



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:14 PM UTC

PDB ID : 3CQ4 / pdb_00003cq4
Title : Histidinol-phosphate aminotransferase from *Corynebacterium glutamicum*
Authors : Sandalova, T.; Marienhagen, J.; Schneider, G.
Deposited on : 2008-04-02
Resolution : 2.20 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

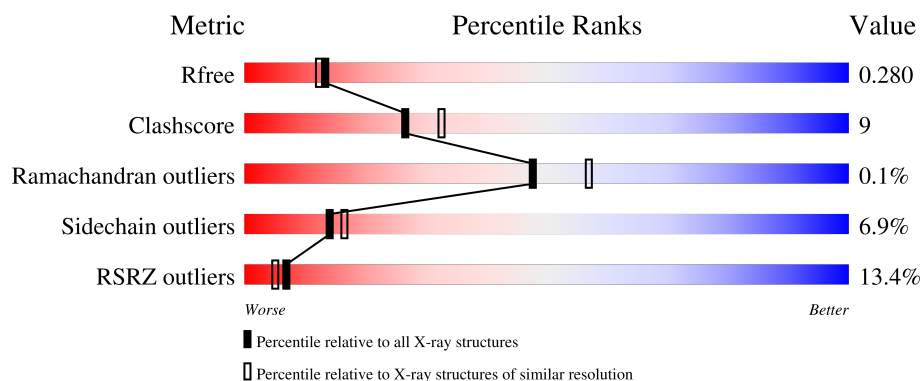
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	376	11% 79% 12% • 5%
1	B	376	14% 76% 14% • 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5636 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.

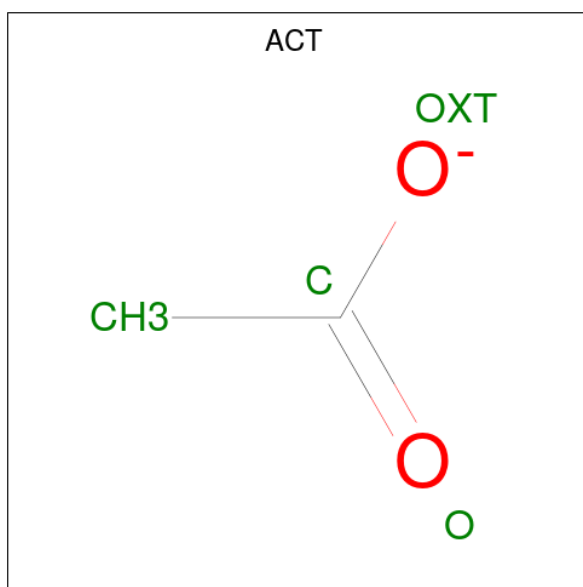
- Molecule 1 is a protein called Histidinol-phosphate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2751	1750	470	527	4			
1	B	347	Total	C	N	O	S	0	0	0
			2660	1692	453	511	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	SER	-	expression tag	UNP Q9KJU4
A	368	ALA	-	expression tag	UNP Q9KJU4
A	369	TRP	-	expression tag	UNP Q9KJU4
A	370	SER	-	expression tag	UNP Q9KJU4
A	371	HIS	-	expression tag	UNP Q9KJU4
A	372	PRO	-	expression tag	UNP Q9KJU4
A	373	GLN	-	expression tag	UNP Q9KJU4
A	374	PHE	-	expression tag	UNP Q9KJU4
A	375	GLU	-	expression tag	UNP Q9KJU4
A	376	LYS	-	expression tag	UNP Q9KJU4
B	367	SER	-	expression tag	UNP Q9KJU4
B	368	ALA	-	expression tag	UNP Q9KJU4
B	369	TRP	-	expression tag	UNP Q9KJU4
B	370	SER	-	expression tag	UNP Q9KJU4
B	371	HIS	-	expression tag	UNP Q9KJU4
B	372	PRO	-	expression tag	UNP Q9KJU4
B	373	GLN	-	expression tag	UNP Q9KJU4
B	374	PHE	-	expression tag	UNP Q9KJU4
B	375	GLU	-	expression tag	UNP Q9KJU4
B	376	LYS	-	expression tag	UNP Q9KJU4

