



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:56 PM UTC

PDB ID : 4KXK / pdb_00004kxk
Title : Alanine-glyoxylate aminotransferase variant K390A/K391A in complex with the TPR domain of human Pex5p
Authors : Fodor, K.; Lou, Y.; Wilmanns, M.
Deposited on : 2013-05-27
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

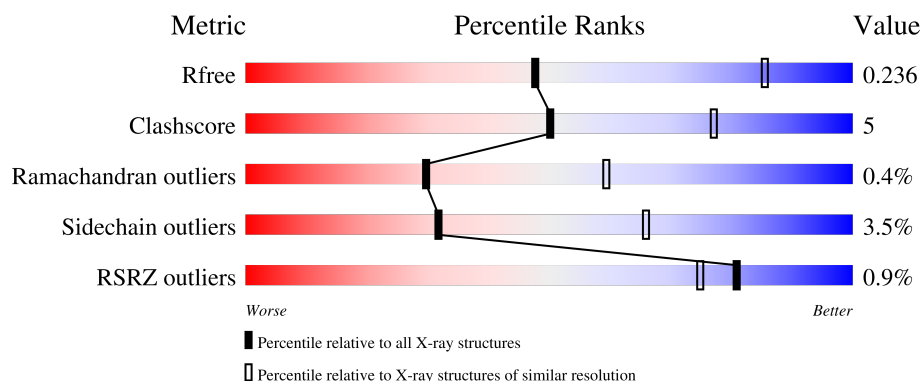
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	A	394	
1	C	394	
2	B	328	
2	D	328	

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	C	401	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10542 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 Serine–pyruvate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	1	0
			2985	1908	520	541	16			
1	C	387	Total	C	N	O	S	0	1	0
			2981	1906	520	539	16			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P21549
A	0	ALA	-	expression tag	UNP P21549
A	390	ALA	LYS	engineered mutation	UNP P21549
A	391	ALA	LYS	engineered mutation	UNP P21549
C	-1	GLY	-	expression tag	UNP P21549
C	0	ALA	-	expression tag	UNP P21549
C	390	ALA	LYS	engineered mutation	UNP P21549
C	391	ALA	LYS	engineered mutation	UNP P21549

- Molecule 2 is a protein called Peroxisomal targeting signal 1 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	288	Total	C	N	O	S	0	1	0
			2259	1419	395	434	11			
2	D	288	Total	C	N	O	S	0	1	0
			2263	1421	395	436	11			

There are 6 discrepancies between the modelled and reference sequences:

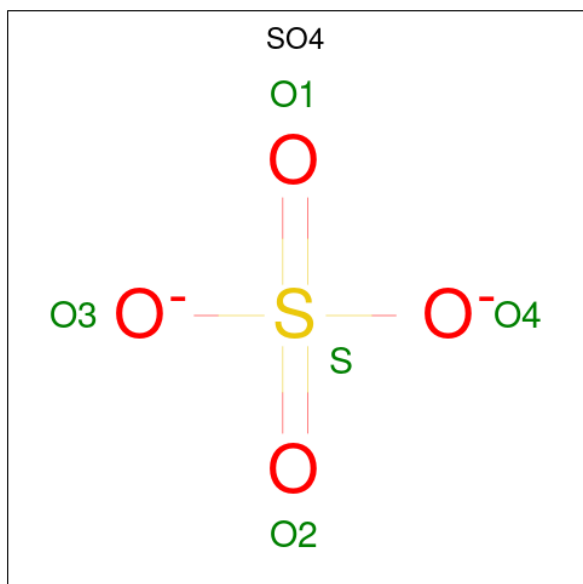
Chain	Residue	Modelled	Actual	Comment	Reference
B	312	GLY	-	expression tag	UNP P50542
B	313	ALA	-	expression tag	UNP P50542
B	314	MET	-	expression tag	UNP P50542
D	312	GLY	-	expression tag	UNP P50542

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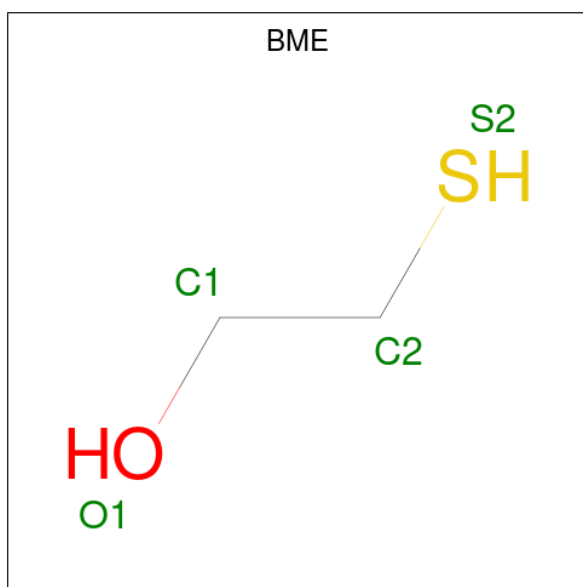
Chain	Residue	Modelled	Actual	Comment	Reference
D	313	ALA	-	expression tag	UNP P50542
D	314	MET	-	expression tag	UNP P50542

