



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:54 AM GMT

PDB ID : 3CMS  
Title : ENGINEERING ENZYME SUB-SITE SPECIFICITY: PREPARATION, KINETIC CHARACTERIZATION AND X-RAY ANALYSIS AT 2.0-ANGSTROMS RESOLUTION OF VAL111PHE SITE-MUTATED CALF CHYMOSIN  
Authors : Newman, M.; Frazao, C.; Shearer, A.; Tickle, I.J.; Blundell, T.L.  
Deposited on : 1990-02-26  
Resolution : 2.00 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

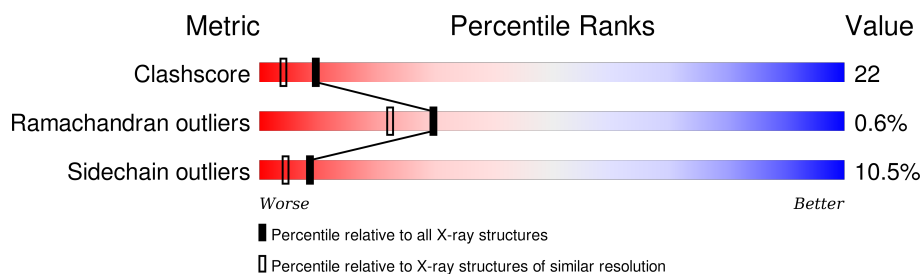
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	323	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2692 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 CHYMOSIN B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	8	0
			2547	1624	405	504	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	111	PHE	VAL	CONFLICT	UNP P00794

- Molecule 2 is water.

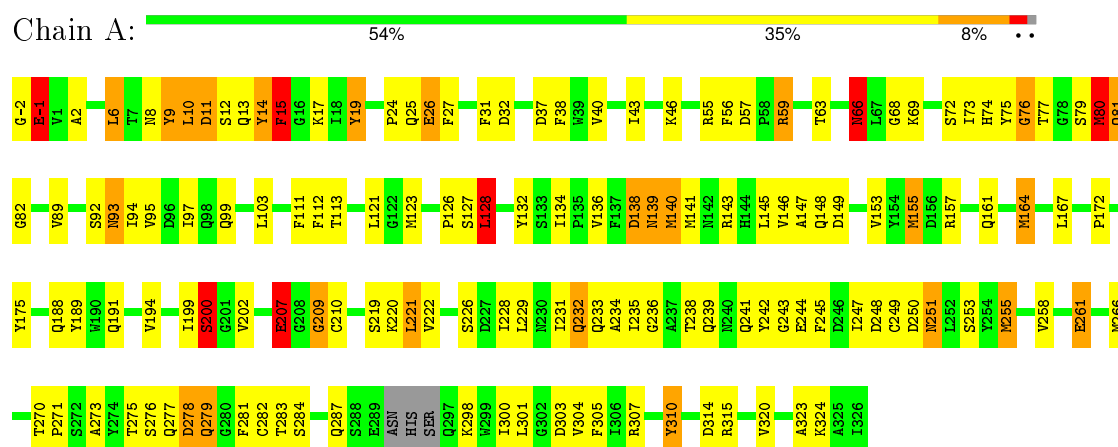
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	145	Total	O	0	0
			145	145		

### 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.

Note EDS was not executed.

#### • Molecule 1: CHYMOSIN B



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.21Å 114.56Å 72.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	RESTRAIN	Depositor
R, $R_{free}$	0.195 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2692	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	0.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	1.27	18/2611 (0.7%)	1.65	54/3555 (1.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	PHE	C-N	10.55	1.58	1.34
1	A	258	VAL	C-N	10.32	1.57	1.34
1	A	15	PHE	C-N	10.28	1.51	1.33
1	A	273	ALA	C-N	9.92	1.56	1.34
1	A	202	VAL	C-N	-9.24	1.12	1.34
1	A	66	ASN	C-N	-8.82	1.13	1.34
1	A	6	LEU	C-N	-8.15	1.15	1.34
1	A	11	ASP	C-N	7.56	1.51	1.34
1	A	12	SER	N-CA	6.87	1.60	1.46
1	A	243	GLY	C-N	-6.18	1.19	1.34
1	A	210	CYS	C-N	-5.95	1.20	1.34
1	A	255	MET	C-N	5.86	1.45	1.34
1	A	251	ASN	C-N	-5.47	1.21	1.34
1	A	236	GLY	C-N	5.38	1.46	1.34
1	A	164	MET	C-N	5.31	1.46	1.34
1	A	113	THR	C-N	5.29	1.46	1.34
1	A	233	GLN	CD-OE1	5.25	1.35	1.24
1	A	148	GLN	CD-OE1	5.17	1.35	1.24

