEN AND ITS COMPLEXES WITH INHIBITORS
Authors : Huber, R.; Bode, W.; Deisenhofer, J.; Schwager, P.
Deposited on : 1982-09-27
Resolution : 1.90 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

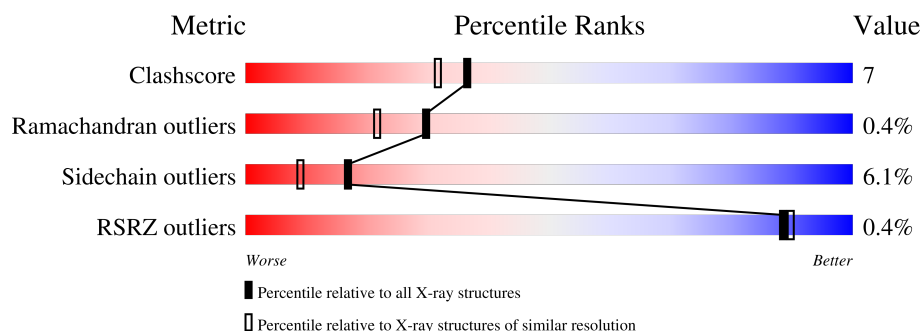
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	Z	229	
2	I	58	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2232 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 TRYPSINOGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	Z	223	1629	1012	279	324	14	66	0	0

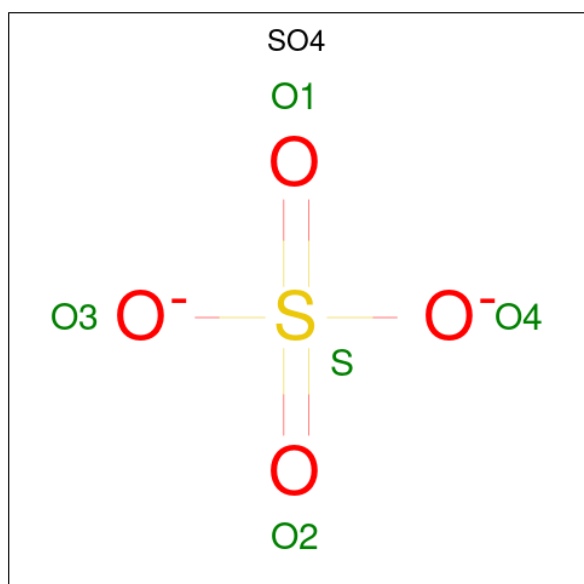
- Molecule 2 is a protein called TRYPSIN INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	I	58	454	284	84	79	7	37	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	Z	1	Total	Ca	0	0
			1	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

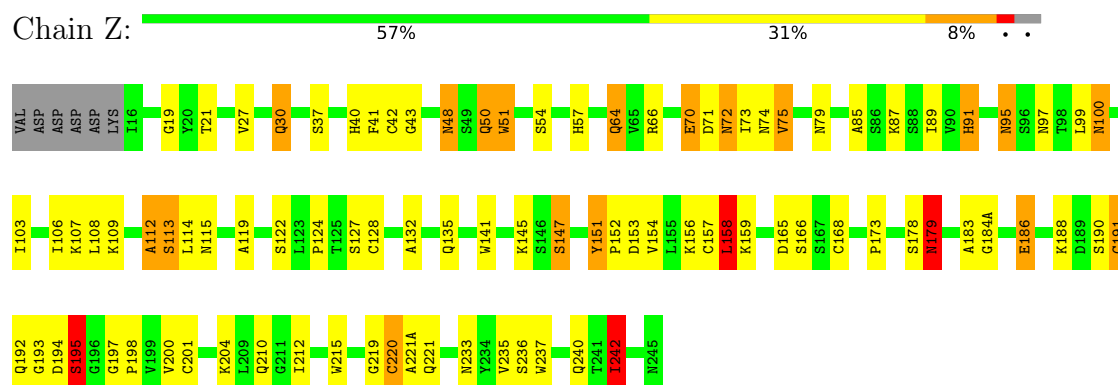
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	Z	104	Total	O	0	0
			104	104		
5	I	34	Total	O	0	0
			34	34		

