



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:30 PM GMT

PDB ID : 4CBM  
Title : Pestivirus NS3 helicase  
Authors : Tortorici, M.A.; Duquerroy, S.; Kwok, J.; Vonnrhein, C.; Perez, J.; Lamp, B.;  
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Deposited on : 2013-10-14  
Resolution : 3.27 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

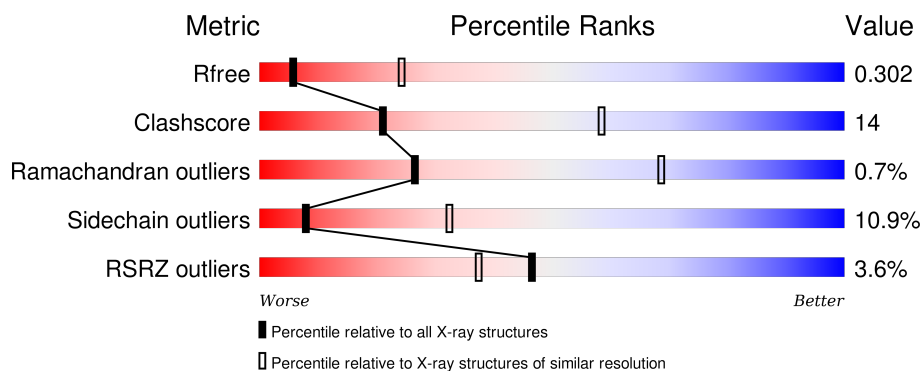
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.27 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	1756 (3.36-3.20)
Clashscore	102246	1941 (3.36-3.20)
Ramachandran outliers	100387	1905 (3.36-3.20)
Sidechain outliers	100360	1903 (3.36-3.20)
RSRZ outliers	91569	1764 (3.36-3.20)

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 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	516	 2% 61% 26% • 9%
1	B	516	 3% 58% 27% • 11%
1	C	516	 3% 61% 24% • 11%
1	D	516	 5% 60% 24% • 12%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 14616 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 SERINE PROTEASE NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3704	2349	632	702	21			
1	B	458	Total	C	N	O	S	0	0	0
			3641	2310	622	688	21			
1	C	461	Total	C	N	O	S	0	0	0
			3672	2331	624	695	22			
1	D	453	Total	C	N	O	S	0	0	0
			3598	2282	611	683	22			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	176	MET	-	EXPRESSION TAG	UNP P19712
A	177	ALA	-	EXPRESSION TAG	UNP P19712
A	178	SER	-	EXPRESSION TAG	UNP P19712
A	179	HIS	-	EXPRESSION TAG	UNP P19712
A	180	HIS	-	EXPRESSION TAG	UNP P19712
A	181	HIS	-	EXPRESSION TAG	UNP P19712
A	182	HIS	-	EXPRESSION TAG	UNP P19712
A	183	HIS	-	EXPRESSION TAG	UNP P19712
A	184	HIS	-	EXPRESSION TAG	UNP P19712
A	185	HIS	-	EXPRESSION TAG	UNP P19712
A	186	GLU	-	EXPRESSION TAG	UNP P19712
A	187	ASN	-	EXPRESSION TAG	UNP P19712
A	188	LEU	-	EXPRESSION TAG	UNP P19712
A	189	TYR	-	EXPRESSION TAG	UNP P19712
A	190	PHE	-	EXPRESSION TAG	UNP P19712
A	191	GLN	-	EXPRESSION TAG	UNP P19712
A	192	GLY	-	EXPRESSION TAG	UNP P19712
A	600	LYS	GLN	ENGINEERED MUTATION	UNP P19712
B	176	MET	-	EXPRESSION TAG	UNP P19712
B	177	ALA	-	EXPRESSION TAG	UNP P19712
B	178	SER	-	EXPRESSION TAG	UNP P19712

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Chain	Residue	Modelled	Actual	Comment	Reference
B	179	HIS	-	EXPRESSION TAG	UNP P19712
B	180	HIS	-	EXPRESSION TAG	UNP P19712
B	181	HIS	-	EXPRESSION TAG	UNP P19712
B	182	HIS	-	EXPRESSION TAG	UNP P19712
B	183	HIS	-	EXPRESSION TAG	UNP P19712
B	184	HIS	-	EXPRESSION TAG	UNP P19712
B	185	HIS	-	EXPRESSION TAG	UNP P19712
B	186	GLU	-	EXPRESSION TAG	UNP P19712
B	187	ASN	-	EXPRESSION TAG	UNP P19712
B	188	LEU	-	EXPRESSION TAG	UNP P19712
B	189	TYR	-	EXPRESSION TAG	UNP P19712
B	190	PHE	-	EXPRESSION TAG	UNP P19712
B	191	GLN	-	EXPRESSION TAG	UNP P19712
B	192	GLY	-	EXPRESSION TAG	UNP P19712
B	600	LYS	GLN	ENGINEERED MUTATION	UNP P19712
C	176	MET	-	EXPRESSION TAG	UNP P19712
C	177	ALA	-	EXPRESSION TAG	UNP P19712
C	178	SER	-	EXPRESSION TAG	UNP P19712
C	179	HIS	-	EXPRESSION TAG	UNP P19712
C	180	HIS	-	EXPRESSION TAG	UNP P19712
C	181	HIS	-	EXPRESSION TAG	UNP P19712
C	182	HIS	-	EXPRESSION TAG	UNP P19712
C	183	HIS	-	EXPRESSION TAG	UNP P19712
C	184	HIS	-	EXPRESSION TAG	UNP P19712
C	185	HIS	-	EXPRESSION TAG	UNP P19712
C	186	GLU	-	EXPRESSION TAG	UNP P19712
C	187	ASN	-	EXPRESSION TAG	UNP P19712
C	188	LEU	-	EXPRESSION TAG	UNP P19712
C	189	TYR	-	EXPRESSION TAG	UNP P19712
C	190	PHE	-	EXPRESSION TAG	UNP P19712
C	191	GLN	-	EXPRESSION TAG	UNP P19712
C	192	GLY	-	EXPRESSION TAG	UNP P19712
C	600	LYS	GLN	ENGINEERED MUTATION	UNP P19712
D	176	MET	-	EXPRESSION TAG	UNP P19712
D	177	ALA	-	EXPRESSION TAG	UNP P19712
D	178	SER	-	EXPRESSION TAG	UNP P19712
D	179	HIS	-	EXPRESSION TAG	UNP P19712
D	180	HIS	-	EXPRESSION TAG	UNP P19712
D	181	HIS	-	EXPRESSION TAG	UNP P19712
D	182	HIS	-	EXPRESSION TAG	UNP P19712
D	183	HIS	-	EXPRESSION TAG	UNP P19712
D	184	HIS	-	EXPRESSION TAG	UNP P19712