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

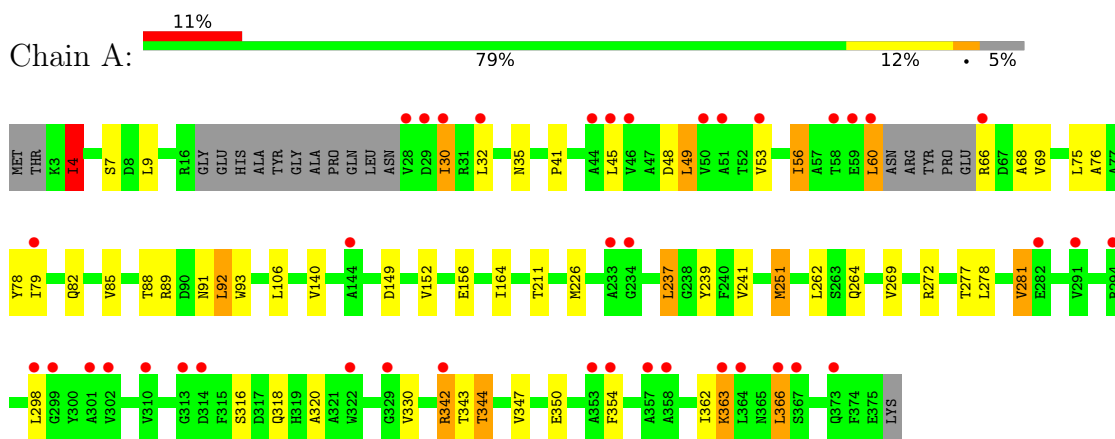
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	111	Total	O	0	0
			111	111		

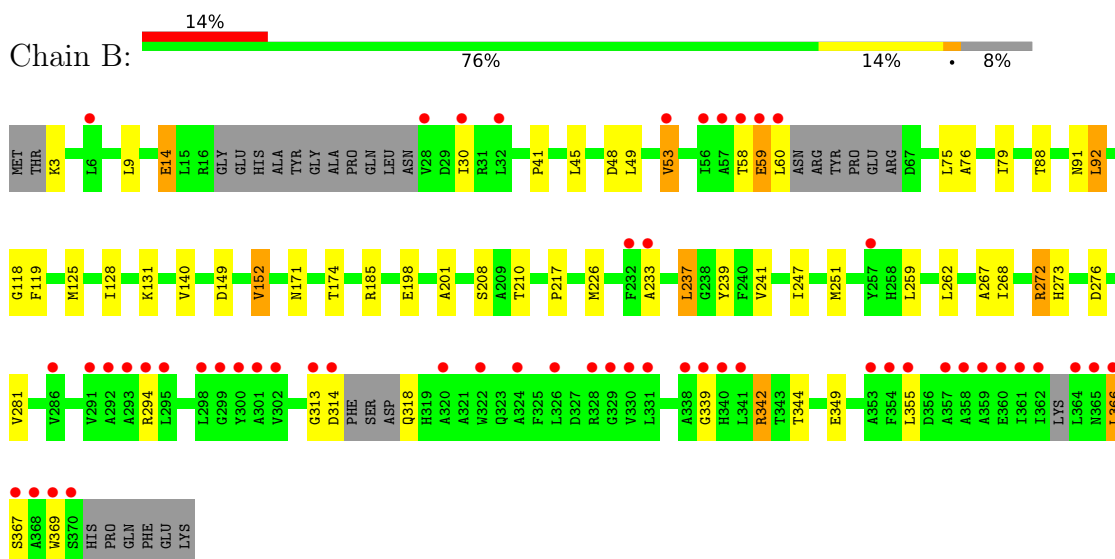
3 Residue-property plots [i](#)