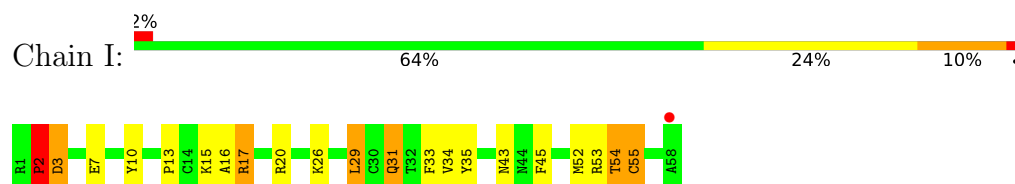
3 Residue-property plots [i](#)

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: TRYPSINOGEN



• Molecule 2: TRYPSIN INHIBITOR



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	75.50Å 85.70Å 122.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.80 – 1.90 6.80 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.80-1.90) 71.7 (6.80-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	0.200 , (Not available) 0.202 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	15.4	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 60.1	EDS
L-test for twinning ¹	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2232	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: CA, SO4

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	Z	1.58	16/1660 (1.0%)	2.05	50/2250 (2.2%)
2	I	1.41	2/465 (0.4%)	2.03	10/622 (1.6%)
All	All	1.55	18/2125 (0.8%)	2.05	60/2872 (2.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	31
2	I	0	10
All	All	0	41

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Z	57	HIS	ND1-CE1	10.60	1.43	1.32
1	Z	91	HIS	CE1-NE2	10.19	1.42	1.32
1	Z	237	TRP	NE1-CE2	-9.22	1.27	1.37
1	Z	57	HIS	CE1-NE2	9.07	1.41	1.32
1	Z	215	TRP	NE1-CE2	-8.96	1.27	1.37
1	Z	43	GLY	N-CA	7.50	1.50	1.44
1	Z	40	HIS	CE1-NE2	7.22	1.39	1.32
1	Z	51	TRP	NE1-CE2	-7.16	1.29	1.37
2	I	16	ALA	C-N	-6.62	1.25	1.33
2	I	3	ASP	N-CA	6.60	1.54	1.46
1	Z	141	TRP	NE1-CE2	-6.54	1.30	1.37
1	Z	91	HIS	ND1-CE1	6.10	1.38	1.32
1	Z	183	ALA	C-N	-5.65	1.27	1.33
1	Z	40	HIS	ND1-CE1	5.48	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Z	151	TYR	CZ-OH	5.39	1.49	1.38
1	Z	201	CYS	C-N	-5.25	1.26	1.33
1	Z	132	ALA	C-N	-5.23	1.26	1.33
1	Z	42	CYS	C-N	-5.19	1.28	1.33

