



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:57 PM GMT

PDB ID : 1VYV  
Title : BETA4 SUBUNIT OF CA2+ CHANNEL  
Authors : Chen, Y.-H.; Li, M.-H.; Zhang, Y.; He, L.-L.; Yamada, Y.; Fitzmaurice, A.;  
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Deposited on : 2004-05-07  
Resolution : 3.00 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

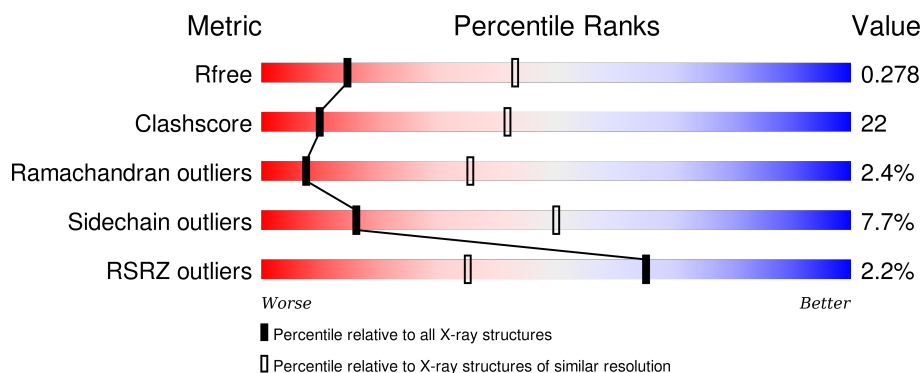
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	359	
1	B	359	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4361 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.

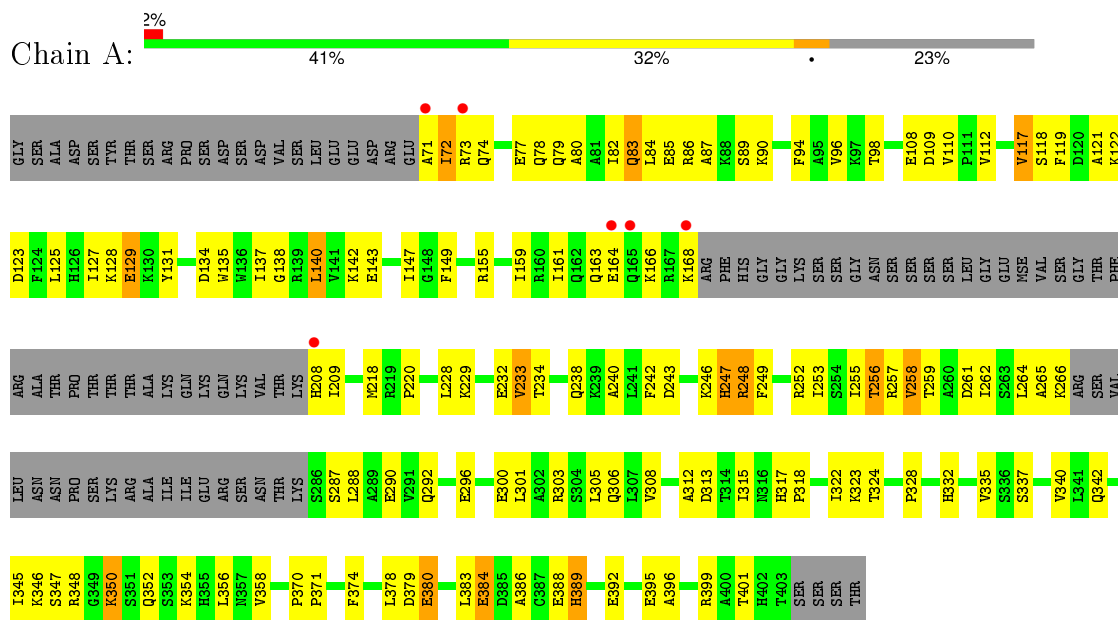
- Molecule 1 is a protein called CALCIUM CHANNEL BETA-4SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	Se	0	0	1
			2176	1384	382	402	4	4			
1	B	276	Total	C	N	O	S	Se	0	0	1
			2185	1389	383	405	4	4			