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Chain	Residue	Modelled	Actual	Comment	Reference
D	185	HIS	-	EXPRESSION TAG	UNP P19712
D	186	GLU	-	EXPRESSION TAG	UNP P19712
D	187	ASN	-	EXPRESSION TAG	UNP P19712
D	188	LEU	-	EXPRESSION TAG	UNP P19712
D	189	TYR	-	EXPRESSION TAG	UNP P19712
D	190	PHE	-	EXPRESSION TAG	UNP P19712
D	191	GLN	-	EXPRESSION TAG	UNP P19712
D	192	GLY	-	EXPRESSION TAG	UNP P19712
D	600	LYS	GLN	ENGINEERED MUTATION	UNP P19712

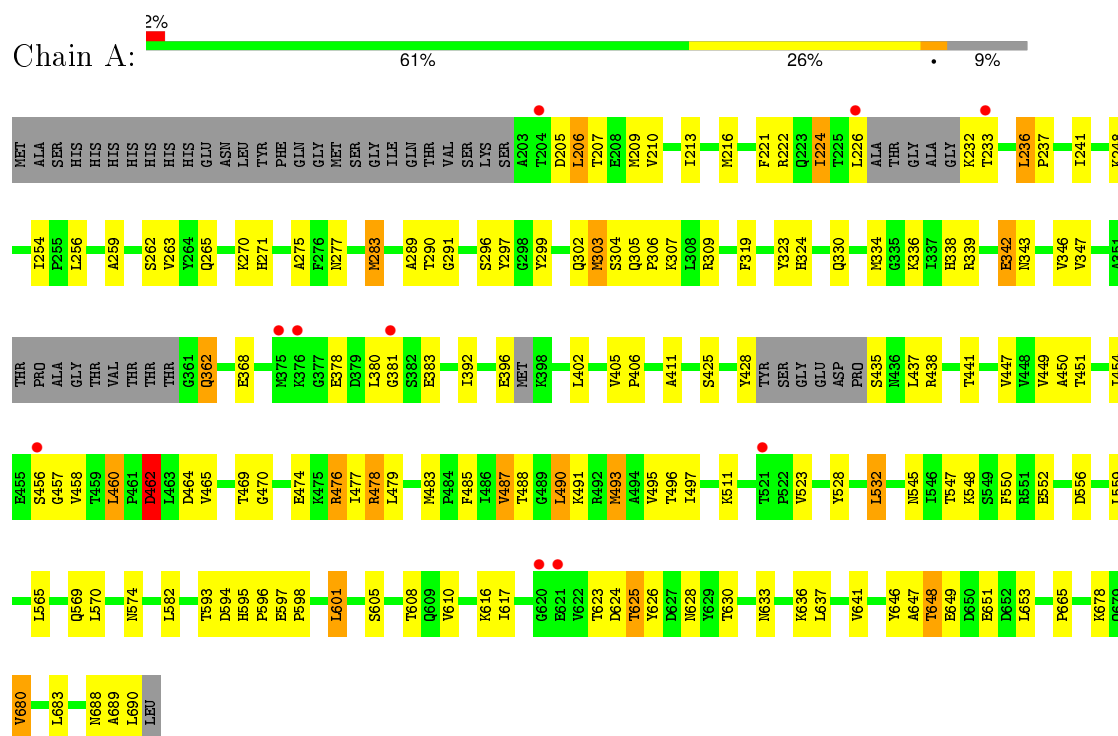
- Molecule 2 is water.

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

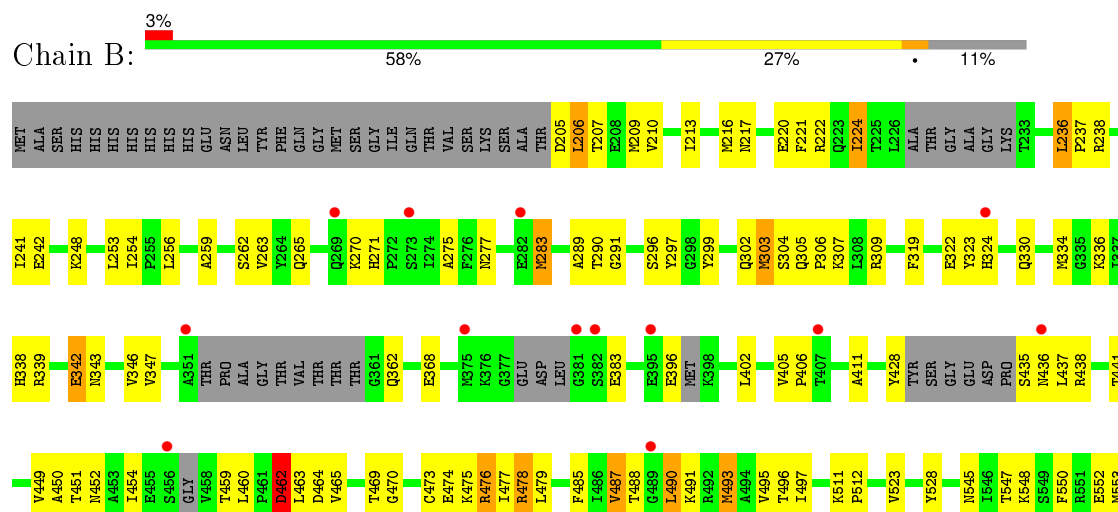
### 3 Residue-property plots

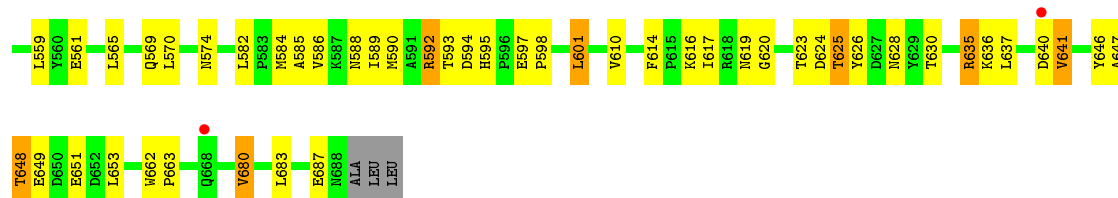
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: SERINE PROTEASE NS3

