



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:40 AM GMT

PDB ID : 2XXX  
Title : Crystal structure of the GluK2 (GluR6) D776K LBD dimer in complex with glutamate (P21 21 21)  
Authors : Nayeem, N.; Mayans, O.; Green, T.  
Deposited on : 2010-11-12  
Resolution : 2.10 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

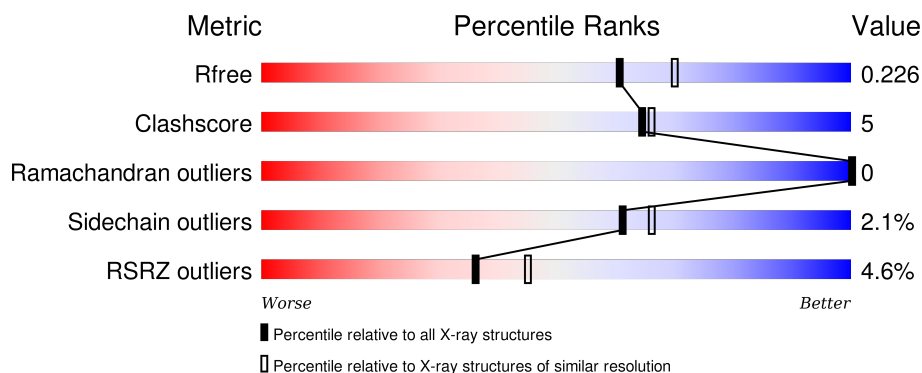
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	261	<div> <div>3%</div> <div>84% 10% 5%</div> </div>
1	B	261	<div> <div>6%</div> <div>84% 10% 5%</div> </div>
1	C	261	<div> <div>5%</div> <div>83% 11% • 5%</div> </div>
1	D	261	<div> <div>3%</div> <div>78% 14% • 6%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8354 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 GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1983	1272	325	375	11			
1	B	248	Total	C	N	O	S	0	0	0
			1983	1272	325	375	11			
1	C	248	Total	C	N	O	S	0	0	0
			1983	1272	325	375	11			
1	D	246	Total	C	N	O	S	0	0	0
			1971	1265	325	370	11			

There are 24 discrepancies between the modelled and reference sequences:

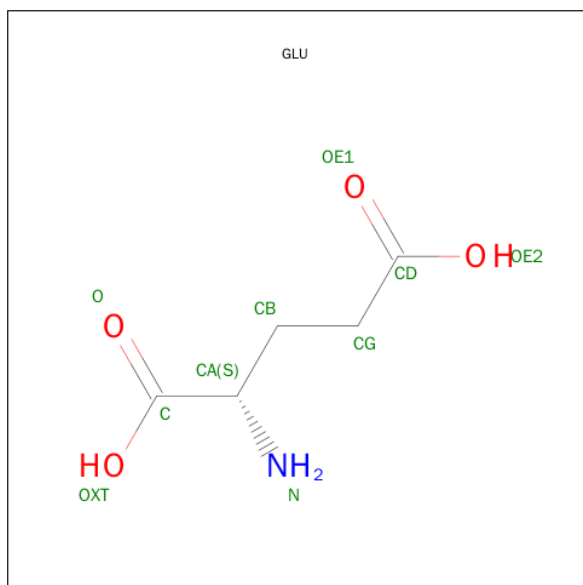
Chain	Residue	Modelled	Actual	Comment	Reference
A	428	GLY	-	EXPRESSION TAG	UNP P42260
A	555	GLY	-	LINKER	UNP P42260
A	566	THR	-	LINKER	UNP P42260
A	776	LYS	ASP	ENGINEERED MUTATION	UNP P42260
A	807	PRO	-	EXPRESSION TAG	UNP P42260
A	808	ARG	-	EXPRESSION TAG	UNP P42260
B	428	GLY	-	EXPRESSION TAG	UNP P42260
B	555	GLY	-	LINKER	UNP P42260
B	566	THR	-	LINKER	UNP P42260
B	776	LYS	ASP	ENGINEERED MUTATION	UNP P42260
B	807	PRO	-	EXPRESSION TAG	UNP P42260
B	808	ARG	-	EXPRESSION TAG	UNP P42260
C	428	GLY	-	EXPRESSION TAG	UNP P42260
C	555	GLY	-	LINKER	UNP P42260
C	566	THR	-	LINKER	UNP P42260
C	776	LYS	ASP	ENGINEERED MUTATION	UNP P42260
C	807	PRO	-	EXPRESSION TAG	UNP P42260
C	808	ARG	-	EXPRESSION TAG	UNP P42260
D	428	GLY	-	EXPRESSION TAG	UNP P42260
D	555	GLY	-	LINKER	UNP P42260
D	566	THR	-	LINKER	UNP P42260

