Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:57 PM UTC

PDB ID	:	2ZEH / pdb_00002zeh
Title	:	Crystal structure of the human glutaminyl cyclase mutant E201Q at 1.8 angstrom resolution
Authors	:	Huang, K.F.; Wang, Y.R.; Chang, E.C.; Chou, T.L.; Wang, A.H.
Deposited on	:	2007-12-12
Resolution	:	1.80 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:

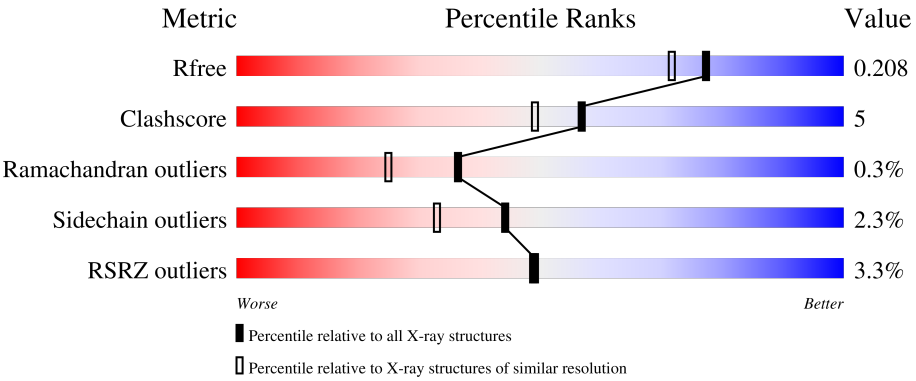
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 <=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	329	2% 87% 9%
1	B	329	5% 84% 13%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6099 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 Glutaminyl-peptide cyclotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	5	0	0
			2610	1673	451	477	9			
1	B	323	Total	C	N	O	S	5	0	0
			2610	1673	451	477	9			

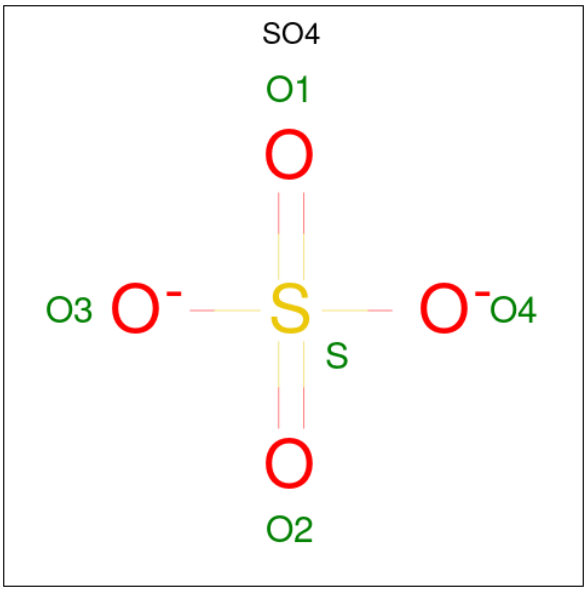
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLN	GLU	engineered mutation	UNP Q16769
B	201	GLN	GLU	engineered mutation	UNP Q16769

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

- Molecule 4 is water.

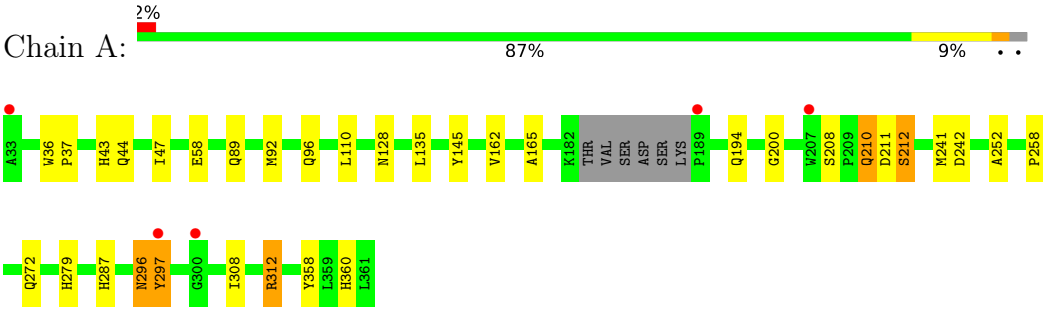
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	492	Total O 492 492	0	0
4	B	375	Total O 375 375	0	0

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.