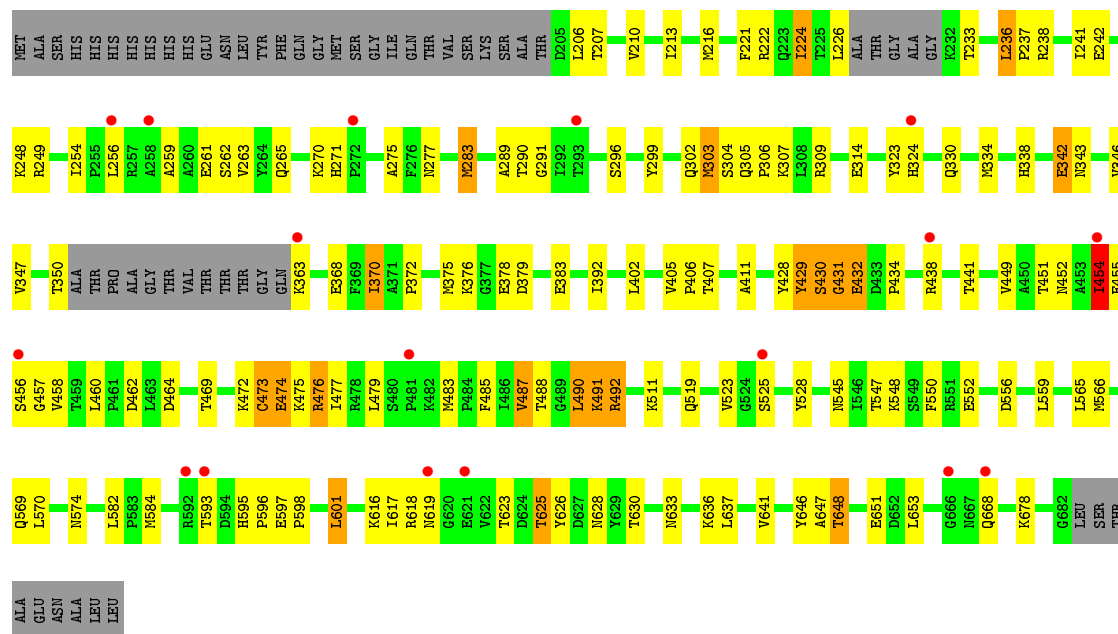


#### • Molecule 1: SERINE PROTEASE NS3

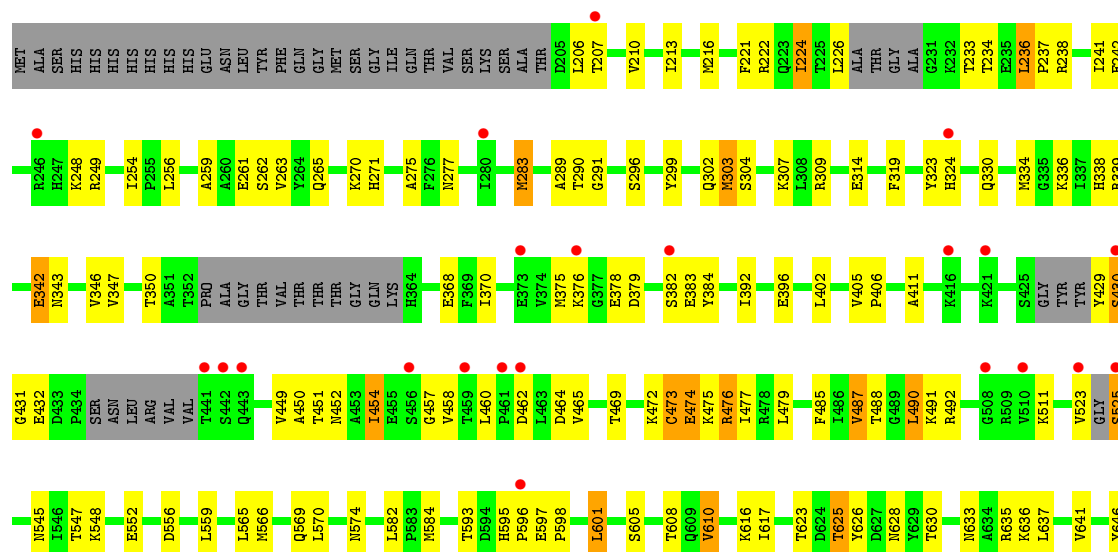


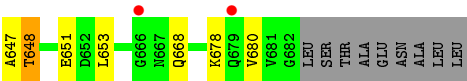


• Molecule 1: SERINE PROTEASE NS3



• Molecule 1: SERINE PROTEASE NS3





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.10 Å   159.59 Å   99.23 Å 90.00°   97.24°   90.00°	Depositor
Resolution (Å)	20.00 – 3.27 19.98 – 3.27	Depositor EDS
% Data completeness (in resolution range)	94.0 (20.00-3.27) 94.0 (19.98-3.27)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 3.29 Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, $R_{free}$	0.233   ,   0.283 0.254   ,   0.302	Depositor DCC
$R_{free}$ test set	1585 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.2	Xtriage
Anisotropy	1.199	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 59.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	2 of 31359 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	14616	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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

### 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	0.51	0/3771	0.71	3/5098 (0.1%)
1	B	0.53	0/3706	0.71	4/5007 (0.1%)
1	C	0.53	0/3743	0.73	3/5062 (0.1%)
1	D	0.49	0/3664	0.68	1/4951 (0.0%)
All	All	0.52	0/14884	0.71	11/20118 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	ILE	N-CA-C	-8.15	89.00	111.00
1	B	497	ILE	N-CA-C	-8.03	89.33	111.00
1	C	454	ILE	C-N-CA	8.03	141.76	121.70
1	C	431	GLY	C-N-CA	7.21	139.74	121.70
1	A	462	ASP	CA-CB-CG	6.46	127.62	113.40
1	B	561	GLU	CB-CG-CD	-6.27	97.26	114.20
1	B	462	ASP	CA-CB-CG	6.22	127.08	113.40
1	B	322	GLU	CB-CA-C	-6.12	98.16	110.40
1	A	457	GLY	C-N-CA	6.01	136.73	121.70
1	D	457	GLY	C-N-CA	5.63	135.78	121.70
1	C	457	GLY	C-N-CA	5.10	134.45	121.70

There are no chirality outliers.

There are no planarity outliers.

### 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	3704	0	3724	119	0
1	B	3641	0	3657	120	0
1	C	3672	0	3685	102	0
1	D	3598	0	3602	98	0
2	A	1	0	0	2	0
All	All	14616	0	14668	419	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 14.