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: Histidinol-phosphate aminotransferase



- Molecule 1: Histidinol-phosphate aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	102.34Å 102.34Å 140.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.20 25.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (25.00-2.20) 99.2 (25.00-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.09 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.237 , 0.277 0.240 , 0.280	Depositor DCC
R_{free} test set	2177 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	36.6	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5636	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACT

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	0.70	0/2805	0.86	1/3822 (0.0%)
1	B	0.76	0/2708	0.87	1/3689 (0.0%)
All	All	0.73	0/5513	0.87	2/7511 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	ILE	N-CA-CB	5.50	118.72	110.13
1	B	58	THR	N-CA-C	-5.48	102.90	110.35

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	2751	0	2736	53	0
1	B	2660	0	2653	49	0
2	A	4	0	3	1	0
2	B	4	0	3	0	0
3	A	106	0	0	0	0
3	B	111	0	0	0	0
All	All	5636	0	5395	100	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 9.

All (100) 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:75:LEU:HD21	1:A:226:MET:HE2	1.35	1.07
1:A:226:MET:HE3	1:A:237:LEU:HD12	1.49	0.94
1:B:75:LEU:HD21	1:B:226:MET:HE2	1.48	0.93
1:A:79:ILE:HD11	1:A:239:TYR:HE2	1.37	0.90
1:A:75:LEU:HD21	1:A:226:MET:CE	2.04	0.88
1:A:320:ALA:HB1	1:A:366:LEU:HD12	1.58	0.85
1:B:79:ILE:HD12	1:B:92:LEU:HD21	1.58	0.84
1:B:79:ILE:HD11	1:B:239:TYR:HE2	1.43	0.81
1:B:49:LEU:O	1:B:53:VAL:HG12	1.88	0.73
1:A:75:LEU:CD2	1:A:226:MET:HE2	2.16	0.72
1:A:78:TYR:CZ	1:A:82:GLN:HG3	2.24	0.72
1:A:79:ILE:HD13	1:A:241:VAL:CG2	2.21	0.71
1:B:79:ILE:HD13	1:B:241:VAL:CG2	2.20	0.70
1:B:171:ASN:ND2	1:B:174:THR:OG1	2.24	0.70
1:B:41:PRO:HB2	1:B:45:LEU:HD23	1.72	0.70
1:A:48:ASP:OD2	1:A:272:ARG:HD2	1.93	0.69
1:B:60:LEU:C	1:B:60:LEU:HD23	2.18	0.69
1:A:79:ILE:HD12	1:A:92:LEU:HD21	1.76	0.67
1:B:79:ILE:CD1	1:B:92:LEU:HD21	2.24	0.67
1:B:79:ILE:HD13	1:B:241:VAL:HG21	1.74	0.67
1:B:79:ILE:HD11	1:B:239:TYR:CE2	2.29	0.66
1:A:79:ILE:HD13	1:A:241:VAL:HG21	1.78	0.65
1:A:298:LEU:O	1:A:362:ILE:HD13	1.96	0.65
1:B:247:ILE:O	1:B:251:MET:HG3	1.96	0.65
1:B:342:ARG:HH11	1:B:342:ARG:HG2	1.63	0.63
1:A:79:ILE:HD11	1:A:239:TYR:CE2	2.26	0.63
1:B:48:ASP:OD2	1:B:273:HIS:HE1	1.82	0.62
1:A:88:THR:H	1:A:91:ASN:HD22	1.47	0.61
1:B:226:MET:HE3	1:B:237:LEU:CG	2.30	0.60
1:B:41:PRO:CB	1:B:45:LEU:HD23	2.31	0.59
1:B:294:ARG:HD3	1:B:355:LEU:HD13	1.86	0.58
1:A:41:PRO:CB	1:A:45:LEU:HD23	2.35	0.56
1:A:342:ARG:HH11	1:A:342:ARG:HG2	1.69	0.56
1:B:198:GLU:HB3	1:B:201:ALA:HB2	1.86	0.56
1:A:79:ILE:HD13	1:A:241:VAL:HG22	1.87	0.56
1:A:93:TRP:CH2	1:A:251:MET:HE3	2.41	0.56
1:A:49:LEU:HD13	1:A:269:VAL:HG11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:MET:HE3	1:A:237:LEU:CD1	2.32	0.55