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	33	PHE	CA-C-O	-8.12	112.54	121.23
1	Z	221	GLN	N-CA-C	7.79	122.50	110.20
1	Z	21	THR	N-CA-CB	-7.71	97.60	109.94
2	I	2	PRO	CA-C-N	7.67	135.83	122.79
2	I	2	PRO	C-N-CA	7.67	135.83	122.79
1	Z	190	SER	CA-C-N	-7.64	109.96	122.11
1	Z	190	SER	C-N-CA	-7.64	109.96	122.11
2	I	53	ARG	CD-NE-CZ	7.46	134.84	124.40
1	Z	112	ALA	CA-C-N	-7.45	112.72	123.00
1	Z	112	ALA	C-N-CA	-7.45	112.72	123.00
1	Z	166	SER	O-C-N	6.77	129.40	122.09
2	I	10	TYR	N-CA-CB	-6.76	99.97	110.65
1	Z	95	ASN	CB-CA-C	-6.56	99.56	110.19
1	Z	191	CYS	CA-C-O	-6.50	114.47	121.36
1	Z	42	CYS	CA-C-N	-6.47	115.96	122.69
1	Z	42	CYS	C-N-CA	-6.47	115.96	122.69
1	Z	168	CYS	N-CA-C	-6.43	104.35	111.36
1	Z	147	SER	CA-C-O	-6.31	113.89	120.70
1	Z	219	GLY	CA-C-N	-6.19	112.96	122.62
1	Z	219	GLY	C-N-CA	-6.19	112.96	122.62
1	Z	173	PRO	N-CA-C	6.17	121.31	111.26
1	Z	112	ALA	O-C-N	-5.90	116.06	122.79
1	Z	197	GLY	CA-C-O	-5.83	116.38	122.38
1	Z	210	GLN	N-CA-C	5.81	120.50	113.41
1	Z	89	ILE	N-CA-C	5.79	115.07	106.85
1	Z	242	ILE	CB-CA-C	-5.78	104.33	112.14
1	Z	70	GLU	CA-C-O	-5.72	115.06	121.81
1	Z	119	ALA	CA-C-N	-5.70	112.86	123.05
1	Z	119	ALA	C-N-CA	-5.70	112.86	123.05
1	Z	179	ASN	CB-CG-ND2	-5.66	107.92	116.40
1	Z	54	SER	CA-C-O	-5.63	115.34	121.14
1	Z	215	TRP	CA-C-N	5.57	128.16	120.92
1	Z	215	TRP	C-N-CA	5.57	128.16	120.92
1	Z	99	LEU	N-CA-C	-5.54	106.47	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Z	108	LEU	CA-C-O	-5.51	115.55	121.56
2	I	45	PHE	CA-CB-CG	-5.49	108.31	113.80
2	I	20	ARG	CA-C-O	-5.45	115.16	121.49
2	I	55	CYS	N-CA-C	5.44	120.19	113.50
2	I	54	THR	O-C-N	5.44	129.30	122.23
1	Z	113	SER	N-CA-C	5.42	117.80	109.07
1	Z	198	PRO	CA-C-N	5.41	130.68	123.10
1	Z	198	PRO	C-N-CA	5.41	130.68	123.10
1	Z	79	ASN	N-CA-CB	5.39	118.75	110.61
1	Z	220	CYS	CA-C-O	-5.35	114.85	121.11
1	Z	236	SER	N-CA-C	5.31	116.75	111.07
2	I	13	PRO	CB-CA-C	-5.28	102.85	111.56
1	Z	64	GLN	CB-CG-CD	-5.25	103.68	112.60
1	Z	186	GLU	CA-C-N	-5.23	114.18	122.65
1	Z	186	GLU	C-N-CA	-5.23	114.18	122.65
1	Z	145	LYS	N-CA-C	5.22	116.92	108.41
1	Z	74	ASN	CA-CB-CG	-5.20	107.41	112.60
1	Z	41	PHE	N-CA-CB	5.19	117.81	110.90
1	Z	30	GLN	O-C-N	5.19	129.11	123.04
1	Z	128	CYS	N-CA-C	5.15	117.69	109.96
1	Z	200	VAL	N-CA-C	5.15	115.51	107.99
1	Z	37	SER	N-CA-CB	-5.12	104.49	111.65
1	Z	106	ILE	CA-C-N	-5.11	115.66	122.72
1	Z	106	ILE	C-N-CA	-5.11	115.66	122.72
1	Z	194	ASP	O-C-N	5.05	129.37	122.46
1	Z	72	ASN	OD1-CG-ND2	-5.03	117.57	122.60

There are no chirality outliers.

All (41) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	2	PRO	Mainchain,Peptide
2	I	26	LYS	Mainchain
2	I	3	ASP	Mainchain
2	I	31	GLN	Sidechain
2	I	34	VAL	Mainchain
2	I	35	TYR	Mainchain
2	I	43	ASN	Sidechain
2	I	55	CYS	Mainchain
2	I	7	GLU	Sidechain
1	Z	100	ASN	Sidechain
1	Z	112	ALA	Mainchain

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Mol	Chain	Res	Type	Group
1	Z	113	SER	Mainchain
1	Z	114	LEU	Mainchain
1	Z	115	ASN	Sidechain
1	Z	147	SER	Mainchain
1	Z	151	TYR	Sidechain
1	Z	154	VAL	Mainchain
1	Z	157	CYS	Mainchain
1	Z	158	LEU	Mainchain
1	Z	159	LYS	Mainchain
1	Z	165	ASP	Sidechain
1	Z	179	ASN	Sidechain
1	Z	184(A)	GLY	Mainchain
1	Z	19	GLY	Mainchain
1	Z	192	GLN	Sidechain
1	Z	193	GLY	Mainchain
1	Z	195	SER	Mainchain
1	Z	220	CYS	Mainchain
1	Z	221(A)	ALA	Mainchain
1	Z	233	ASN	Mainchain
1	Z	235	VAL	Mainchain
1	Z	240	GLN	Sidechain
1	Z	27	VAL	Mainchain
1	Z	30	GLN	Sidechain
1	Z	50	GLN	Sidechain
1	Z	70	GLU	Sidechain,Mainchain
1	Z	71	ASP	Mainchain
1	Z	85	ALA	Mainchain
1	Z	95	ASN	Sidechain

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	Z	1629	0	1588	26	1
2	I	454	0	438	6	1
3	Z	1	0	0	0	0
4	I	10	0	0	0	0
5	I	34	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Z	104	0	0	1	0
All	All	2232	0	2026	28	1