All (419) 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:450:ALA:CB	1:A:454:ILE:HG21	1.46	1.44
1:A:450:ALA:HB1	1:A:454:ILE:CG2	1.47	1.43
1:B:450:ALA:CB	1:B:454:ILE:HG21	1.48	1.42
1:B:450:ALA:HB1	1:B:454:ILE:CG2	1.49	1.41
1:C:324:HIS:HD2	1:C:350:THR:OG1	1.10	1.33
1:C:324:HIS:CD2	1:C:350:THR:OG1	1.88	1.24
1:D:324:HIS:HD2	1:D:350:THR:OG1	1.11	1.23
1:D:324:HIS:CD2	1:D:350:THR:OG1	1.90	1.23
1:A:323:TYR:CE1	1:A:324:HIS:CE1	2.28	1.22
1:A:323:TYR:CZ	1:A:324:HIS:CE1	2.36	1.14
1:B:428:TYR:CD1	1:B:454:ILE:HG22	1.98	0.99
1:A:428:TYR:CD1	1:A:454:ILE:HG22	1.98	0.98
1:A:428:TYR:HD1	1:A:454:ILE:HG22	1.25	0.96
1:B:428:TYR:HD1	1:B:454:ILE:HG22	1.26	0.94
1:D:323:TYR:CE1	1:D:324:HIS:CE1	2.55	0.93
1:C:323:TYR:CE1	1:C:324:HIS:CE1	2.57	0.93
1:B:641:VAL:HG22	1:B:663:PRO:HD3	1.48	0.93
1:D:450:ALA:HB1	1:D:454:ILE:HG13	1.48	0.92
1:B:323:TYR:HA	1:B:330:GLN:NE2	1.83	0.92
1:B:428:TYR:HB2	1:B:437:LEU:HD11	1.54	0.89
1:B:402:LEU:HD12	1:B:460:LEU:HD22	1.55	0.86
1:A:428:TYR:HB2	1:A:437:LEU:HD11	1.57	0.86
1:A:323:TYR:CZ	1:A:324:HIS:HE1	1.87	0.86
1:C:593:THR:HG22	1:C:595:HIS:H	1.44	0.82
1:C:454:ILE:HA	1:C:456:SER:N	1.95	0.82
1:D:593:THR:HG22	1:D:595:HIS:H	1.46	0.81
1:B:593:THR:HG22	1:B:595:HIS:H	1.46	0.80
1:A:593:THR:HG22	1:A:595:HIS:H	1.45	0.79
1:A:593:THR:HG23	1:A:630:THR:O	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:593:THR:HG23	1:C:630:THR:O	1.85	0.77
1:D:593:THR:HG23	1:D:630:THR:O	1.85	0.76
1:B:402:LEU:HD12	1:B:460:LEU:CD2	2.16	0.76
1:C:259:ALA:O	1:C:263:VAL:HG23	1.86	0.76
1:B:236:LEU:HB3	1:B:237:PRO:HD3	1.68	0.76
1:A:236:LEU:HB3	1:A:237:PRO:HD3	1.68	0.75
1:D:595:HIS:CD2	1:D:597:GLU:H	2.05	0.74
1:B:595:HIS:CD2	1:B:597:GLU:H	2.05	0.74
1:B:593:THR:HG23	1:B:630:THR:O	1.86	0.74
1:A:259:ALA:O	1:A:263:VAL:HG23	1.88	0.73
1:A:595:HIS:CD2	1:A:597:GLU:H	2.06	0.73
1:A:323:TYR:OH	1:A:324:HIS:HE1	1.71	0.73
1:C:595:HIS:CD2	1:C:597:GLU:H	2.05	0.73
1:B:595:HIS:HD2	1:B:597:GLU:H	1.38	0.72
1:B:259:ALA:O	1:B:263:VAL:HG23	1.89	0.72
1:D:259:ALA:O	1:D:263:VAL:HG23	1.88	0.72
1:B:406:PRO:HD3	1:B:469:THR:HG21	1.72	0.71
1:A:406:PRO:HD3	1:A:469:THR:HG21	1.71	0.71
1:C:595:HIS:HD2	1:C:597:GLU:H	1.39	0.71
1:A:595:HIS:HD2	1:A:597:GLU:H	1.39	0.71
1:C:236:LEU:HB3	1:C:237:PRO:HD3	1.71	0.71
1:D:236:LEU:HB3	1:D:237:PRO:HD3	1.73	0.71
1:D:595:HIS:HD2	1:D:597:GLU:H	1.38	0.70
1:B:299:TYR:O	1:B:302:GLN:HG3	1.90	0.70
1:D:406:PRO:HD3	1:D:469:THR:HG21	1.74	0.69
1:C:406:PRO:HD3	1:C:469:THR:HG21	1.72	0.69
1:D:226:LEU:CD2	1:D:233:THR:HG22	2.22	0.69
1:C:324:HIS:HD2	1:C:350:THR:HG1	1.38	0.69
1:C:226:LEU:CD2	1:C:233:THR:HG22	2.23	0.69
1:B:323:TYR:CE1	1:B:559:LEU:HD22	2.27	0.69
1:A:342:GLU:HG2	1:D:545:ASN:CB	2.22	0.69
1:B:585:ALA:HA	1:B:588:ASN:HD22	1.58	0.69
1:A:323:TYR:OH	1:A:324:HIS:CE1	2.44	0.68
1:B:309:ARG:HH21	1:B:343:ASN:HD21	1.39	0.68
1:D:490:LEU:O	1:D:491:LYS:HG2	1.93	0.68
1:D:450:ALA:HB1	1:D:454:ILE:CG1	2.21	0.68
1:B:614:PHE:CD2	1:B:637:LEU:HD12	2.29	0.67
1:A:299:TYR:O	1:A:302:GLN:HG3	1.94	0.67
1:C:324:HIS:NE2	1:C:350:THR:HG21	2.09	0.67
1:A:616:LYS:HE3	1:A:625:THR:CG2	2.25	0.67
1:B:585:ALA:O	1:B:589:ILE:HG13	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:342:GLU:HG2	1:C:545:ASN:CB	2.26	0.66
1:C:324:HIS:CD2	1:C:350:THR:CB	2.78	0.66
1:D:324:HIS:CD2	1:D:350:THR:CB	2.78	0.66
1:D:299:TYR:O	1:D:302:GLN:HG3	1.96	0.66
1:B:616:LYS:HE3	1:B:625:THR:CG2	2.25	0.66
1:A:226:LEU:CD2	1:A:233:THR:HG22	2.25	0.66
1:D:323:TYR:HE1	1:D:324:HIS:CE1	2.10	0.66
1:C:616:LYS:HE3	1:C:625:THR:CG2	2.26	0.65
1:A:213:ILE:HD11	1:A:224:ILE:HD11	1.77	0.65
1:A:309:ARG:HH21	1:A:343:ASN:HD21	1.45	0.65
1:A:487:VAL:HA	1:A:647:ALA:O	1.96	0.65
1:C:299:TYR:O	1:C:302:GLN:HG3	1.97	0.65