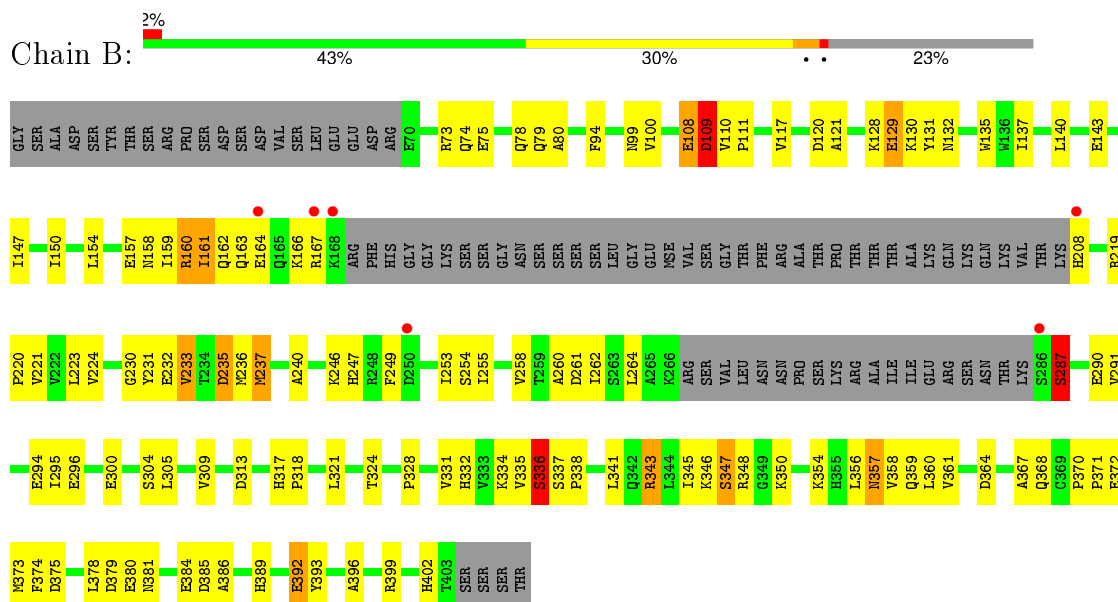
### 3 Residue-property plots

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: CALCIUM CHANNEL BETA-4SUBUNIT



- Molecule 1: CALCIUM CHANNEL BETA-4SUBUNIT



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.30Å 83.20Å 72.30Å 90.00° 94.90° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 29.97 – 2.80	Depositor EDS
% Data completeness (in resolution range)	88.8 (30.00-3.00) 91.7 (29.97-2.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.248 , 0.287 0.236 , 0.278	Depositor DCC
$R_{free}$ test set	1413 reflections (11.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.7	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 46.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 16967 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4361	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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	0.52	0/2213	0.71	1/2987 (0.0%)
1	B	0.49	1/2222 (0.0%)	0.68	0/2999
All	All	0.50	1/4435 (0.0%)	0.70	1/5986 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	237	MSE	CG-SE	-5.13	1.78	1.95

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	ILE	N-CA-C	-5.16	97.08	111.00

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	2176	0	2213	110	0
1	B	2185	0	2219	87	0
All	All	4361	0	4432	194	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 22.