- 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		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		

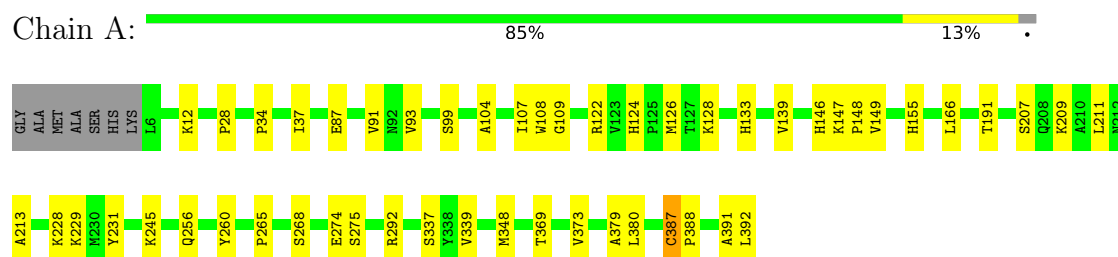
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	C	17	Total	O	0	0
			17	17		
5	B	5	Total	O	0	0
			5	5		
5	D	4	Total	O	0	0
			4	4		

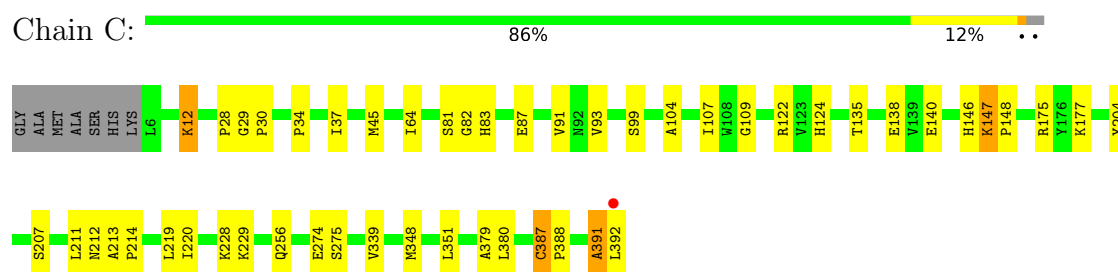
3 Residue-property plots

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.

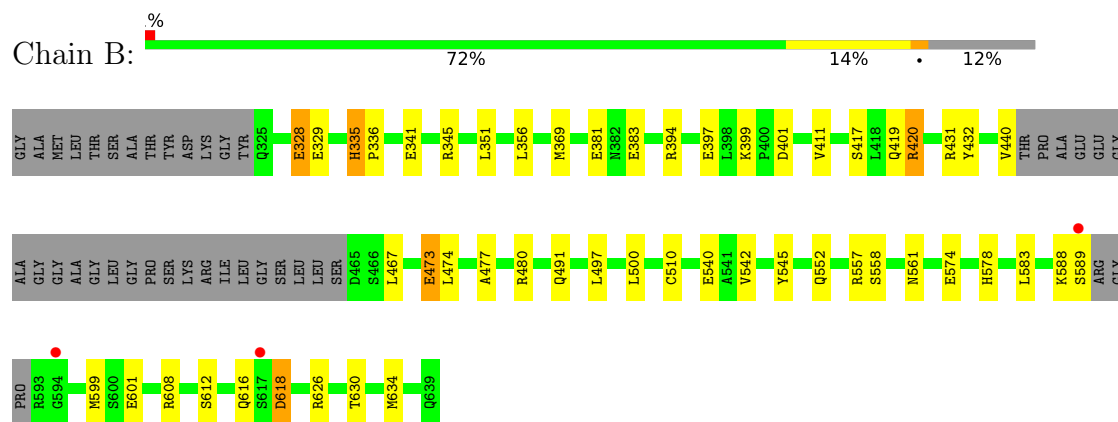
- Molecule 1: Serine-pyruvate aminotransferase