1:B:487:VAL:HA	1:B:647:ALA:O	1.97	0.65
1:B:478:ARG:HD3	1:B:649:GLU:OE2	1.96	0.65
1:D:324:HIS:NE2	1:D:350:THR:HG21	2.11	0.64
1:A:478:ARG:HD3	1:A:649:GLU:OE2	1.97	0.64
1:D:464:ASP:OD1	1:D:511:LYS:HE2	1.97	0.64
1:A:428:TYR:HB2	1:A:437:LEU:CD1	2.28	0.64
1:C:487:VAL:HA	1:C:647:ALA:O	1.98	0.64
1:B:586:VAL:O	1:B:590:MET:HG3	1.97	0.63
1:D:487:VAL:HA	1:D:647:ALA:O	1.97	0.63
1:C:454:ILE:HA	1:C:456:SER:H	1.61	0.63
1:D:616:LYS:HE3	1:D:625:THR:CG2	2.28	0.63
1:B:213:ILE:HD11	1:B:224:ILE:HD11	1.79	0.63
1:C:438:ARG:HA	1:C:441:THR:OG1	1.99	0.62
1:B:428:TYR:HB2	1:B:437:LEU:CD1	2.27	0.62
1:B:641:VAL:CG2	1:B:663:PRO:HD3	2.25	0.62
1:B:451:THR:HG22	1:B:452:ASN:N	2.14	0.62
1:C:309:ARG:HH21	1:C:343:ASN:HD21	1.48	0.62
1:D:324:HIS:HD2	1:D:350:THR:HG1	1.41	0.62
1:C:213:ILE:HD11	1:C:224:ILE:HD11	1.81	0.61
1:C:323:TYR:HE1	1:C:324:HIS:CE1	2.13	0.61
1:A:342:GLU:HG2	1:D:545:ASN:HB3	1.82	0.61
1:B:545:ASN:CB	1:C:342:GLU:HG2	2.29	0.61
1:C:464:ASP:OD1	1:C:511:LYS:HE2	1.99	0.61
1:B:464:ASP:OD1	1:B:511:LYS:HE2	2.01	0.60
1:D:309:ARG:HH21	1:D:343:ASN:HD21	1.50	0.59
1:C:226:LEU:HD21	1:C:233:THR:HG22	1.82	0.59
1:B:283:MET:CE	1:B:307:LYS:HD2	2.32	0.59
1:A:283:MET:CE	1:A:307:LYS:HD2	2.32	0.59
1:C:428:TYR:CE2	1:C:454:ILE:O	2.56	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:342:GLU:HG2	1:C:545:ASN:HB2	1.83	0.59
1:C:221:PHE:HD1	1:C:346:VAL:HG22	1.67	0.59
1:A:323:TYR:CE1	1:A:324:HIS:NE2	2.69	0.58
1:D:213:ILE:HD11	1:D:224:ILE:HD11	1.84	0.58
1:A:342:GLU:HG2	1:D:545:ASN:HB2	1.83	0.58
1:D:226:LEU:HD21	1:D:233:THR:HG22	1.84	0.58
1:D:221:PHE:HD1	1:D:346:VAL:HG22	1.68	0.58
1:B:594:ASP:OD2	1:B:630:THR:HG23	2.04	0.58
1:B:334:MET:HE1	1:B:559:LEU:HD13	1.84	0.58
1:D:334:MET:HE1	1:D:559:LEU:HD13	1.84	0.58
1:A:464:ASP:OD1	1:A:511:LYS:HE2	2.03	0.58
1:A:665:PRO:HD3	2:A:2001:HOH:O	2.03	0.58
1:B:221:PHE:HD1	1:B:346:VAL:HG22	1.69	0.57
1:A:226:LEU:HD21	1:A:233:THR:HG22	1.86	0.57
1:C:623:THR:OG1	1:C:625:THR:HB	2.04	0.57
1:C:473:CYS:SG	1:C:492:ARG:HG3	2.44	0.57
1:D:451:THR:HG22	1:D:452:ASN:N	2.20	0.57
1:B:342:GLU:HG2	1:C:545:ASN:HB3	1.87	0.57
1:B:635:ARG:NH2	1:B:640:ASP:O	2.34	0.57
1:B:545:ASN:HB3	1:C:342:GLU:HG2	1.87	0.56
1:A:283:MET:HE3	1:A:307:LYS:HD2	1.87	0.56
1:A:213:ILE:O	1:A:216:MET:HB2	2.06	0.56
1:A:221:PHE:HD1	1:A:346:VAL:HG22	1.70	0.56
1:B:476:ARG:NE	1:B:493:MET:CE	2.69	0.56
1:D:450:ALA:CB	1:D:454:ILE:HG13	2.32	0.56
1:A:689:ALA:O	1:A:690:LEU:HB2	2.06	0.56
1:B:476:ARG:HE	1:B:493:MET:CE	2.19	0.55
1:A:545:ASN:CB	1:D:342:GLU:HG2	2.36	0.55
1:C:429:TYR:C	1:C:431:GLY:H	2.10	0.55
1:B:490:LEU:O	1:B:491:LYS:HG2	2.07	0.55
1:D:623:THR:OG1	1:D:625:THR:HB	2.06	0.55
1:A:593:THR:HG22	1:A:595:HIS:N	2.19	0.55
1:B:275:ALA:O	1:B:291:GLY:HA3	2.07	0.55
1:D:248:LYS:O	1:D:290:THR:O	2.25	0.55
1:D:275:ALA:O	1:D:291:GLY:HA3	2.07	0.55
1:A:623:THR:OG1	1:A:625:THR:HB	2.07	0.55
1:B:623:THR:OG1	1:B:625:THR:HB	2.07	0.55
1:A:248:LYS:O	1:A:290:THR:O	2.23	0.55
1:C:275:ALA:O	1:C:291:GLY:HA3	2.07	0.54
1:D:450:ALA:HB1	1:D:454:ILE:CB	2.38	0.54
1:D:617:ILE:HD13	1:D:653:LEU:HD23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:MET:HE1	1:A:559:LEU:HD13	1.89	0.54
1:B:248:LYS:O	1:B:290:THR:O	2.25	0.54
1:A:476:ARG:HE	1:A:493:MET:HE1	1.71	0.54
1:C:451:THR:HG22	1:C:452:ASN:N	2.23	0.54
1:C:593:THR:HG21	1:C:595:HIS:HB2	1.90	0.53
1:A:594:ASP:OD2	1:A:630:THR:HG23	2.08	0.53
1:C:407:THR:HG22	1:C:492:ARG:HH11	1.72	0.53
1:D:593:THR:HG21	1:D:595:HIS:HB2	1.90	0.53
1:D:593:THR:HG22	1:D:595:HIS:N	2.19	0.53
1:B:593:THR:HG22	1:B:595:HIS:N	2.19	0.53
1:D:213:ILE:O	1:D:216:MET:HB2	2.08	0.53
1:B:545:ASN:HB2	1:C:342:GLU:HG2	1.90	0.53
1:A:490:LEU:O	1:A:491:LYS:HG2	2.07	0.53
1:D:475:LYS:HG2	1:D:490:LEU:HD13	1.89	0.53