All (194) 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:246:LYS:HG3	1:B:255:ILE:HD12	1.44	0.99
1:A:159:ILE:O	1:A:163:GLN:HB2	1.61	0.98
1:B:380:GLU:O	1:B:381:ASN:HB2	1.64	0.93
1:A:246:LYS:HG2	1:A:255:ILE:HD12	1.52	0.91
1:A:256:THR:HG21	1:A:301:LEU:HD11	1.53	0.90
1:A:296:GLU:O	1:A:300:GLU:HG2	1.72	0.89
1:A:73:ARG:HG3	1:A:74:GLN:N	1.88	0.88
1:B:380:GLU:OE1	1:B:385:ASP:HB3	1.74	0.87
1:B:233:VAL:HG21	1:B:345:ILE:HG12	1.56	0.86
1:A:242:PHE:O	1:A:246:LYS:HG3	1.76	0.85
1:A:265:ALA:HB3	1:A:324:THR:HB	1.61	0.81
1:A:392:GLU:CD	1:B:343:ARG:HH21	1.84	0.81
1:A:259:THR:HG22	1:A:313:ASP:OD2	1.82	0.78
1:A:252:ARG:HA	1:A:306:GLN:OE1	1.83	0.78
1:A:164:GLU:C	1:A:166:LYS:H	1.85	0.78
1:A:228:LEU:HD11	1:A:358:VAL:HG12	1.66	0.78
1:B:332:HIS:HB2	1:B:374:PHE:CD2	2.22	0.74
1:A:140:LEU:HD13	1:A:142:LYS:HB2	1.71	0.72
1:A:233:VAL:HG21	1:A:345:ILE:HG12	1.72	0.72
1:A:249:PHE:O	1:A:253:ILE:HG22	1.90	0.71
1:A:256:THR:HG21	1:A:301:LEU:CD1	2.19	0.71
1:A:73:ARG:HG3	1:A:74:GLN:H	1.55	0.70
1:A:380:GLU:HG3	1:B:347:SER:HA	1.72	0.70
1:B:159:ILE:O	1:B:163:GLN:HG3	1.94	0.68
1:A:246:LYS:CG	1:A:255:ILE:HD12	2.25	0.67
1:A:208:HIS:HB3	1:A:209:ILE:HD12	1.77	0.67
1:A:78:GLN:O	1:A:82:ILE:HG12	1.95	0.66
1:B:380:GLU:OE2	1:B:386:ALA:HA	1.95	0.66
1:A:87:ALA:HA	1:A:90:LYS:HD2	1.78	0.65
1:A:265:ALA:HB3	1:A:324:THR:CB	2.27	0.64
1:A:243:ASP:HA	1:A:246:LYS:HD2	1.78	0.64
1:B:336:SER:OG	1:B:337:SER:N	2.31	0.63
1:B:396:ALA:O	1:B:399:ARG:HG2	1.98	0.63
1:B:287:SER:OG	1:B:290:GLU:HG3	1.98	0.63
1:A:108:GLU:C	1:A:110:VAL:H	2.02	0.62
1:B:370:PRO:HD2	1:B:373:MSE:SE	2.49	0.62
1:A:380:GLU:OE2	1:A:389:HIS:HD2	1.83	0.62
1:A:161:ILE:C	1:A:163:GLN:H	2.02	0.62
1:A:380:GLU:OE2	1:A:389:HIS:CD2	2.53	0.62
1:B:223:LEU:HD23	1:B:331:VAL:HB	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:ARG:HG3	1:A:155:ARG:HH11	1.66	0.61
1:B:260:ALA:HB3	1:B:294:GLU:HG3	1.82	0.61
1:B:80:ALA:HB2	1:B:131:TYR:OH	2.01	0.61
1:B:255:ILE:O	1:B:255:ILE:HG22	2.01	0.60
1:A:332:HIS:HB2	1:A:374:PHE:CD2	2.37	0.59
1:B:262:ILE:C	1:B:264:LEU:H	2.05	0.59
1:B:380:GLU:O	1:B:381:ASN:CB	2.42	0.58
1:B:158:ASN:HB3	1:B:162:GLN:NE2	2.18	0.58
1:A:110:VAL:HG22	1:A:135:TRP:CH2	2.39	0.58
1:A:80:ALA:HB2	1:A:131:TYR:OH	2.03	0.58
1:B:94:PHE:CE2	1:B:130:LYS:HE2	2.38	0.58
1:B:258:VAL:HG11	1:B:262:ILE:HG23	1.85	0.58
1:A:94:PHE:CZ	1:A:127:ILE:HG21	2.39	0.58
1:A:262:ILE:C	1:A:264:LEU:H	2.07	0.58
1:A:155:ARG:HG3	1:A:155:ARG:NH1	2.19	0.57
1:B:258:VAL:HG11	1:B:262:ILE:CG2	2.34	0.57
1:B:379:ASP:O	1:B:380:GLU:CG	2.53	0.57
1:B:392:GLU:HG2	1:B:393:TYR:N	2.18	0.57
1:B:74:GLN:O	1:B:78:GLN:HG3	2.04	0.57
1:A:218:MSE:SE	1:A:401:THR:HG21	2.55	0.56
1:A:125:LEU:HD23	1:A:140:LEU:HA	1.86	0.56
1:A:121:ALA:O	1:A:122:LYS:HB2	2.05	0.55
1:A:380:GLU:N	1:A:380:GLU:OE1	2.40	0.55
1:A:220:PRO:HD2	1:A:328:PRO:HA	1.87	0.55
1:B:120:ASP:OD1	1:B:121:ALA:N	2.39	0.55