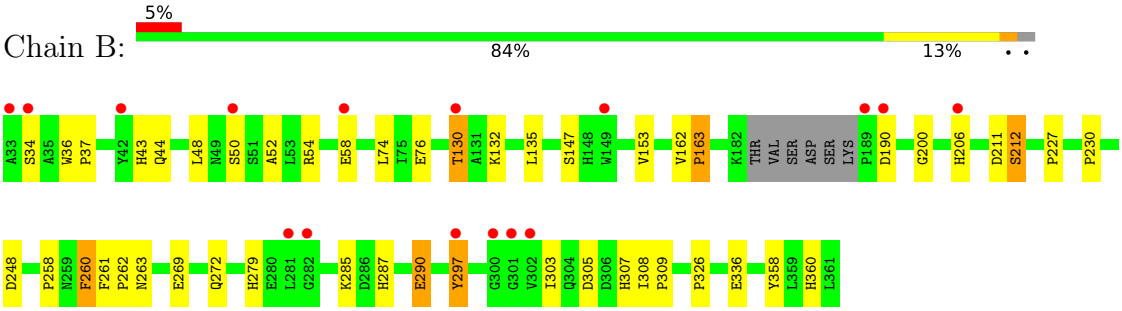
• Molecule 1: Glutaminyl-peptide cyclotransferase

Chain A:



• Molecule 1: Glutaminyl-peptide cyclotransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	119.05Å 119.05Å 332.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.80 30.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.0 (30.00-1.80) 92.0 (30.00-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	3.20 (at 1.79Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.181 , 0.207 0.181 , 0.208	Depositor DCC
R_{free} test set	4190 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	22.3	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 55.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6099	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, ZN

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	1.13	5/2687 (0.2%)	1.13	7/3656 (0.2%)
1	B	0.94	0/2687	1.09	8/3656 (0.2%)
All	All	1.04	5/5374 (0.1%)	1.11	15/7312 (0.2%)

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	A	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	ILE	CA-CB	10.41	1.59	1.54
1	A	162	VAL	CA-CB	8.95	1.59	1.54
1	A	241	MET	SD-CE	-8.65	1.57	1.79
1	A	165	ALA	CA-CB	5.18	1.61	1.53
1	A	252	ALA	CA-CB	5.02	1.60	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	147	SER	N-CA-C	-7.70	100.94	110.41
1	B	260	PHE	N-CA-C	7.22	120.57	111.69
1	B	135	LEU	N-CA-C	-6.78	98.57	109.96
1	B	200	GLY	N-CA-C	6.70	124.21	114.10
1	A	260	PHE	N-CA-C	6.46	119.31	111.82
1	A	135	LEU	N-CA-C	-6.21	99.88	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	128	ASN	CA-C-N	5.94	126.09	119.32
1	A	128	ASN	C-N-CA	5.94	126.09	119.32
1	B	190	ASP	N-CA-C	-5.89	100.79	109.62
1	A	208	SER	N-CA-C	-5.64	101.70	108.25
1	B	303	ILE	N-CA-C	-5.51	100.45	108.17
1	B	132	LYS	N-CA-C	5.43	117.20	111.28
1	A	47	ILE	N-CA-C	5.41	116.06	109.30
1	B	263	ASN	N-CA-C	5.33	119.65	113.20
1	A	200	GLY	N-CA-C	5.02	121.69	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	145	TYR	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	A	2610	0	2531	22	0
1	B	2610	0	2531	26	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	492	0	0	6	0
4	B	375	0	0	3	1
All	All	6099	0	5062	47	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 5.

All (47) 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:58:GLU:HG3	4:A:930:HOH:O	1.55	1.04
1:B:54:ARG:O	1:B:58:GLU:HG2	1.76	0.85
1:A:312:ARG:HD3	4:A:1130:HOH:O	1.94	0.67
1:A:44:GLN:O	1:A:360:HIS:HE1	1.78	0.65
1:B:43:HIS:HD2	4:B:633:HOH:O	1.81	0.64
1:B:43:HIS:HE1	1:B:358:TYR:O	1.82	0.63
1:B:258:PRO:HB3	1:B:297:TYR:CE2	2.33	0.62
1:B:279:HIS:HD2	1:B:287:HIS:ND1	1.96	0.62
1:A:279:HIS:HD2	1:A:287:HIS:ND1	1.98	0.61
1:A:43:HIS:HE1	1:A:358:TYR:O	1.83	0.61
1:A:43:HIS:HD2	4:A:420:HOH:O	1.85	0.59
1:A:110:LEU:HG	1:B:227:PRO:HG3	1.84	0.58
1:A:296:ASN:OD1	1:A:296:ASN:N	2.37	0.57
1:B:290:GLU:O	1:B:290:GLU:HG3	2.03	0.57
1:A:194:GLN:NE2	4:A:480:HOH:O	2.39	0.56
1:A:92:MET:O	1:A:96:GLN:HG3	2.06	0.55
1:B:269:GLU:HA	1:B:272:GLN:HE21	1.72	0.54
1:B:307:HIS:H	1:B:307:HIS:HD1	1.55	0.54
1:B:258:PRO:HB3	1:B:297:TYR:CZ	2.44	0.53
1:B:36:TRP:CG	1:B:37:PRO:HD3	2.45	0.52
1:A:279:HIS:CD2	1:A:287:HIS:ND1	2.76	0.52
1:A:210:GLN:H	1:A:210:GLN:NE2	2.08	0.51
1:A:211:ASP:O	1:A:212:SER:HB3	2.13	0.48
1:A:360:HIS:HD2	4:A:803:HOH:O	1.96	0.48
1:A:258:PRO:HG2	1:A:260:PHE:CZ	2.50	0.47
1:B:162:VAL:HB	1:B:163:PRO:HD3	1.97	0.46
1:B:74:LEU:HD13	1:B:336:GLU:HB2	1.99	0.45
1:B:308:ILE:HB	1:B:309:PRO:HD3	1.97	0.45
1:A:269:GLU:HA	1:A:272:GLN:HE21	1.81	0.45
1:B:43:HIS:CE1	1:B:358:TYR:O	2.66	0.44
1:A:89:GLN:HG3	4:A:1036:HOH:O	2.18	0.44
1:B:258:PRO:HG2	1:B:260:PHE:CZ	2.52	0.44
1:B:130:THR:HG22	4:B:971:HOH:O	2.17	0.44
1:B:48:LEU:HB3	1:B:52:ALA:HB3	2.01	0.43
1:B:285:LYS:HD2	4:B:711:HOH:O	2.19	0.43
1:B:50:SER:O	1:B:54:ARG:HG3	2.19	0.43
1:B:44:GLN:O	1:B:360:HIS:NE2	2.42	0.42
1:B:261:PHE:HA	1:B:262:PRO:HD3	1.85	0.42
1:B:211:ASP:O	1:B:212:SER:HB3	2.19	0.42
1:A:36:TRP:CG	1:A:37:PRO:HD3	2.55	0.42
1:A:296:ASN:O	1:A:297:TYR:HB3	2.20	0.42
1:A:44:GLN:O	1:A:360:HIS:CE1	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:36:TRP:CD2	1:B:37:PRO:HD3	2.55	0.41
1:A:312:ARG:HH11	1:A:312:ARG:HG2	1.85	0.41
1:B:248:ASP:OD2	1:B:305:ASP:OD2	2.38	0.41
1:B:76:GLU:HB2	1:B:153:VAL:CG1	2.51	0.40
1:A:43:HIS:CE1	1:A:358:TYR:O	2.70	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)
4:B:1092:HOH:O	4:B:1092:HOH:O[11_445]	0.95	1.25