1:B:614:PHE:CG	1:B:637:LEU:HD12	2.43	0.53
1:A:477:ILE:HG22	1:A:488:THR:HG22	1.91	0.53
1:D:283:MET:CE	1:D:307:LYS:HD2	2.39	0.53
1:D:323:TYR:CZ	1:D:324:HIS:CE1	2.96	0.53
1:D:309:ARG:HH21	1:D:343:ASN:ND2	2.06	0.53
1:C:334:MET:HE1	1:C:559:LEU:HD13	1.89	0.53
1:C:617:ILE:HD13	1:C:653:LEU:HD23	1.89	0.53
1:C:323:TYR:CZ	1:C:324:HIS:CE1	2.97	0.53
1:C:309:ARG:HH21	1:C:343:ASN:ND2	2.06	0.53
1:C:277:ASN:CG	1:C:289:ALA:HB1	2.30	0.52
1:C:477:ILE:HG22	1:C:488:THR:HG22	1.92	0.52
1:A:593:THR:HG21	1:A:595:HIS:HB2	1.90	0.52
1:A:309:ARG:HH21	1:A:343:ASN:ND2	2.08	0.52
1:D:598:PRO:O	1:D:601:LEU:HB2	2.09	0.52
1:A:275:ALA:O	1:A:291:GLY:HA3	2.10	0.52
1:C:476:ARG:HG2	1:C:491:LYS:HD2	1.91	0.52
1:A:362:GLN:HG2	1:C:372:PRO:HB3	1.90	0.52
1:B:593:THR:HG21	1:B:595:HIS:HB2	1.91	0.52
1:B:283:MET:HE1	1:B:307:LYS:HD2	1.90	0.52
1:B:213:ILE:O	1:B:216:MET:HB2	2.09	0.51
1:C:248:LYS:O	1:C:290:THR:O	2.27	0.51
1:B:451:THR:O	1:B:454:ILE:HG23	2.10	0.51
1:A:476:ARG:NE	1:A:493:MET:CE	2.72	0.51
1:A:648:THR:HG22	1:A:651:GLU:H	1.75	0.51
1:C:213:ILE:O	1:C:216:MET:HB2	2.09	0.51
1:B:476:ARG:HE	1:B:493:MET:HE1	1.75	0.51
1:B:648:THR:HG22	1:B:651:GLU:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:476:ARG:HH11	1:D:476:ARG:HG3	1.75	0.51
1:D:277:ASN:CG	1:D:289:ALA:HB1	2.31	0.51
1:C:475:LYS:HG2	1:C:490:LEU:HD13	1.92	0.51
1:C:283:MET:CE	1:C:307:LYS:HD2	2.40	0.51
1:C:598:PRO:O	1:C:601:LEU:HB2	2.11	0.51
1:B:451:THR:CG2	1:B:452:ASN:N	2.74	0.51
1:B:277:ASN:CG	1:B:289:ALA:HB1	2.31	0.51
1:C:593:THR:HG22	1:C:595:HIS:N	2.18	0.51
1:D:477:ILE:HG22	1:D:488:THR:HG22	1.93	0.51
1:C:648:THR:HG22	1:C:651:GLU:H	1.76	0.50
1:A:598:PRO:O	1:A:601:LEU:HB2	2.11	0.50
1:A:483:MET:HB2	2:A:2001:HOH:O	2.11	0.50
1:A:362:GLN:CG	1:C:372:PRO:HB3	2.41	0.50
1:A:617:ILE:HD13	1:A:653:LEU:HD23	1.94	0.50
1:A:532:LEU:O	1:A:532:LEU:HD22	2.12	0.50
1:A:545:ASN:HB2	1:D:342:GLU:HG2	1.94	0.50
1:D:523:VAL:HG22	1:D:525:SER:HB3	1.92	0.50
1:A:222:ARG:O	1:A:347:VAL:HA	2.12	0.50
1:A:338:HIS:HE1	1:A:556:ASP:OD2	1.95	0.50
1:B:206:LEU:O	1:B:210:VAL:HG23	2.11	0.50
1:D:429:TYR:C	1:D:431:GLY:H	2.15	0.50
1:B:477:ILE:HG22	1:B:488:THR:HG22	1.94	0.50
1:B:277:ASN:OD1	1:B:289:ALA:HB1	2.12	0.49
1:A:451:THR:O	1:A:454:ILE:HG23	2.11	0.49
1:B:462:ASP:OD2	1:B:511:LYS:NZ	2.45	0.49
1:A:236:LEU:HD23	1:A:319:PHE:HE2	1.77	0.49
1:C:476:ARG:HG3	1:C:476:ARG:HH11	1.76	0.49
1:C:338:HIS:HE1	1:C:556:ASP:OD2	1.95	0.49
1:D:323:TYR:CZ	1:D:324:HIS:NE2	2.80	0.49
1:B:334:MET:CE	1:B:559:LEU:HD13	2.42	0.49
1:A:277:ASN:CG	1:A:289:ALA:HB1	2.32	0.49
1:A:323:TYR:CE1	1:A:324:HIS:ND1	2.75	0.49
1:C:454:ILE:HG23	1:C:456:SER:HB3	1.94	0.49
1:B:435:SER:O	1:B:438:ARG:HB2	2.13	0.49
1:A:206:LEU:O	1:A:210:VAL:HG23	2.12	0.49
1:B:309:ARG:HH21	1:B:343:ASN:ND2	2.09	0.49
1:C:472:LYS:HD2	1:C:474:GLU:HG2	1.94	0.49
1:B:338:HIS:CD2	1:B:553:MET:HA	2.48	0.48
1:B:236:LEU:HD23	1:B:319:PHE:HE2	1.78	0.48
1:D:222:ARG:O	1:D:347:VAL:HA	2.13	0.48
1:A:476:ARG:NE	1:A:493:MET:HE1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:ARG:O	1:B:347:VAL:HA	2.12	0.48
1:B:323:TYR:CZ	1:B:559:LEU:HD22	2.49	0.48
1:D:616:LYS:HB2	1:D:625:THR:HG22	1.96	0.48
1:A:323:TYR:HE1	1:A:324:HIS:NE2	2.12	0.48
1:B:588:ASN:O	1:B:592:ARG:HG3	2.13	0.48
1:D:648:THR:HG22	1:D:651:GLU:H	1.77	0.48
1:C:206:LEU:O	1:C:210:VAL:HG23	2.13	0.48
1:B:496:THR:HG22	1:B:523:VAL:HG13	1.96	0.48
1:C:523:VAL:HG22	1:C:525:SER:HB2	1.95	0.48
1:B:598:PRO:O	1:B:601:LEU:HB2	2.14	0.48
1:B:236:LEU:HB3	1:B:237:PRO:CD	2.41	0.47
1:A:435:SER:O	1:A:438:ARG:HB2	2.14	0.47
1:D:226:LEU:HD23	1:D:233:THR:HG22	1.95	0.47
1:A:277:ASN:OD1	1:A:289:ALA:HB1	2.14	0.47
1:D:206:LEU:O	1:D:210:VAL:HG23	2.14	0.47
1:D:472:LYS:HD2	1:D:474:GLU:HG2	1.96	0.47