1:A:342:GLN:HG3	1:A:356:LEU:HD21	1.88	0.55
1:B:161:ILE:C	1:B:163:GLN:H	2.10	0.55
1:A:317:HIS:ND1	1:A:318:PRO:HD2	2.22	0.55
1:A:337:SER:OG	1:A:340:VAL:HG23	2.06	0.55
1:A:164:GLU:C	1:A:166:LYS:N	2.54	0.55
1:B:379:ASP:O	1:B:380:GLU:HG3	2.06	0.54
1:A:84:LEU:O	1:A:87:ALA:HB3	2.07	0.54
1:A:209:ILE:N	1:A:209:ILE:HD12	2.22	0.54
1:A:84:LEU:HD12	1:A:137:ILE:HD13	1.90	0.54
1:B:357:ASN:O	1:B:361:VAL:HG23	2.09	0.53
1:B:94:PHE:HE2	1:B:130:LYS:HE2	1.74	0.53
1:A:228:LEU:CD1	1:A:358:VAL:HG12	2.38	0.53
1:A:94:PHE:CE2	1:A:127:ILE:HG21	2.44	0.53
1:B:399:ARG:HB3	1:B:399:ARG:NH1	2.25	0.52
1:B:249:PHE:O	1:B:253:ILE:HG22	2.10	0.52
1:B:137:ILE:CG2	1:B:147:ILE:HD11	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:VAL:HG22	1:A:312:ALA:HA	1.92	0.52
1:B:164:GLU:C	1:B:166:LYS:H	2.12	0.52
1:A:378:LEU:HB3	1:A:386:ALA:HB1	1.92	0.52
1:A:350:LYS:O	1:A:354:LYS:HB2	2.09	0.52
1:B:117:VAL:CG2	1:B:150:ILE:HG12	2.40	0.52
1:A:265:ALA:CB	1:A:324:THR:HB	2.37	0.51
1:A:83:GLN:HG3	1:A:83:GLN:O	2.10	0.51
1:B:371:PRO:HG2	1:B:372:GLU:OE2	2.11	0.50
1:B:253:ILE:HG12	1:B:254:SER:N	2.26	0.50
1:A:110:VAL:HG12	1:A:112:VAL:O	2.12	0.50
1:B:75:GLU:O	1:B:79:GLN:HG2	2.11	0.50
1:B:346:LYS:C	1:B:348:ARG:H	2.14	0.50
1:A:164:GLU:O	1:A:164:GLU:HG2	2.10	0.50
1:A:379:ASP:O	1:A:380:GLU:C	2.49	0.50
1:B:73:ARG:NH2	1:B:74:GLN:HE21	2.10	0.50
1:B:128:LYS:O	1:B:129:GLU:CB	2.59	0.50
1:A:229:LYS:HE3	1:A:315:ILE:O	2.12	0.50
1:B:99:ASN:O	1:B:100:VAL:HG13	2.12	0.49
1:A:140:LEU:HD11	1:A:142:LYS:HD2	1.93	0.49
1:B:317:HIS:ND1	1:B:318:PRO:HD2	2.27	0.49
1:A:240:ALA:HB1	1:A:383:LEU:HD21	1.93	0.49
1:B:232:GLU:O	1:B:236:MSE:HG3	2.13	0.49
1:A:306:GLN:O	1:A:308:VAL:HG23	2.12	0.49
1:B:304:SER:O	1:B:305:LEU:HB2	2.12	0.49
1:A:396:ALA:HA	1:A:399:ARG:NH1	2.28	0.49
1:B:158:ASN:HB3	1:B:162:GLN:HE21	1.77	0.49
1:A:234:THR:HG23	1:A:238:GLN:HE21	1.78	0.48
1:A:287:SER:HB3	1:A:290:GLU:HG3	1.95	0.48
1:A:96:VAL:CG2	1:A:125:LEU:HB2	2.43	0.48
1:A:248:ARG:NH1	1:A:395:GLU:OE1	2.43	0.48
1:B:364:ASP:O	1:B:368:GLN:HG3	2.14	0.48
1:A:84:LEU:HD13	1:A:149:PHE:CE1	2.49	0.48
1:A:134:ASP:C	1:A:135:TRP:CD1	2.87	0.48
1:B:291:VAL:O	1:B:295:ILE:HG12	2.14	0.48
1:B:117:VAL:HG21	1:B:150:ILE:HG12	1.96	0.47
1:B:358:VAL:HG23	1:B:359:GLN:N	2.28	0.47
1:A:384:GLU:H	1:A:384:GLU:HG2	1.23	0.47
1:A:266:LYS:HG2	1:A:266:LYS:O	2.14	0.47
1:A:143:GLU:OE2	1:A:399:ARG:HD2	2.14	0.47
1:A:346:LYS:C	1:A:348:ARG:H	2.17	0.47
1:A:292:GLN:O	1:A:296:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:MSE:HE2	1:A:305:LEU:O	2.14	0.47
1:B:399:ARG:NH1	1:B:399:ARG:CB	2.78	0.47
1:B:131:TYR:CD2	1:B:132:ASN:ND2	2.83	0.47
1:A:232:GLU:OE1	1:A:352:GLN:HG3	2.15	0.47
1:A:71:ALA:N	1:A:73:ARG:HG2	2.30	0.46
1:B:73:ARG:HH21	1:B:74:GLN:HE21	1.63	0.46
1:A:256:THR:OG1	1:A:257:ARG:N	2.48	0.46
1:A:322:ILE:HG22	1:A:323:LYS:HG3	1.98	0.46
1:A:90:LYS:O	1:A:128:LYS:HE2	2.15	0.46