1:B:226:MET:HE3	1:B:237:LEU:HG	1.88	0.55
1:B:171:ASN:HD21	1:B:174:THR:HG23	1.72	0.55
1:A:53:VAL:HG11	1:B:53:VAL:HG11	1.88	0.55
1:A:69:VAL:HG13	1:A:89:ARG:NH1	2.21	0.54
1:B:171:ASN:ND2	1:B:174:THR:H	2.06	0.53
1:A:149:ASP:O	1:A:152:VAL:HG12	2.09	0.53
1:A:49:LEU:HD13	1:A:269:VAL:CG1	2.39	0.53
1:B:226:MET:HE1	1:B:267:ALA:HB1	1.91	0.52
1:A:85:VAL:HG21	1:A:211:THR:HA	1.91	0.52
1:A:56:ILE:HD13	1:A:56:ILE:N	2.25	0.51
1:A:93:TRP:HH2	1:A:251:MET:HE3	1.75	0.51
1:B:79:ILE:HD13	1:B:241:VAL:HG22	1.93	0.50
1:A:41:PRO:HB2	1:A:45:LEU:HD23	1.94	0.50
1:B:49:LEU:HD21	1:B:233:ALA:HB2	1.93	0.49
1:A:277:THR:O	1:A:281:VAL:HG13	2.13	0.49
1:A:60:LEU:C	1:A:60:LEU:HD22	2.37	0.49
1:A:79:ILE:CD1	1:A:241:VAL:HG22	2.42	0.49
1:B:226:MET:HE3	1:B:237:LEU:HD12	1.95	0.49
1:A:30:ILE:HD11	1:A:330:VAL:HG22	1.94	0.49
1:A:75:LEU:CB	1:A:92:LEU:HD22	2.44	0.48
1:B:149:ASP:OD1	1:B:152:VAL:HG12	2.13	0.48
1:A:76:ALA:HB2	1:A:92:LEU:HD13	1.95	0.48
1:A:79:ILE:CD1	1:A:241:VAL:CG2	2.90	0.47
1:A:69:VAL:CG1	1:A:89:ARG:NH1	2.77	0.47
1:B:59:GLU:HG3	1:B:59:GLU:O	2.13	0.47
1:B:88:THR:H	1:B:91:ASN:HD22	1.61	0.47
1:B:75:LEU:HB3	1:B:92:LEU:HD22	1.97	0.46
1:A:69:VAL:HG13	1:A:89:ARG:CZ	2.46	0.46
1:A:75:LEU:HB3	1:A:92:LEU:CD2	2.46	0.46
1:B:118:GLY:HA3	1:B:125:MET:SD	2.56	0.46
1:B:14:GLU:O	1:B:131:LYS:NZ	2.47	0.45
1:A:342:ARG:NH1	1:A:344:THR:HG22	2.32	0.45
1:B:149:ASP:HB3	1:B:152:VAL:CG1	2.47	0.45
1:A:30:ILE:CD1	1:A:330:VAL:HG22	2.46	0.45
1:B:149:ASP:CG	1:B:152:VAL:HG12	2.41	0.45
1:B:268:ILE:O	1:B:272:ARG:HG2	2.17	0.45
1:B:366:LEU:HD12	1:B:367:SER:H	1.82	0.45
1:A:32:LEU:C	1:A:344:THR:HG23	2.42	0.44
1:B:60:LEU:C	1:B:60:LEU:CD2	2.88	0.44
1:B:208:SER:OG	1:B:210:THR:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:PHE:HA	1:B:140:VAL:O	2.16	0.44
1:A:69:VAL:HG13	1:A:89:ARG:HD3	2.00	0.44
1:A:347:VAL:HG22	1:A:350:GLU:OE1	2.18	0.44
1:B:149:ASP:HB3	1:B:152:VAL:HG13	2.00	0.43
1:A:35:ASN:HB2	2:A:401:ACT:H2	2.00	0.43
1:A:4:ILE:HD13	1:B:217:PRO:HB2	2.01	0.43
1:B:313:GLY:O	1:B:314:ASP:HB2	2.19	0.43
1:A:278:LEU:O	1:A:281:VAL:HG22	2.18	0.43
1:A:106:LEU:HD23	1:A:164:ILE:CD1	2.49	0.43
1:B:226:MET:HE3	1:B:237:LEU:CD1	2.49	0.43
1:B:75:LEU:CB	1:B:92:LEU:HD22	2.49	0.42
1:B:76:ALA:HB2	1:B:92:LEU:HD13	2.01	0.42
1:A:75:LEU:HB2	1:A:92:LEU:HD22	2.01	0.42
1:B:314:ASP:N	1:B:339:GLY:O	2.52	0.42
1:B:226:MET:HE3	1:B:237:LEU:CB	2.50	0.42
1:B:149:ASP:CG	1:B:152:VAL:CG1	2.93	0.42
1:B:226:MET:HE3	1:B:237:LEU:HB3	2.01	0.41
1:A:68:ALA:HA	1:A:264:GLN:NE2	2.36	0.41
1:A:88:THR:H	1:A:91:ASN:ND2	2.17	0.41
1:A:363:LYS:HE3	1:A:363:LYS:HA	2.02	0.41
1:A:140:VAL:HG22	1:A:156:GLU:HG2	2.02	0.41
1:A:343:THR:HG21	1:A:354:PHE:CZ	2.56	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	351/376 (93%)	339 (97%)	12 (3%)	0	100	100
1	B	337/376 (90%)	327 (97%)	9 (3%)	1 (0%)	36	42
All	All	688/752 (92%)	666 (97%)	21 (3%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	366	LEU