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Chain	Residue	Modelled	Actual	Comment	Reference
D	776	LYS	ASP	ENGINEERED MUTATION	UNP P42260
D	807	PRO	-	EXPRESSION TAG	UNP P42260
D	808	ARG	-	EXPRESSION TAG	UNP P42260

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula:  $C_5H_9NO_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		
2	C	1	Total	C	N	O	0	0
			10	5	1	4		
2	D	1	Total	C	N	O	0	0
			10	5	1	4		

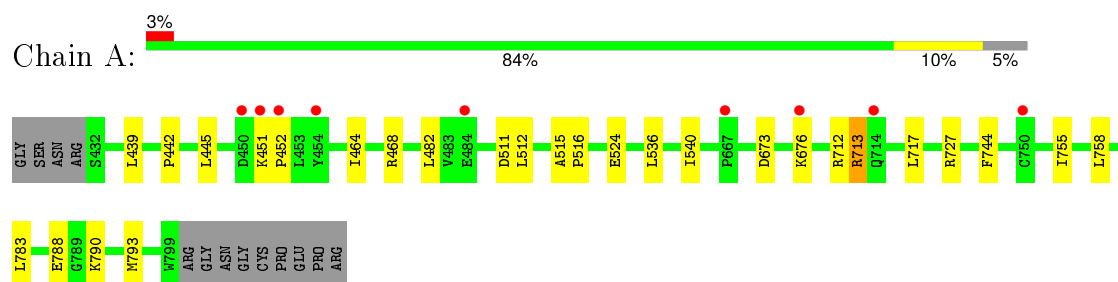
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	118	Total	O	0	0
			118	118		
3	B	79	Total	O	0	0
			79	79		
3	C	100	Total	O	0	0
			100	100		
3	D	97	Total	O	0	0
			97	97		

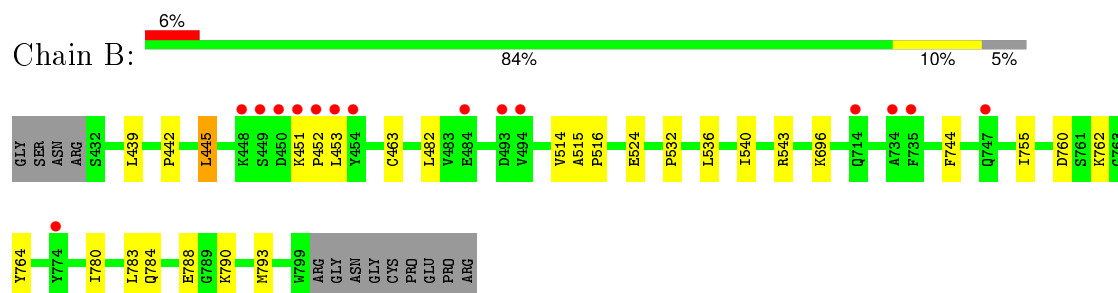
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

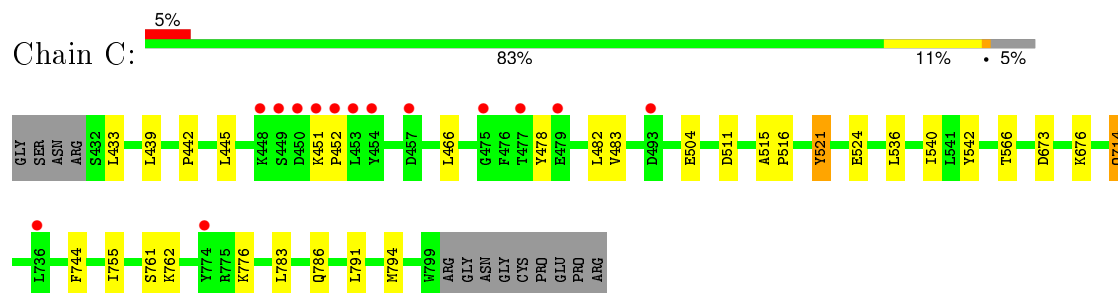
#### • Molecule 1: GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2