1:A:87:ALA:O	1:A:128:LYS:HD3	2.16	0.46
1:A:108:GLU:C	1:A:110:VAL:N	2.69	0.46
1:A:80:ALA:CB	1:A:131:TYR:OH	2.64	0.46
1:A:265:ALA:O	1:A:266:LYS:C	2.54	0.45
1:A:71:ALA:N	1:A:74:GLN:HG3	2.32	0.45
1:A:128:LYS:O	1:A:129:GLU:CB	2.63	0.45
1:B:364:ASP:O	1:B:367:ALA:HB3	2.16	0.45
1:B:163:GLN:O	1:B:166:LYS:HB2	2.15	0.45
1:B:253:ILE:HD11	1:B:255:ILE:HD11	1.99	0.45
1:B:143:GLU:OE2	1:B:399:ARG:HD3	2.17	0.45
1:B:399:ARG:HB3	1:B:399:ARG:CZ	2.46	0.45
1:A:370:PRO:HA	1:A:371:PRO:HD3	1.85	0.45
1:A:303:ARG:HH11	1:A:303:ARG:HG3	1.82	0.45
1:A:380:GLU:CD	1:A:380:GLU:H	2.18	0.45
1:B:220:PRO:HD2	1:B:328:PRO:HA	1.98	0.45
1:A:258:VAL:CG2	1:A:258:VAL:O	2.65	0.45
1:B:262:ILE:C	1:B:264:LEU:N	2.69	0.44
1:A:83:GLN:OE1	1:A:86:ARG:NH2	2.51	0.44
1:B:237:MSE:O	1:B:240:ALA:HB3	2.18	0.44
1:B:109:ASP:N	1:B:109:ASP:OD1	2.50	0.44
1:B:164:GLU:C	1:B:166:LYS:N	2.70	0.44
1:A:389:HIS:C	1:A:389:HIS:ND1	2.71	0.44
1:A:98:THR:HG21	1:A:119:PHE:CD1	2.53	0.44
1:B:378:LEU:HB3	1:B:386:ALA:HB1	1.99	0.43
1:A:96:VAL:HG23	1:A:125:LEU:HB2	2.00	0.43
1:A:262:ILE:C	1:A:264:LEU:N	2.70	0.43
1:B:219:ARG:HA	1:B:220:PRO:HD3	1.75	0.43
1:B:230:GLY:N	1:B:235:ASP:OD1	2.36	0.43
1:A:288:LEU:O	1:A:292:GLN:HG3	2.18	0.43
1:A:110:VAL:HA	1:A:135:TRP:CH2	2.54	0.43
1:A:135:TRP:CD1	1:A:135:TRP:N	2.87	0.43
1:B:131:TYR:HD2	1:B:132:ASN:ND2	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:GLU:C	1:B:110:VAL:H	2.22	0.43
1:B:305:LEU:O	1:B:402:HIS:NE2	2.51	0.43
1:B:384:GLU:OE1	1:B:384:GLU:N	2.45	0.43
1:B:110:VAL:HG22	1:B:135:TRP:CH2	2.53	0.43
1:B:350:LYS:O	1:B:354:LYS:HB2	2.18	0.43
1:A:74:GLN:O	1:A:77:GLU:HB3	2.19	0.43
1:B:364:ASP:OD1	1:B:368:GLN:NE2	2.52	0.42
1:A:392:GLU:CD	1:B:343:ARG:NH2	2.63	0.42
1:A:164:GLU:HG3	1:A:168:LYS:HB2	2.00	0.42
1:B:231:TYR:N	1:B:231:TYR:CD1	2.87	0.42
1:A:117:VAL:CG2	1:A:118:SER:N	2.82	0.42
1:B:233:VAL:HG21	1:B:345:ILE:CG1	2.40	0.42
1:B:356:LEU:HD11	1:B:360:LEU:HD11	2.01	0.42
1:B:332:HIS:CE1	1:B:334:LYS:HE3	2.55	0.42
1:A:123:ASP:OD1	1:A:140:LEU:HD21	2.20	0.42
1:B:221:VAL:HB	1:B:309:VAL:HG22	2.02	0.42
1:A:138:GLY:O	1:A:147:ILE:HA	2.21	0.41
1:A:87:ALA:O	1:A:90:LYS:HB2	2.20	0.41
1:A:247:HIS:C	1:A:247:HIS:ND1	2.72	0.41
1:A:138:GLY:O	1:A:147:ILE:HG13	2.21	0.41
1:B:335:VAL:HG11	1:B:341:LEU:HB2	2.03	0.41
1:A:77:GLU:O	1:A:78:GLN:C	2.58	0.41
1:A:110:VAL:CG1	1:A:112:VAL:O	2.68	0.41
1:A:242:PHE:HB3	1:A:246:LYS:HE3	2.03	0.41
1:B:260:ALA:O	1:B:262:ILE:N	2.54	0.41
1:A:265:ALA:HB3	1:A:324:THR:CG2	2.51	0.41
1:B:337:SER:HA	1:B:338:PRO:HD3	1.86	0.41
1:B:317:HIS:HA	1:B:318:PRO:HD3	1.96	0.41
1:B:296:GLU:O	1:B:300:GLU:HB2	2.21	0.41
1:B:160:ARG:HE	1:B:161:ILE:HG13	1.86	0.40
1:B:321:LEU:HA	1:B:324:THR:HG23	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	269/359 (75%)	239 (89%)	24 (9%)	6 (2%)	8	38
1	B	270/359 (75%)	234 (87%)	29 (11%)	7 (3%)	7	33
All	All	539/718 (75%)	473 (88%)	53 (10%)	13 (2%)	7	35