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	293/308 (95%)	274 (94%)	19 (6%)	15	18
1	B	283/308 (92%)	262 (93%)	21 (7%)	13	14
All	All	576/616 (94%)	536 (93%)	40 (7%)	14	16

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	7	SER
1	A	9	LEU
1	A	30	ILE
1	A	49	LEU
1	A	56	ILE
1	A	60	LEU
1	A	66	ARG
1	A	92	LEU
1	A	237	LEU
1	A	251	MET
1	A	262	LEU
1	A	281	VAL
1	A	316	SER
1	A	318	GLN
1	A	342	ARG
1	A	344	THR
1	A	363	LYS
1	A	366	LEU
1	B	3	LYS
1	B	9	LEU
1	B	14	GLU

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Mol	Chain	Res	Type
1	B	30	ILE
1	B	53	VAL
1	B	59	GLU
1	B	92	LEU
1	B	128	ILE
1	B	152	VAL
1	B	185	ARG
1	B	237	LEU
1	B	259	LEU
1	B	262	LEU
1	B	272	ARG
1	B	276	ASP
1	B	281	VAL
1	B	318	GLN
1	B	342	ARG
1	B	344	THR
1	B	349	GLU
1	B	369	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	ASN
1	A	99	ASN
1	A	264	GLN
1	A	273	HIS
1	A	319	HIS
1	A	371	HIS
1	B	82	GLN
1	B	91	ASN
1	B	99	ASN
1	B	103	GLN
1	B	171	ASN
1	B	188	ASN
1	B	264	GLN
1	B	273	HIS

5.3.3 RNA ⓘ

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](#)