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ARG	NE-CZ-NH1	15.73	128.17	120.30
1	A	149	ASP	CB-CG-OD1	12.16	129.25	118.30
1	A	123	MET	CG-SD-CE	11.35	118.36	100.20
1	A	32	ASP	CB-CG-OD2	10.72	127.95	118.30
1	A	315	ARG	NE-CZ-NH2	-9.71	115.45	120.30
1	A	121	LEU	C-N-CA	9.34	141.90	122.30
1	A	103	LEU	CB-CG-CD2	8.39	125.26	111.00
1	A	26	GLU	OE1-CD-OE2	8.03	132.93	123.30
1	A	11	ASP	O-C-N	-7.72	110.35	122.70
1	A	189	TYR	CB-CG-CD1	-7.69	116.39	121.00
1	A	189	TYR	CG-CD1-CE1	-7.52	115.28	121.30
1	A	307	ARG	NE-CZ-NH2	7.52	124.06	120.30
1	A	55	ARG	NE-CZ-NH2	7.43	124.02	120.30
1	A	157	ARG	NE-CZ-NH2	7.34	123.97	120.30
1	A	314	ASP	CB-CG-OD1	7.32	124.89	118.30
1	A	59	ARG	NE-CZ-NH2	7.27	123.93	120.30
1	A	143	ARG	NE-CZ-NH2	7.23	123.92	120.30
1	A	26	GLU	O-C-N	7.20	134.22	122.70
1	A	9	TYR	O-C-N	7.19	134.20	122.70
1	A	304	VAL	CA-CB-CG2	7.17	121.65	110.90
1	A	40	VAL	CA-CB-CG2	7.01	121.42	110.90
1	A	320	VAL	O-C-N	-6.54	112.08	123.20
1	A	95	VAL	C-N-CA	6.46	137.85	121.70
1	A	310	TYR	O-C-N	-6.42	112.42	122.70
1	A	232	GLN	O-C-N	-6.42	112.42	122.70
1	A	200	SER	CB-CA-C	-6.34	98.06	110.10
1	A	207	GLU	O-C-N	-6.27	112.53	123.20
1	A	26	GLU	CB-CG-CD	-6.20	97.46	114.20
1	A	37	ASP	CB-CG-OD1	6.15	123.84	118.30
1	A	255	MET	CG-SD-CE	6.15	110.03	100.20
1	A	305	PHE	C-N-CA	-6.13	106.36	121.70
1	A	258	VAL	C-N-CA	-6.13	106.39	121.70
1	A	19	TYR	CB-CG-CD1	-6.12	117.33	121.00
1	A	140	MET	CG-SD-CE	6.11	109.98	100.20
1	A	141	MET	CG-SD-CE	6.09	109.95	100.20
1	A	164	MET	CG-SD-CE	6.09	109.95	100.20
1	A	207	GLU	C-N-CA	-6.09	109.50	122.30
1	A	266	MET	CG-SD-CE	6.08	109.92	100.20
1	A	155	MET	CG-SD-CE	6.05	109.88	100.20
1	A	80	MET	CG-SD-CE	6.00	109.80	100.20
1	A	236	GLY	C-N-CA	-5.84	107.10	121.70
1	A	236	GLY	O-C-N	5.70	131.82	122.70
1	A	31	PHE	C-N-CA	5.66	135.85	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	VAL	CA-CB-CG2	5.65	119.38	110.90
1	A	89	VAL	O-C-N	5.63	131.71	122.70
1	A	38	PHE	O-C-N	-5.52	113.86	122.70
1	A	273	ALA	C-N-CA	-5.45	108.07	121.70
1	A	9	TYR	CA-C-N	-5.45	105.22	117.20
1	A	-1	GLU	O-C-N	5.36	131.27	122.70
1	A	303	ASP	O-C-N	-5.27	114.27	122.70
1	A	12	SER	CB-CA-C	-5.25	100.12	110.10
1	A	11	ASP	CA-C-N	5.17	128.57	117.20
1	A	9	TYR	CB-CG-CD1	-5.01	118.00	121.00
1	A	209	GLY	CA-C-O	5.00	129.61	120.60