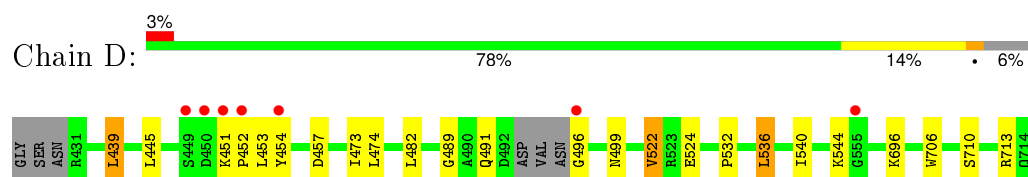
#### • Molecule 1: GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2

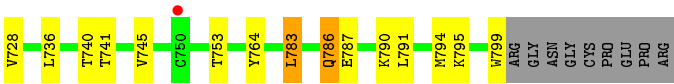


#### • Molecule 1: GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2



#### • Molecule 1: GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.56Å 101.34Å 125.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 2.10 19.93 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.5 (19.93-2.10) 98.5 (19.93-2.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.50 (at 2.09Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.179 , 0.231 0.173 , 0.226	Depositor DCC
$R_{free}$ test set	3234 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 51.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63558 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8354	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.29	0/2021	0.46	0/2724
1	B	0.27	0/2021	0.44	0/2724
1	C	0.26	0/2021	0.44	0/2724
1	D	0.28	0/2008	0.45	0/2703
All	All	0.27	0/8071	0.45	0/10875

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	A	1983	0	2003	17	0
1	B	1983	0	2003	18	0
1	C	1983	0	2003	22	0
1	D	1971	0	1996	33	0
2	A	10	0	5	0	0
2	B	10	0	5	0	0
2	C	10	0	5	0	0
2	D	10	0	5	0	0
3	A	118	0	0	2	0
3	B	79	0	0	0	0
3	C	100	0	0	0	0
3	D	97	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8354	0	8025	81	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 5.