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	350	LYS
1	B	167	ARG
1	B	261	ASP
1	B	336	SER
1	A	261	ASP
1	A	347	SER
1	A	380	GLU
1	A	109	ASP
1	A	129	GLU
1	B	129	GLU
1	B	287	SER
1	B	347	SER
1	B	109	ASP

### 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	241/312 (77%)	225 (93%)	16 (7%)	21	57
1	B	242/312 (78%)	221 (91%)	21 (9%)	13	43
All	All	483/624 (77%)	446 (92%)	37 (8%)	16	50

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ILE
1	A	79	GLN
1	A	83	GLN
1	A	85	GLU
1	A	89	SER
1	A	117	VAL
1	A	140	LEU
1	A	233	VAL
1	A	247	HIS
1	A	248	ARG
1	A	256	THR
1	A	258	VAL
1	A	335	VAL
1	A	384	GLU
1	A	388	GLU
1	A	389	HIS
1	B	108	GLU
1	B	109	ASP
1	B	111	PRO
1	B	140	LEU
1	B	154	LEU
1	B	157	GLU
1	B	160	ARG
1	B	161	ILE
1	B	208	HIS
1	B	224	VAL
1	B	233	VAL
1	B	235	ASP
1	B	247	HIS
1	B	287	SER
1	B	313	ASP
1	B	336	SER
1	B	343	ARG
1	B	357	ASN
1	B	375	ASP
1	B	389	HIS
1	B	392	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	GLN
1	A	238	GLN