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	LEU	Mainchain
1	A	261	GLU	Mainchain
1	A	278	ASP	Mainchain
1	A	310	TYR	Mainchain
1	A	323	ALA	Mainchain
1	A	80	MET	Mainchain

## 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	2547	0	2404	111	0
2	A	145	0	0	5	0
All	All	2692	0	2404	111	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 (111) 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:6:LEU:HD13	1:A:14:TYR:CE2	2.01	0.96
1:A:247:ILE:HG23	1:A:255:MET:HE2	1.52	0.91
1:A:270:THR:HB	1:A:271:PRO:HD2	1.53	0.90
1:A:6:LEU:HD13	1:A:14:TYR:CZ	2.11	0.85
1:A:247:ILE:HG23	1:A:255:MET:CE	2.06	0.85
1:A:73[B]:ILE:HG21	1:A:75[B]:TYR:CZ	2.11	0.84
1:A:9:TYR:HB2	1:A:15:PHE:HZ	1.45	0.79
1:A:2:ALA:HB2	1:A:94:ILE:HG13	1.69	0.74
1:A:19:TYR:CE1	1:A:26:GLU:HB2	2.22	0.74
1:A:25:GLN:HE22	1:A:57:ASP:H	1.35	0.74
1:A:128:LEU:HD13	1:A:188:GLN:CG	2.20	0.72
1:A:239:GLN:HA	1:A:244:GLU:O	1.89	0.72
1:A:77[B]:THR:HG22	1:A:111:PHE:CD1	2.25	0.71
1:A:77[B]:THR:HG21	1:A:111:PHE:CE1	2.24	0.71
1:A:140:MET:HA	1:A:145:LEU:HD12	1.75	0.69
1:A:9:TYR:HB2	1:A:15:PHE:CZ	2.25	0.68
1:A:161:GLN:HG2	1:A:161:GLN:O	1.92	0.67
1:A:172:PRO:HA	1:A:175:TYR:CE2	2.29	0.66
1:A:278:ASP:O	1:A:279:GLN:C	2.32	0.65
1:A:73[B]:ILE:HD13	2:A:1104:HOH:O	1.96	0.65
1:A:128:LEU:CD1	1:A:188:GLN:HG2	2.26	0.65
1:A:220:LYS:HD3	1:A:287:GLN:HB2	1.78	0.64
1:A:80:MET:HE2	1:A:81:GLN:C	2.18	0.64
1:A:2:ALA:HB1	1:A:92:SER:HB3	1.79	0.64
1:A:270:THR:HB	1:A:271:PRO:CD	2.27	0.64
1:A:250:ASP:OD1	1:A:250:ASP:O	2.16	0.64
1:A:128:LEU:HD13	1:A:188:GLN:HG2	1.80	0.64
1:A:19:TYR:CD1	1:A:26:GLU:HB2	2.33	0.63
1:A:6:LEU:CD1	1:A:14:TYR:CZ	2.80	0.63
1:A:73[B]:ILE:CG2	1:A:75[B]:TYR:CZ	2.83	0.62
1:A:249:CYS:SG	1:A:282:CYS:N	2.72	0.62
1:A:75[B]:TYR:O	1:A:76[B]:GLY:C	2.38	0.62
1:A:73[A]:ILE:HD13	2:A:1104:HOH:O	2.00	0.61
1:A:231:ILE:O	1:A:235:ILE:HG12	2.01	0.60
1:A:244:GLU:HG2	1:A:245:PHE:N	2.16	0.60
1:A:247:ILE:CG2	1:A:255:MET:CE	2.78	0.60
1:A:77[B]:THR:CG2	1:A:111:PHE:CD1	2.84	0.60
1:A:6:LEU:CD1	1:A:14:TYR:CE2	2.83	0.59
1:A:128:LEU:HD13	1:A:188:GLN:HG3	1.85	0.59