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	319/329 (97%)	311 (98%)	7 (2%)	1 (0%)	36	25
1	B	319/329 (97%)	308 (97%)	10 (3%)	1 (0%)	36	25
All	All	638/658 (97%)	619 (97%)	17 (3%)	2 (0%)	36	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	SER
1	B	212	SER

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	284/290 (98%)	279 (98%)	5 (2%)	51 43
1	B	284/290 (98%)	276 (97%)	8 (3%)	38 26
All	All	568/580 (98%)	555 (98%)	13 (2%)	44 33

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	210	GLN
1	A	242	ASP
1	A	296	ASN
1	A	297	TYR
1	A	312	ARG
1	B	34	SER
1	B	130	THR
1	B	163	PRO
1	B	206	HIS
1	B	230	PRO
1	B	290	GLU
1	B	297	TYR
1	B	326	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	43	HIS
1	A	55	GLN
1	A	67	GLN
1	A	68	ASN
1	A	93	GLN
1	A	150	ASN
1	A	210	GLN
1	A	272	GLN
1	A	276	HIS
1	A	279	HIS
1	A	360	HIS
1	B	43	HIS
1	B	55	GLN

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Mol	Chain	Res	Type
1	B	128	ASN
1	B	148	HIS
1	B	201	GLN
1	B	272	GLN
1	B	279	HIS
1	B	304	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 4 ligands modelled in this entry, 2 are 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	$\#\|Z\| > 2$
3	SO4	A	395	-	4,4,4	0.46	0	6,6,6	0.62	0
3	SO4	B	396	-	4,4,4	0.64	0	6,6,6	0.41	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 (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, 95^{th} 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	322/329 (97%)	-0.40	5 (1%) 70 71	15, 21, 35, 48	0
1	B	322/329 (97%)	0.22	16 (4%) 34 33	16, 28, 46, 65	0
All	All	644/658 (97%)	-0.09	21 (3%) 49 49	15, 24, 44, 65	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	33	ALA	6.3
1	A	33	ALA	4.7
1	A	207	TRP	3.7
1	B	297	TYR	3.7
1	B	189	PRO	3.7
1	B	301	GLY	3.5
1	A	189	PRO	3.1
1	B	58	GLU	2.7
1	B	300	GLY	2.6
1	B	190	ASP	2.4
1	B	302	VAL	2.4
1	A	297	TYR	2.3
1	B	130	THR	2.2
1	B	149	TRP	2.2
1	B	281	LEU	2.2
1	B	282	GLY	2.2
1	B	34	SER	2.1
1	A	300	GLY	2.1
1	B	50	SER	2.1
1	B	42	TYR	2.0
1	B	206	HIS	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, 95^{th} 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	395	5/5	0.91	0.13	43,44,45,45	0
3	SO4	B	396	5/5	0.92	0.12	41,42,42,43	0
2	ZN	B	392	1/1	0.99	0.02	21,21,21,21	0
2	ZN	A	391	1/1	1.00	0.01	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.