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 (28) 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:Z:195:SER:HB2	2:I:15:LYS:C	2.14	0.73
1:Z:48:ASN:HD22	1:Z:50:GLN:H	1.40	0.69
1:Z:124:PRO:HA	1:Z:204:LYS:HD3	1.77	0.66
1:Z:152:PRO:HG3	1:Z:156:LYS:HD3	1.79	0.65
1:Z:158:LEU:HD11	1:Z:188:LYS:HB3	1.78	0.65
1:Z:195:SER:HB2	2:I:15:LYS:O	2.03	0.59
1:Z:64:GLN:HE21	1:Z:66:ARG:HE	1.55	0.54
1:Z:64:GLN:HE22	1:Z:66:ARG:HH21	1.56	0.53
1:Z:64:GLN:NE2	1:Z:66:ARG:HE	2.07	0.53
1:Z:51:TRP:CD2	1:Z:242:ILE:HD12	2.47	0.49
1:Z:87:LYS:HB2	1:Z:107:LYS:HB3	1.95	0.48
1:Z:48:ASN:ND2	1:Z:50:GLN:H	2.09	0.47
1:Z:186:GLU:HB2	5:Z:476:HOH:O	2.14	0.47
1:Z:158:LEU:CD1	1:Z:188:LYS:HB3	2.45	0.47
1:Z:51:TRP:CD1	1:Z:242:ILE:HG23	2.50	0.47
1:Z:103:ILE:HD12	1:Z:212:ILE:HD11	1.98	0.46
2:I:29:LEU:HD13	2:I:31:GLN:HG2	1.98	0.46
1:Z:48:ASN:HD22	1:Z:48:ASN:C	2.24	0.45
1:Z:195:SER:CB	2:I:15:LYS:C	2.89	0.44
1:Z:100:ASN:HD21	1:Z:179:ASN:HD22	1.66	0.44
2:I:17:ARG:HH11	2:I:17:ARG:HD3	1.52	0.44
1:Z:91:HIS:HB2	1:Z:103:ILE:HG23	2.00	0.44
1:Z:51:TRP:CE3	1:Z:242:ILE:HD12	2.54	0.43
1:Z:64:GLN:NE2	1:Z:66:ARG:HH21	2.16	0.42
1:Z:73:ILE:HD13	1:Z:73:ILE:HG21	1.81	0.42
1:Z:51:TRP:CH2	1:Z:107:LYS:HB2	2.55	0.41
1:Z:191:CYS:HA	2:I:15:LYS:HD3	2.03	0.40
1:Z:72:ASN:ND2	1:Z:75:VAL:HG13	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:109:LYS:NZ	2:I:54:THR:O[2_575]	1.78	0.42

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	Z	221/229 (96%)	215 (97%)	6 (3%)	0	100	100
2	I	56/58 (97%)	52 (93%)	3 (5%)	1 (2%)	6	1
All	All	277/287 (96%)	267 (96%)	9 (3%)	1 (0%)	30	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	2	PRO

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	Z	184/190 (97%)	173 (94%)	11 (6%)	17	9
2	I	46/46 (100%)	43 (94%)	3 (6%)	15	8
All	All	230/236 (98%)	216 (94%)	14 (6%)	17	9

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Z	48	ASN
1	Z	75	VAL
1	Z	97	ASN
1	Z	122	SER
1	Z	127	SER
1	Z	135	GLN
1	Z	153	ASP
1	Z	158	LEU
1	Z	178	SER
1	Z	195	SER
1	Z	242	ILE
2	I	17	ARG
2	I	29	LEU
2	I	52	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	25	ASN
1	Z	30	GLN
1	Z	48	ASN
1	Z	64	GLN
1	Z	100	ASN
1	Z	175	GLN
1	Z	210	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
4	SO4	I	60	-	4,4,4	0.78	0	6,6,6	0.48	0
4	SO4	I	59	-	4,4,4	0.74	0	6,6,6	0.59	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.

No monomer is involved in short contacts.

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	Z	220/229 (96%)	-0.48	0	100 100	6, 17, 31, 52	26 (11%)
2	I	56/58 (96%)	-0.59	1 (1%)	67 71	9, 14, 23, 31	7 (12%)
All	All	276/287 (96%)	-0.51	1 (0%)	88 90	6, 16, 31, 52	33 (11%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	58	ALA	2.1

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	CA	Z	462	1/1	0.94	0.09	37,37,37,37	0
4	SO4	I	59	5/5	0.97	0.07	39,39,39,39	0
4	SO4	I	60	5/5	0.98	0.07	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.