1:A:2:ALA:HB3	1:A:167:LEU:HD12	1.86	0.58
1:A:14:TYR:OH	1:A:153:VAL:HG13	2.02	0.58
1:A:57:ASP:OD1	1:A:59:ARG:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:-1:GLU:O	1:A:147:ALA:N	2.33	0.57
1:A:277:GLN:HB2	1:A:282:CYS:SG	2.45	0.57
1:A:74[A]:HIS:HD2	1:A:79[A]:SER:OG	1.87	0.57
1:A:247:ILE:HG23	1:A:255:MET:HE1	1.87	0.56
1:A:244:GLU:CG	1:A:245:PHE:N	2.69	0.56
1:A:80:MET:HE2	1:A:81:GLN:O	2.05	0.56
1:A:14:TYR:CD2	1:A:155:MET:HG2	2.42	0.55
1:A:75[B]:TYR:O	1:A:77[B]:THR:N	2.39	0.55
1:A:244:GLU:CG	1:A:245:PHE:H	2.20	0.54
1:A:278:ASP:O	1:A:279:GLN:O	2.26	0.54
1:A:43:ILE:HG23	1:A:56:PHE:O	2.08	0.54
1:A:126:PRO:HG3	1:A:138:ASP:OD2	2.07	0.54
1:A:283:THR:HG22	1:A:284:SER:N	2.22	0.54
1:A:221:LEU:HD21	1:A:301:LEU:HD23	1.90	0.53
1:A:199:ILE:O	1:A:200:SER:HB2	2.07	0.52
1:A:247:ILE:O	1:A:282:CYS:HB2	2.10	0.52
1:A:93:ASN:ND2	1:A:94:ILE:HG13	2.25	0.52
1:A:199:ILE:HD12	1:A:234:ALA:HB1	1.92	0.51
1:A:112:PHE:HD2	2:A:1121:HOH:O	1.91	0.51
1:A:228:ILE:O	1:A:232:GLN:HG2	2.09	0.51
1:A:235:ILE:O	1:A:255:MET:HG2	2.10	0.51
1:A:69:LYS:HD2	1:A:132:TYR:CE2	2.46	0.51
1:A:93:ASN:HD22	1:A:94:ILE:N	2.08	0.51
1:A:238:THR:O	1:A:245:PHE:HA	2.11	0.50
1:A:77[B]:THR:CG2	1:A:111:PHE:CE1	2.94	0.50
1:A:222:VAL:HB	1:A:300:ILE:HB	1.93	0.50
1:A:247:ILE:CG2	1:A:255:MET:HE2	2.33	0.50
1:A:238:THR:HG22	1:A:239:GLN:N	2.27	0.49
1:A:80:MET:CE	1:A:81:GLN:C	2.80	0.49
1:A:194:VAL:O	1:A:209:GLY:HA2	2.11	0.49
1:A:80:MET:HE1	1:A:82:GLY:N	2.28	0.48
1:A:10:LEU:O	1:A:11:ASP:HB2	2.13	0.48
1:A:19:TYR:HB3	1:A:24:PRO:HB2	1.94	0.48
1:A:14:TYR:CZ	1:A:153:VAL:HG13	2.48	0.48
1:A:19:TYR:HE1	1:A:26:GLU:HB2	1.75	0.47
1:A:80:MET:SD	1:A:80:MET:C	2.93	0.47
1:A:271:PRO:O	1:A:275:THR:HB	2.15	0.47
1:A:13:GLN:HB2	1:A:15:PHE:CE2	2.50	0.47
1:A:191:GLN:HE22	1:A:298:LYS:CE	2.28	0.47
1:A:199:ILE:O	1:A:200:SER:CB	2.59	0.47
1:A:251:ASN:HB3	1:A:255:MET:HE1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ILE:CG2	1:A:255:MET:HE1	2.44	0.46
1:A:191:GLN:NE2	1:A:298:LYS:CE	2.78	0.46
1:A:-1:GLU:O	1:A:146:VAL:HA	2.16	0.46
1:A:93:ASN:HD22	1:A:94:ILE:HG13	1.81	0.46
1:A:19:TYR:CE1	1:A:26:GLU:HG3	2.51	0.45