2 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	ACT	A	401	-	3,3,3	0.70	0	3,3,3	1.26	0
2	ACT	B	401	-	3,3,3	0.73	0	3,3,3	1.22	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	ACT	1	0

5.7 Other polymers [i](#)

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, 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	357/376 (94%)	0.60	40 (11%) 10 8	22, 35, 66, 75	0
1	B	347/376 (92%)	0.79	54 (15%) 5 4	21, 34, 67, 76	0
All	All	704/752 (93%)	0.69	94 (13%) 7 5	21, 35, 66, 76	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	ALA	5.5
1	A	60	LEU	5.4
1	B	364	LEU	5.1
1	B	358	ALA	5.0
1	A	58	THR	4.9
1	B	329	GLY	4.8
1	B	361	ILE	4.7
1	B	359	ALA	4.6
1	A	313	GLY	4.3
1	B	357	ALA	4.3
1	B	362	ILE	4.3
1	B	339	GLY	4.0
1	B	58	THR	4.0
1	A	28	VAL	3.9
1	B	331	LEU	3.9
1	A	294	ARG	3.9
1	B	60	LEU	3.8
1	B	30	ILE	3.8
1	B	365	ASN	3.8
1	B	301	ALA	3.7
1	B	300	TYR	3.7
1	B	326	LEU	3.6
1	B	340	HIS	3.6
1	B	299	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	366	LEU	3.6
1	B	28	VAL	3.5
1	B	313	GLY	3.5
1	B	293	ALA	3.5
1	B	330	VAL	3.4
1	B	292	ALA	3.3
1	B	314	ASP	3.3
1	A	366	LEU	3.3
1	B	368	ALA	3.3
1	B	354	PHE	3.3
1	B	341	LEU	3.3
1	B	369	TRP	3.2
1	B	355	LEU	3.2
1	B	294	ARG	3.1
1	B	6	LEU	3.1
1	B	298	LEU	3.1
1	B	320	ALA	3.0
1	B	57	ALA	2.8
1	B	324	ALA	2.8
1	B	59	GLU	2.8
1	A	357	ALA	2.8
1	A	50	VAL	2.8
1	B	295	LEU	2.8
1	A	353	ALA	2.8
1	B	32	LEU	2.7
1	A	51	ALA	2.7
1	A	364	LEU	2.7
1	A	44	ALA	2.7
1	B	370	SER	2.6
1	A	299	GLY	2.5
1	A	32	LEU	2.5
1	A	354	PHE	2.5
1	A	53	VAL	2.5
1	B	328	ARG	2.5
1	A	367	SER	2.4
1	A	46	VAL	2.4
1	A	291	VAL	2.4
1	A	310	VAL	2.4
1	B	322	TRP	2.4
1	B	302	VAL	2.4
1	A	314	ASP	2.4
1	A	282	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	360	GLU	2.4
1	A	322	TRP	2.4
1	A	358	ALA	2.3
1	A	66	ARG	2.3
1	A	373	GLN	2.3
1	A	29	ASP	2.3
1	A	144	ALA	2.3
1	A	233	ALA	2.3
1	A	329	GLY	2.3
1	B	56	ILE	2.3
1	B	233	ALA	2.3
1	B	232	PHE	2.2
1	A	45	LEU	2.2
1	A	301	ALA	2.2
1	B	338	ALA	2.2
1	A	298	LEU	2.2
1	B	286	VAL	2.2
1	A	234	GLY	2.2
1	A	342	ARG	2.1
1	B	257	TYR	2.1
1	A	302	VAL	2.1
1	B	53	VAL	2.1
1	B	367	SER	2.1
1	A	79	ILE	2.1
1	A	363	LYS	2.0
1	A	59	GLU	2.0
1	A	30	ILE	2.0
1	B	291	VAL	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, 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(Å ²)	Q<0.9
2	ACT	A	401	4/4	0.79	0.17	48,49,49,50	0
2	ACT	B	401	4/4	0.89	0.15	62,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.