1:B:283:MET:HE3	1:B:307:LYS:HD2	1.96	0.47
1:A:462:ASP:OD2	1:A:511:LYS:NZ	2.45	0.47
1:A:334:MET:CE	1:A:559:LEU:HD13	2.45	0.47
1:A:476:ARG:HE	1:A:493:MET:CE	2.27	0.47
1:C:277:ASN:OD1	1:C:289:ALA:HB1	2.15	0.47
1:C:283:MET:HE3	1:C:307:LYS:HD2	1.95	0.47
1:A:683:LEU:HD21	1:B:687:GLU:HA	1.95	0.47
1:A:428:TYR:CE1	1:A:454:ILE:HA	2.50	0.47
1:C:236:LEU:HB3	1:C:237:PRO:CD	2.44	0.47
1:D:277:ASN:OD1	1:D:289:ALA:HB1	2.15	0.47
1:B:548:LYS:O	1:B:552:GLU:HG3	2.14	0.47
1:D:304:SER:OG	1:D:307:LYS:HE3	2.15	0.47
1:C:616:LYS:HB2	1:C:625:THR:HG22	1.97	0.46
1:A:548:LYS:O	1:A:552:GLU:HG3	2.15	0.46
1:C:548:LYS:O	1:C:552:GLU:HG3	2.14	0.46
1:A:496:THR:HG22	1:A:523:VAL:HG13	1.96	0.46
1:D:236:LEU:HD23	1:D:319:PHE:HE2	1.80	0.46
1:B:474:GLU:HB2	1:B:493:MET:SD	2.55	0.46
1:A:545:ASN:HB3	1:D:342:GLU:HG2	1.96	0.46
1:A:474:GLU:HB2	1:A:493:MET:SD	2.55	0.46
1:C:411:ALA:HA	1:C:449:VAL:CG1	2.46	0.46
1:C:270:LYS:HG2	1:C:271:HIS:CD2	2.51	0.46
1:D:338:HIS:HE1	1:D:556:ASP:OD2	1.97	0.46
1:A:411:ALA:HA	1:A:449:VAL:CG1	2.46	0.46
1:D:451:THR:CG2	1:D:452:ASN:N	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:411:ALA:HA	1:B:449:VAL:CG1	2.46	0.46
1:B:616:LYS:HG3	1:B:625:THR:HG22	1.96	0.46
1:A:616:LYS:HG3	1:A:625:THR:HG22	1.98	0.46
1:D:334:MET:CE	1:D:559:LEU:HD13	2.46	0.46
1:B:476:ARG:NE	1:B:493:MET:HE2	2.31	0.46
1:D:626:TYR:CZ	1:D:636:LYS:HD3	2.51	0.46
1:B:428:TYR:HD1	1:B:454:ILE:CG2	2.13	0.46
1:D:411:ALA:HA	1:D:449:VAL:CG1	2.46	0.46
1:B:512:PRO:HG3	1:D:384:TYR:OH	2.16	0.46
1:D:283:MET:HE3	1:D:307:LYS:HD2	1.97	0.45
1:A:402:LEU:HD12	1:A:460:LEU:HD12	1.99	0.45
1:A:428:TYR:HD1	1:A:454:ILE:CG2	2.13	0.45
1:A:323:TYR:HA	1:A:330:GLN:NE2	2.32	0.45
1:C:304:SER:OG	1:C:307:LYS:HE3	2.15	0.45
1:A:470:GLY:O	1:A:495:VAL:HG22	2.17	0.45
1:B:265:GLN:OE1	1:B:265:GLN:HA	2.15	0.45
1:C:323:TYR:CZ	1:C:324:HIS:NE2	2.84	0.45
1:A:265:GLN:OE1	1:A:265:GLN:HA	2.16	0.45
1:B:438:ARG:HA	1:B:441:THR:OG1	2.17	0.45
1:D:548:LYS:O	1:D:552:GLU:HG3	2.16	0.45
1:C:451:THR:CG2	1:C:452:ASN:N	2.80	0.45
1:C:222:ARG:O	1:C:347:VAL:HA	2.16	0.45
1:D:323:TYR:HA	1:D:330:GLN:NE2	2.32	0.45
1:C:565:LEU:O	1:C:569:GLN:HG3	2.17	0.45
1:C:334:MET:CE	1:C:559:LEU:HD13	2.46	0.44
1:A:565:LEU:O	1:A:569:GLN:HG3	2.17	0.44
1:B:451:THR:CG2	1:B:452:ASN:H	2.30	0.44
1:B:428:TYR:CE1	1:B:454:ILE:HA	2.51	0.44
1:A:616:LYS:HB2	1:A:625:THR:HG22	1.99	0.44
1:C:254:ILE:O	1:C:296:SER:HA	2.18	0.44
1:A:304:SER:OG	1:A:307:LYS:HE3	2.18	0.44
1:A:222:ARG:HB2	1:A:347:VAL:HG22	1.99	0.44
1:B:547:THR:H	1:B:574:ASN:ND2	2.16	0.44
1:D:565:LEU:O	1:D:569:GLN:HG3	2.17	0.44
1:B:460:LEU:HD23	1:B:463:LEU:HD13	1.99	0.44
1:B:305:GLN:N	1:B:306:PRO:HD2	2.33	0.44
1:B:565:LEU:O	1:B:569:GLN:HG3	2.17	0.44
1:A:283:MET:HE1	1:A:307:LYS:HD2	2.00	0.44
1:D:610:VAL:CG2	1:D:635:ARG:HG2	2.48	0.44
1:A:305:GLN:N	1:A:306:PRO:HD2	2.32	0.44
1:D:270:LYS:HG2	1:D:271:HIS:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:470:GLY:O	1:B:495:VAL:HG22	2.18	0.43
1:A:236:LEU:HB3	1:A:237:PRO:CD	2.41	0.43
1:A:690:LEU:O	1:B:683:LEU:HD11	2.18	0.43
1:C:303:MET:HB3	1:C:307:LYS:HB3	2.00	0.43
1:C:547:THR:H	1:C:574:ASN:ND2	2.16	0.43
1:B:336:LYS:O	1:B:339:ARG:HB2	2.18	0.43
1:B:584:MET:O	1:B:588:ASN:ND2	2.51	0.43
1:B:614:PHE:CD2	1:B:637:LEU:CD1	3.00	0.43
1:A:226:LEU:HD23	1:A:233:THR:HG22	1.98	0.43
1:C:595:HIS:CD2	1:C:596:PRO:HD2	2.53	0.43
1:B:303:MET:HB3	1:B:307:LYS:HB3	2.00	0.43
1:A:303:MET:HB3	1:A:307:LYS:HB3	2.01	0.43
1:B:254:ILE:O	1:B:296:SER:HA	2.18	0.43
1:C:626:TYR:CZ	1:C:636:LYS:HD3	2.53	0.43
1:A:438:ARG:HA	1:A:441:THR:OG1	2.18	0.43
1:B:616:LYS:HB2	1:B:625:THR:HG22	1.99	0.43
1:C:249:ARG:HD2	1:C:289:ALA:O	2.19	0.43
1:B:222:ARG:HB2	1:B:347:VAL:HG22	2.00	0.43