1:A:66:ASN:ND2	1:A:68:GLY:H	2.15	0.45
1:A:-2:GLY:C	1:A:-1:GLU:HG2	2.37	0.45
1:A:26:GLU:HG2	1:A:27:PHE:N	2.32	0.44
1:A:221:LEU:HD21	1:A:301:LEU:CD2	2.47	0.44
1:A:283:THR:CG2	1:A:284:SER:N	2.81	0.44
1:A:207:GLU:H	1:A:207:GLU:HG3	1.18	0.44
1:A:14:TYR:CD1	1:A:14:TYR:O	2.71	0.44
1:A:99:GLN:NE2	1:A:136:VAL:HA	2.33	0.43
1:A:-1:GLU:HB2	1:A:145:LEU:O	2.18	0.43
1:A:261:GLU:HB2	2:A:1089:HOH:O	2.18	0.43
1:A:161:GLN:CG	1:A:161:GLN:O	2.65	0.43
1:A:9:TYR:CB	1:A:15:PHE:CZ	2.99	0.43
1:A:128:LEU:CD1	1:A:188:GLN:CG	2.88	0.43
1:A:74[A]:HIS:CD2	1:A:79[A]:SER:OG	2.70	0.42
1:A:324:LYS:HE2	2:A:1108:HOH:O	2.20	0.42
1:A:229:LEU:HA	1:A:229:LEU:HD12	1.63	0.42
1:A:127:SER:OG	1:A:188:GLN:HA	2.19	0.42
1:A:43:ILE:HG21	1:A:43:ILE:HD13	1.73	0.42
1:A:238:THR:CG2	1:A:239:GLN:N	2.83	0.41
1:A:80:MET:CE	1:A:82:GLY:HA3	2.50	0.41
1:A:134:ILE:HG21	1:A:139:ASN:ND2	2.35	0.41
1:A:73[B]:ILE:HG21	1:A:75[B]:TYR:OH	2.19	0.40
1:A:80:MET:CE	1:A:82:GLY:N	2.84	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	324/323 (100%)	308 (95%)	13 (4%)	3 (1%)	21 13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	76[A]	GLY
1	A	76[B]	GLY
1	A	279	GLN

### 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	283/280 (101%)	253 (89%)	30 (11%)	8 4

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	GLU
1	A	8	ASN
1	A	10	LEU
1	A	14	TYR
1	A	15	PHE
1	A	17	LYS
1	A	46	LYS
1	A	63	THR
1	A	66	ASN
1	A	72[A]	SER
1	A	72[B]	SER
1	A	80	MET
1	A	81	GLN
1	A	93	ASN
1	A	97	ILE
1	A	128	LEU
1	A	138	ASP
1	A	139	ASN

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Mol	Chain	Res	Type
1	A	164	MET
1	A	200	SER
1	A	207	GLU
1	A	219	SER
1	A	221	LEU
1	A	226	SER
1	A	241	GLN
1	A	242	TYR
1	A	248	ASP
1	A	253	SER
1	A	276	SER
1	A	281	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	52	ASN
1	A	54	GLN
1	A	66	ASN
1	A	93	ASN
1	A	99	GLN
1	A	139	ASN
1	A	142	ASN
1	A	180	HIS
1	A	191	GLN
1	A	230	ASN
1	A	297	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 [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](#)

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.