- Molecule 1: Serine-pyruvate aminotransferase

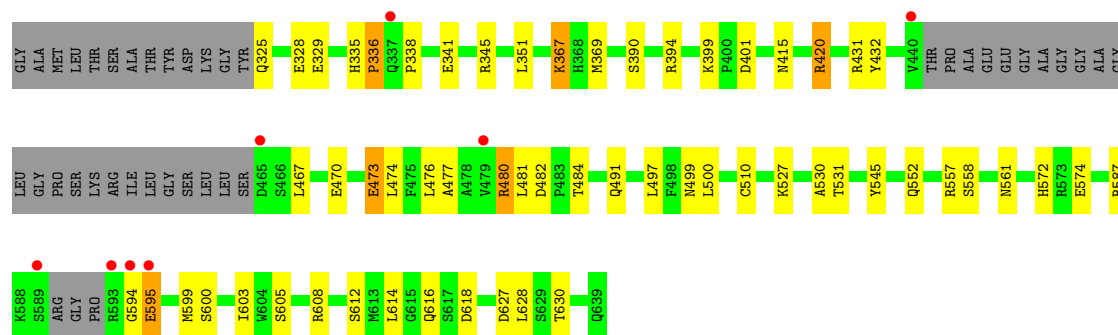


- Molecule 2: Peroxisomal targeting signal 1 receptor



- Molecule 2: Peroxisomal targeting signal 1 receptor





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.59Å 74.70Å 91.21Å 87.85° 83.62° 89.79°	Depositor
Resolution (Å)	19.80 – 2.90 19.80 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.80-2.90) 96.8 (19.80-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.88Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.184 , 0.238 0.186 , 0.236	Depositor DCC
R_{free} test set	1643 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.015 for -h,k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10542	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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: BME, 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	A	0.83	0/3057	0.98	0/4149
1	C	0.86	1/3053 (0.0%)	1.01	4/4144 (0.1%)
2	B	0.71	0/2304	0.93	3/3122 (0.1%)
2	D	0.74	1/2308 (0.0%)	0.95	3/3127 (0.1%)
All	All	0.79	2/10722 (0.0%)	0.97	10/14542 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	214	PRO	CA-C	5.85	1.55	1.51
2	D	420	ARG	CZ-NH2	5.81	1.41	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	480	ARG	CG-CD-NE	-7.04	96.51	112.00
2	D	431	ARG	CB-CG-CD	-6.13	97.20	111.30
1	C	12	LYS	CB-CA-C	-5.87	101.42	110.81
2	D	480	ARG	N-CA-CB	-5.65	101.86	110.33
1	C	212	ASN	N-CA-C	5.42	119.05	111.90

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	2985	0	3028	30	0
1	C	2981	0	3024	30	0
2	B	2259	0	2200	29	1
2	D	2263	0	2204	31	1
3	A	5	0	0	0	0
3	C	5	0	0	2	0
4	A	4	0	6	0	0
5	A	14	0	0	1	0
5	B	5	0	0	2	0
5	C	17	0	0	1	0
5	D	4	0	0	0	0
All	All	10542	0	10462	112	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.

The worst 5 of 112 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:292:ARG:NH1	5:A:512:HOH:O	2.04	0.90
1:A:28:PRO:HD2	1:A:348:MET:HG3	1.51	0.90
1:C:28:PRO:HD2	1:C:348:MET:HG3	1.59	0.83
1:A:87:GLU:O	1:A:91:VAL:HG23	1.78	0.82
1:C:87:GLU:O	1:C:91:VAL:HG23	1.84	0.78

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)
2:B:540:GLU:OE2	2:D:367:LYS:NZ[1_564]	2.09	0.11

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	386/394 (98%)	374 (97%)	11 (3%)	1 (0%)	36	65
1	C	386/394 (98%)	368 (95%)	17 (4%)	1 (0%)	36	65
2	B	283/328 (86%)	272 (96%)	10 (4%)	1 (0%)	30	59
2	D	283/328 (86%)	267 (94%)	14 (5%)	2 (1%)	18	48
All	All	1338/1444 (93%)	1281 (96%)	52 (4%)	5 (0%)	30	59

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	336	PRO
2	D	336	PRO
2	D	594	GLY
1	A	387	CYS
1	C	387	CYS

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	320/324 (99%)	313 (98%)	7 (2%)	45	77
1	C	319/324 (98%)	312 (98%)	7 (2%)	45	77
2	B	236/264 (89%)	223 (94%)	13 (6%)	19	50
2	D	237/264 (90%)	223 (94%)	14 (6%)	18	48
All	All	1112/1176 (95%)	1071 (96%)	41 (4%)	32	64

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	367	LYS
2	D	558	SER
2	D	394[A]	ARG

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Mol	Chain	Res	Type
2	D	473	GLU
2	D	595	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	536	ASN
2	D	572	HIS
2	D	616	GLN
1	C	124	HIS
1	C	146	HIS

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](#)

3 ligands are modelled in this entry.

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	BME	A	402	-	3,3,3	0.15	0	2,2,2	1.06	0
3	SO4	A	401	-	4,4,4	0.35	0	6,6,6	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	C	401	-	4,4,4	0.47	0	6,6,6	0.81	0

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
4	BME	A	402	-	-	0/1/1/1	-

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	C	401	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	387/394 (98%)	-0.74	0 100 100	14, 22, 39, 51	1 (0%)
1	C	387/394 (98%)	-0.72	1 (0%) 90 87	11, 22, 37, 50	1 (0%)
2	B	288/328 (87%)	-0.22	3 (1%) 79 73	21, 41, 71, 102	1 (0%)
2	D	288/328 (87%)	-0.14	8 (2%) 55 46	19, 40, 78, 107	1 (0%)
All	All	1350/1444 (93%)	-0.50	12 (0%) 81 75	11, 27, 66, 107	4 (0%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	440	VAL	3.5
2	B	617	SER	3.4
2	B	589	SER	3.1
2	D	594	GLY	3.1
2	D	595	GLU	2.3

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
4	BME	A	402	4/4	0.84	0.13	27,31,36,45	0
3	SO4	A	401	5/5	0.97	0.06	36,38,39,40	0
3	SO4	C	401	5/5	0.98	0.06	34,34,36,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.