All (81) 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:D:790:LYS:HG3	1:D:794:MET:HE2	1.41	1.02
1:D:710:SER:HB2	1:D:713:ARG:HH21	1.39	0.87
1:D:791:LEU:HD23	1:D:794:MET:HE3	1.66	0.76
1:A:788:GLU:HG3	1:A:790:LYS:HG3	1.68	0.75
1:A:713:ARG:HD3	1:A:717:LEU:HD12	1.73	0.71
1:C:442:PRO:HG3	1:C:744:PHE:CD1	2.27	0.69
1:B:451:LYS:HG3	1:B:452:PRO:HD2	1.75	0.68
1:C:786:GLN:HG3	1:C:791:LEU:HD12	1.74	0.68
1:D:791:LEU:HA	1:D:794:MET:HE3	1.80	0.62
1:D:710:SER:HB2	1:D:713:ARG:NH2	2.14	0.62
1:D:439:LEU:HD22	1:D:482:LEU:HD22	1.82	0.61
1:D:795:LYS:HD2	1:D:799:TRP:CE3	2.36	0.61
1:D:791:LEU:HD23	1:D:794:MET:CE	2.33	0.57
1:B:780:ILE:O	1:B:784:GLN:HG3	2.04	0.57
1:D:491:GLN:HB2	1:D:496:GLY:O	2.05	0.56
1:A:439:LEU:HD22	1:A:482:LEU:HD22	1.88	0.54
1:B:439:LEU:HD22	1:B:482:LEU:HD22	1.89	0.54
1:B:442:PRO:HG3	1:B:744:PHE:CD1	2.42	0.53
1:D:451:LYS:HG2	1:D:452:PRO:HD2	1.89	0.53
1:A:511:ASP:O	1:A:512:LEU:HD12	2.08	0.52
1:B:515:ALA:HB1	1:B:516:PRO:HD2	1.91	0.52
1:B:788:GLU:HG3	1:B:790:LYS:HG3	1.91	0.52
1:A:793:MET:HE3	3:A:2112:HOH:O	2.09	0.52
1:C:439:LEU:HD22	1:C:482:LEU:HD22	1.92	0.51
1:C:673:ASP:HA	1:C:676:LYS:HE2	1.93	0.50
1:D:544:LYS:HG2	1:D:753:THR:HB	1.92	0.50
1:C:483:VAL:HG23	1:C:504:GLU:OE2	2.12	0.50
1:A:451:LYS:HB3	1:A:452:PRO:HD2	1.94	0.50
1:D:451:LYS:CG	1:D:452:PRO:HD2	2.43	0.49
1:A:727:ARG:HD3	3:A:2077:HOH:O	2.12	0.49
1:C:540:ILE:HB	1:C:755:ILE:HB	1.94	0.49
1:D:473:ILE:HG22	1:D:474:LEU:HD23	1.95	0.48
1:C:483:VAL:HA	1:C:504:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:433:LEU:HA	1:C:511:ASP:OD2	2.14	0.47
1:C:433:LEU:O	1:C:478:TYR:HA	2.14	0.47
1:C:783:LEU:CD1	1:D:524:GLU:HG3	2.44	0.47
1:A:515:ALA:HB1	1:A:516:PRO:HD2	1.96	0.47
1:A:540:ILE:HB	1:A:755:ILE:HB	1.96	0.47
1:D:536:LEU:HB3	1:D:740:THR:HG23	1.97	0.47
1:A:712:ARG:HH11	1:A:712:ARG:HG3	1.80	0.47
1:A:783:LEU:CD1	1:B:524:GLU:HG3	2.45	0.46
1:C:524:GLU:HG3	1:D:783:LEU:HD23	1.97	0.46
1:D:451:LYS:HG2	1:D:452:PRO:CD	2.45	0.46
1:D:540:ILE:HG12	1:D:736:LEU:HD13	1.98	0.46
1:A:524:GLU:HG3	1:B:783:LEU:CD1	2.46	0.46
1:C:515:ALA:HB1	1:C:516:PRO:HD2	1.97	0.46
1:C:521:TYR:HD2	1:D:787:GLU:OE1	1.98	0.46
1:A:442:PRO:HG3	1:A:744:PHE:CD1	2.51	0.46
1:B:790:LYS:HA	1:B:793:MET:CE	2.46	0.45
1:D:706:TRP:CE2	1:D:710:SER:HB3	2.52	0.45
1:D:715:SER:O	1:D:727:ARG:NH1	2.51	0.44
1:B:540:ILE:HB	1:B:755:ILE:HB	2.00	0.44
1:C:451:LYS:HB3	1:C:452:PRO:HD2	1.99	0.44
1:D:522:VAL:HG11	1:D:696:LYS:HE3	2.01	0.43
1:B:696:LYS:HA	1:B:696:LYS:HD2	1.88	0.43
1:D:439:LEU:HD13	1:D:439:LEU:HA	1.85	0.43
1:B:532:PRO:HA	1:B:764:TYR:O	2.19	0.43
1:D:724:GLY:O	1:D:728:VAL:HG23	2.18	0.43
1:B:784:GLN:O	1:B:788:GLU:HG2	2.19	0.43
1:B:463:CYS:HB3	1:B:514:VAL:HG12	2.01	0.43
1:C:776:LYS:HE3	1:D:524:GLU:O	2.18	0.42
1:C:524:GLU:HG3	1:D:783:LEU:CD2	2.49	0.42
1:D:741:THR:O	1:D:745:VAL:HG23	2.19	0.42
1:B:790:LYS:HA	1:B:793:MET:HE3	2.01	0.42
1:C:761:SER:O	1:D:786:GLN:CD	2.57	0.42
1:A:511:ASP:C	1:A:512:LEU:HD12	2.39	0.42
1:B:760:ASP:OD2	1:B:762:LYS:HE3	2.19	0.42
1:A:464:ILE:O	1:A:468:ARG:HG3	2.20	0.42
1:A:673:ASP:HA	1:A:676:LYS:HE2	2.02	0.42
1:C:714:GLN:HG2	1:C:714:GLN:H	1.64	0.41
1:D:532:PRO:HA	1:D:764:TYR:O	2.19	0.41
1:A:439:LEU:CD2	1:A:482:LEU:HD22	2.49	0.41
1:C:542:TYR:CE2	1:C:566:THR:HG21	2.56	0.41
1:C:762:LYS:HB3	1:C:762:LYS:HE2	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:TYR:HB3	1:D:783:LEU:HB3	2.03	0.41
1:B:543:ARG:HE	1:B:543:ARG:HB2	1.67	0.41
1:B:439:LEU:HD12	1:B:445:LEU:HA	2.02	0.41
1:D:790:LYS:O	1:D:794:MET:HG3	2.22	0.40
1:D:454:TYR:O	1:D:457:ASP:HB2	2.22	0.40
1:D:489:GLY:HA2	1:D:499:ASN:O	2.21	0.40
1:C:466:LEU:HB2	1:C:794:MET:HE1	2.04	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	246/261 (94%)	242 (98%)	4 (2%)	0	100	100
1	B	246/261 (94%)	242 (98%)	4 (2%)	0	100	100
1	C	246/261 (94%)	242 (98%)	4 (2%)	0	100	100
1	D	242/261 (93%)	236 (98%)	6 (2%)	0	100	100
All	All	980/1044 (94%)	962 (98%)	18 (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	217/227 (96%)	213 (98%)	4 (2%)	66	72
1	B	217/227 (96%)	214 (99%)	3 (1%)	74	80
1	C	217/227 (96%)	213 (98%)	4 (2%)	66	72
1	D	215/227 (95%)	208 (97%)	7 (3%)	45	47
All	All	866/908 (95%)	848 (98%)	18 (2%)	61	66