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Mol	Chain	Res	Type
1	A	292	GLN
1	A	342	GLN
1	A	359	GLN
1	A	381	ASN
1	A	382	GLN
1	A	389	HIS
1	A	402	HIS
1	B	74	GLN
1	B	78	GLN
1	B	162	GLN
1	B	165	GLN
1	B	292	GLN
1	B	306	GLN
1	B	320	GLN
1	B	332	HIS
1	B	342	GLN
1	B	359	GLN
1	B	368	GLN
1	B	382	GLN
1	B	402	HIS

### 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 ⓘ

There are no ligands in this entry.

## 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, 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	271/359 (75%)	-0.30	6 (2%) 65 35	17, 41, 80, 107	0
1	B	272/359 (75%)	-0.28	6 (2%) 65 35	23, 46, 83, 105	0
All	All	543/718 (75%)	-0.29	12 (2%) 65 35	17, 45, 82, 107	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	164	GLU	3.7
1	A	71	ALA	2.9
1	A	168	LYS	2.7
1	A	165	GLN	2.7
1	B	168	LYS	2.7
1	B	167	ARG	2.5
1	B	208	HIS	2.2
1	B	250	ASP	2.2
1	B	286	SER	2.2
1	A	73	ARG	2.1
1	A	164	GLU	2.1
1	A	208	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 carbohydrates 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.