

wwPDB X-ray Structure Validation Summary Report (i)

Sep 17, 2023 – 02:41 AM EDT

PDB ID	:	4TK2
Title	:	Geph E in complex with a GABA receptor alpha3 subunit derived peptide in
		space group P61
Authors	:	Kasaragod, V.B.; Maric, H.M.; Schindelin, H.
Deposited on		
Resolution	:	4.10 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 (i) 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 (1)) were used in the production of this report:

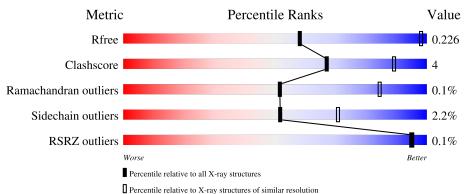
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 4.10 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1193 (4.50-3.70)
Clashscore	141614	1003 (4.44 - 3.76)
Ramachandran outliers	138981	1005 (4.48-3.72)
Sidechain outliers	138945	1199 (4.50-3.70)
RSRZ outliers	127900	1034 (4.50-3.70)

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	Q	uality of chain	
1	А	419		88%	9% ••
1	В	419		86%	11% ••
2	С	11	36%	45%	18%
2	D	11	73%		27%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6411 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.

- AltConf Mol Residues ZeroOcc Chain Atoms Total С Ν Ο S 1 0 0 А 411 1979313854559618 С Ν Total Ο S 1 В 0 0 411 3138198054559419
- Molecule 1 is a protein called Gephyrin.

• Molecule 2 is a protein called Gamma-aminobutyric acid receptor subunit alpha-3.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	С	9	Total C N O	Ο	Ο	0
2	U	5	71 48 10 13	0	0	0
0	Л	0	Total C N O	0	0	0
	D	0	64 43 9 12	0	0	0



Trace

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.

Chain A:	88%	99	6 ••
MET SER P320 V369 V369 A415 P415 P415 1433 I433 S436	Diage Diage Diage Diage Diage Diage Diage Edd Edd Edd Edd Edd Edd Edd Edd Edd Edd Edd Edd Edd Pid5 Pid5 Pid63 Pid63 Pid64 Pid64 Pid64 Pid64	L544 L544 Contraction L544 Contraction L544 Contraction L544 Contraction L544 Contraction L546 Contraction L547 Contraction L547 Contraction L547 Contraction L547 Contraction L	L590 K602 P603 T608 A623
N627 P628 R644 R644 L678 L678 V680	P687 N694 GLN MET MET S698 P713 P713 P713 V730 V730 L736		
• Molecule 1: G	ephyrin		
Chain B:	86%	11%	ý • •
MET SER 9326 1365 1365 1365 1365 1366 1366 1366 1378	L432 L432 L432 L433 R434 E435 S435 S435 S435 S435 E441 L443 L443 E441 L443 R446 L443 R446 L443 R446 L443 R458 R458 R458	L484 1491 1492 1493 1493 1493 1493 1514 1514 1514 1554	S575 MET GLY GLV L586 L586
L590 K602 P603 T608 T611	4623 1643 1644 1644 1644 1644 1678 1678 1678 1678 1678 1678 1678 1678	SER 869 609 871 8715 8715 8715 8715 8720 1720 1720 1720 1720 1730	
• Molecule 2: G	amma-aminobutyric acid recepto	or subunit alpha-3	
Chain C:	36% 45%	% 18%	_
F368 N369 1370 1373 1374 7374 1374 1376 1376 1115 ASN			
• Molecule 2: G	amma-aminobutyric acid recepto	or subunit alpha-3	
Chain D:	73%	27%	
F368 Y375 PRO ILLE ASN			

• Molecule 1: Gephyrin



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Depositor
Resolution (Å)	$\begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	Depositor EDS
% Data completeness	99.8 (47.90-4.10)	Depositor
(in resolution range)	$100.0 \ (47.90-4.10)$	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.20	Depositor
$< I/\sigma(I) > 1$	$1.87 (at 4.14 \text{\AA})$	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
D D	0.183 , 0.236	Depositor
R, R_{free}	0.177 , 0.226	DCC
R_{free} test set	824 reflections $(5.25%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	134.8	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32, 122.8	EDS
L-test for $twinning^2$	$< L >=0.41, < L^2>=0.23$	Xtriage
Estimated twinning fraction	0.094 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6411	wwPDB-VP
Average B, all atoms $(Å^2)$	160.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

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	s Bond angles		
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.20	0/3197	0.39	0/4347	
1	В	0.20	0/3197	0.39	0/4348	
2	С	0.33	0/73	0.49	0/100	
2	D	0.27	0/65	0.46	0/88	
All	All	0.20	0/6532	0.39	0/8883	

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	А	3138	0	3177	25	0
1	В	3138	0	3179	27	0
2	С	71	0	67	3	0
2	D	64	0	60	0	0
All	All	6411	0	6483	50	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 4.

The worst 5 of 50 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:B:692:THR:O	1:B:695:GLN:NE2	2.23	0.72
1:A:440:THR:HG22	1:A:441:GLU:H	1.58	0.67
1:B:608:THR:HB	1:B:623:ALA:HB3	1.81	0.61
1:B:433:ILE:HD11	1:B:446:ARG:HG2	1.84	0.59
1:A:678:LEU:HD21	1:A:730:VAL:HG11	1.85	0.59

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	Percentil	es
1	А	405/419~(97%)	397~(98%)	7 (2%)	1 (0%)	47 80	
1	В	405/419~(97%)	399~(98%)	6(2%)	0	100 10	0
2	С	7/11~(64%)	6 (86%)	1 (14%)	0	100 10	0
2	D	6/11~(54%)	6 (100%)	0	0	100 10	0
All	All	823/860~(96%)	808 (98%)	14 (2%)	1 (0%)	51 84	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	437	ASP

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	А	349/356~(98%)	343~(98%)	6(2%)	60	78
1	В	349/356~(98%)	341~(98%)	8 (2%)	50	70
2	С	8/10 (80%)	6~(75%)	2(25%)	0	4
2	D	7/10~(70%)	7~(100%)	0	100	100
All	All	713/732~(97%)	697~(98%)	16 (2%)	52	71

5 of 16 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
2	С	368	PHE
1	В	696	MET
1	В	436	SER
1	В	554	LEU
1	В	435	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	695	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.



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, 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 $>$	$\# RSRZ {>}2$	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	411/419 (98%)	-0.20	0 100 100	95, 144, 214, 277	0
1	В	411/419 (98%)	-0.09	1 (0%) 95 93	102, 159, 229, 298	0
2	С	9/11~(81%)	0.86	0 100 100	201, 220, 245, 250	0
2	D	8/11~(72%)	0.20	0 100 100	176, 205, 239, 255	0
All	All	839/860~(97%)	-0.13	1 (0%) 95 95	95, 153, 225, 298	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	442	GLU	3.7

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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