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	445	LEU
1	A	536	LEU
1	A	713	ARG
1	A	758	LEU
1	B	445	LEU
1	B	453	LEU
1	B	536	LEU
1	C	445	LEU
1	C	521	TYR
1	C	536	LEU
1	C	714	GLN
1	D	439	LEU
1	D	445	LEU
1	D	453	LEU
1	D	522	VAL
1	D	536	LEU
1	D	783	LEU
1	D	786	GLN

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

Mol	Chain	Res	Type
1	A	714	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

4 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	$\# Z  > 2$
2	GLU	A	900	-	3,9,9	0.30	0	2,11,11	0.07	0
2	GLU	B	900	-	3,9,9	0.36	0	2,11,11	0.06	0
2	GLU	C	900	-	3,9,9	0.38	0	2,11,11	0.15	0
2	GLU	D	900	-	3,9,9	0.35	0	2,11,11	0.17	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
2	GLU	A	900	-	-	0/3/9/9	0/0/0/0
2	GLU	B	900	-	-	0/3/9/9	0/0/0/0
2	GLU	C	900	-	-	0/3/9/9	0/0/0/0
2	GLU	D	900	-	-	0/3/9/9	0/0/0/0

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 ⓘ

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	248/261 (95%)	-0.12	9 (3%) 46 55	18, 37, 78, 126	0
1	B	248/261 (95%)	0.04	15 (6%) 25 33	23, 46, 83, 149	0
1	C	248/261 (95%)	0.05	14 (5%) 28 36	23, 45, 86, 174	0
1	D	246/261 (94%)	-0.08	8 (3%) 50 59	21, 42, 71, 109	0
All	All	990/1044 (94%)	-0.03	46 (4%) 36 45	18, 42, 81, 174	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	496	GLY	7.6
1	C	450	ASP	5.2
1	C	451	LYS	4.9
1	B	450	ASP	4.7
1	B	449	SER	4.7
1	C	454	TYR	4.3
1	C	448	LYS	4.3
1	B	451	LYS	4.2
1	C	457	ASP	4.1
1	D	450	ASP	4.0
1	C	449	SER	3.9
1	A	714	GLN	3.7
1	A	450	ASP	3.6
1	B	448	LYS	3.4
1	B	493	ASP	3.4
1	A	452	PRO	3.3
1	A	451	LYS	3.3
1	A	750	CYS	3.3
1	C	452	PRO	3.2
1	C	774	TYR	3.2
1	A	454	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	494	VAL	3.1
1	C	453	LEU	3.0
1	B	734	ALA	2.7
1	B	452	PRO	2.7
1	D	449	SER	2.6
1	C	477	THR	2.5
1	D	750	CYS	2.5
1	B	774	TYR	2.4
1	C	475	GLY	2.4
1	D	454	TYR	2.4
1	B	714	GLN	2.3
1	D	555	GLY	2.3
1	D	452	PRO	2.3
1	C	479	GLU	2.3
1	A	667	PRO	2.3
1	B	747	GLN	2.3
1	B	454	TYR	2.3
1	D	451	LYS	2.2
1	A	676	LYS	2.2
1	A	484	GLU	2.2
1	C	493	ASP	2.2
1	C	736	LEU	2.1
1	B	735	PHE	2.1
1	B	484	GLU	2.1
1	B	453	LEU	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLU	A	900	10/10	0.97	0.15	0.83	24,26,29,29	0
2	GLU	D	900	10/10	0.97	0.11	-0.12	19,29,31,31	0
2	GLU	C	900	10/10	0.97	0.09	-0.25	20,25,30,32	0
2	GLU	B	900	10/10	0.97	0.08	-0.99	24,28,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.