1:B:565:LEU:HD12	1:B:680:VAL:HG13	2.00	0.43
1:C:323:TYR:HA	1:C:330:GLN:NE2	2.33	0.43
1:D:616:LYS:HG3	1:D:625:THR:HG22	2.00	0.43
1:C:238:ARG:NH1	1:C:242:GLU:OE1	2.51	0.43
1:B:641:VAL:HG21	1:B:662:TRP:HA	2.01	0.43
1:D:396:GLU:HG3	1:D:465:VAL:HG11	2.01	0.43
1:B:304:SER:OG	1:B:307:LYS:HE3	2.18	0.42
1:C:370:ILE:HD11	1:C:519:GLN:HA	2.00	0.42
1:A:547:THR:H	1:A:574:ASN:ND2	2.17	0.42
1:A:254:ILE:O	1:A:296:SER:HA	2.19	0.42
1:C:324:HIS:NE2	1:C:350:THR:CB	2.82	0.42
1:D:595:HIS:CD2	1:D:596:PRO:HD2	2.53	0.42
1:D:490:LEU:C	1:D:491:LYS:HG2	2.39	0.42
1:A:565:LEU:HD12	1:A:680:VAL:HG13	2.00	0.42
1:B:619:ASN:HB3	1:B:620:GLY:H	1.57	0.42
1:D:238:ARG:NH1	1:D:242:GLU:OE1	2.52	0.42
1:B:396:GLU:HG3	1:B:465:VAL:HG11	2.01	0.42
1:D:547:THR:H	1:D:574:ASN:ND2	2.16	0.42
1:C:222:ARG:HB2	1:C:347:VAL:HG22	2.02	0.42
1:D:473:CYS:SG	1:D:492:ARG:HG2	2.59	0.42
1:B:209:MET:O	1:B:213:ILE:HG12	2.19	0.42
1:D:411:ALA:HA	1:D:449:VAL:HG12	2.02	0.42
1:B:528:TYR:CE2	1:B:550:PHE:CZ	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:ILE:O	1:D:296:SER:HA	2.20	0.42
1:D:475:LYS:O	1:D:476:ARG:HD3	2.20	0.42
1:B:435:SER:HB3	1:B:438:ARG:HG3	2.02	0.42
1:C:249:ARG:HH21	1:C:314:GLU:CB	2.33	0.42
1:A:435:SER:HB3	1:A:438:ARG:HG3	2.00	0.42
1:C:411:ALA:HA	1:C:449:VAL:HG12	2.02	0.42
1:B:617:ILE:HD13	1:B:653:LEU:HD23	2.02	0.42
1:A:209:MET:O	1:A:213:ILE:HG12	2.20	0.42
1:D:249:ARG:HD2	1:D:289:ALA:O	2.20	0.42
1:D:565:LEU:HD12	1:D:680:VAL:HG13	2.01	0.42
1:D:605:SER:HA	1:D:608:THR:O	2.20	0.42
1:C:324:HIS:NE2	1:C:350:THR:CG2	2.81	0.41
1:A:690:LEU:O	1:B:683:LEU:CD1	2.68	0.41
1:A:626:TYR:CZ	1:A:636:LYS:HD3	2.55	0.41
1:B:626:TYR:CZ	1:B:636:LYS:HD3	2.54	0.41
1:C:479:LEU:HA	1:C:485:PHE:O	2.19	0.41
1:B:238:ARG:NH1	1:B:242:GLU:OE1	2.52	0.41
1:A:362:GLN:HE22	1:C:370:ILE:HG12	1.85	0.41
1:A:396:GLU:HG3	1:A:465:VAL:HG11	2.01	0.41
1:C:593:THR:CG2	1:C:595:HIS:H	2.25	0.41
1:D:303:MET:HB3	1:D:307:LYS:HB3	2.01	0.41
1:D:249:ARG:HH21	1:D:314:GLU:CB	2.34	0.41
1:C:270:LYS:HD3	1:C:271:HIS:HE2	1.84	0.41
1:D:479:LEU:HA	1:D:485:PHE:O	2.21	0.41
1:A:595:HIS:CD2	1:A:596:PRO:HD2	2.55	0.41
1:C:434:PRO:O	1:C:438:ARG:HG2	2.19	0.41
1:B:475:LYS:O	1:B:476:ARG:HD3	2.20	0.41
1:A:411:ALA:HA	1:A:449:VAL:HG12	2.01	0.41
1:A:336:LYS:O	1:A:339:ARG:HB2	2.20	0.41
1:D:283:MET:HE1	1:D:307:LYS:HD2	2.01	0.41
1:D:222:ARG:HB2	1:D:347:VAL:HG22	2.03	0.41
1:C:265:GLN:OE1	1:C:265:GLN:HA	2.21	0.41
1:A:593:THR:CG2	1:A:595:HIS:H	2.26	0.41
1:B:253:LEU:HD22	1:B:297:TYR:HA	2.03	0.41
1:A:593:THR:CG2	1:A:595:HIS:HB2	2.51	0.41
1:D:224:ILE:HG22	1:D:226:LEU:HD22	2.02	0.41
1:D:221:PHE:CD1	1:D:346:VAL:HG22	2.52	0.41
1:B:411:ALA:HA	1:B:449:VAL:HG12	2.03	0.41
1:C:528:TYR:CE2	1:C:550:PHE:CZ	3.09	0.41
1:A:528:TYR:CE2	1:A:550:PHE:CZ	3.09	0.41
1:A:221:PHE:CD1	1:A:346:VAL:HG22	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:476:ARG:HH11	1:B:476:ARG:HG3	1.87	0.41
1:C:429:TYR:O	1:C:431:GLY:N	2.51	0.41
1:A:476:ARG:HH11	1:A:476:ARG:HG3	1.86	0.41
1:C:305:GLN:N	1:C:306:PRO:HD2	2.36	0.41
1:B:593:THR:CG2	1:B:595:HIS:HB2	2.51	0.40
1:C:221:PHE:CD1	1:C:346:VAL:HG22	2.52	0.40
1:C:483:MET:HE2	1:C:485:PHE:CE2	2.56	0.40
1:A:270:LYS:HG2	1:A:271:HIS:CD2	2.57	0.40
1:B:217:ASN:HB2	1:B:220:GLU:OE2	2.21	0.40
1:A:362:GLN:HE21	1:C:519:GLN:CD	2.24	0.40
1:A:479:LEU:HA	1:A:485:PHE:O	2.22	0.40
1:C:618:ARG:O	1:C:619:ASN:HB2	2.22	0.40
1:B:270:LYS:HG2	1:B:271:HIS:CD2	2.56	0.40
1:D:336:LYS:O	1:D:339:ARG:HB2	2.21	0.40
1:B:479:LEU:HA	1:B:485:PHE:O	2.20	0.40
1:D:265:GLN:HA	1:D:265:GLN:OE1	2.20	0.40
1:A:605:SER:HA	1:A:608:THR:O	2.21	0.40
1:A:425:SER:HA	1:A:447:VAL:O	2.22	0.40
1:A:297:TYR:CZ	1:A:330:GLN:HG3	2.57	0.40
1:B:297:TYR:CZ	1:B:330:GLN:HG3	2.56	0.40
1:D:477:ILE:HD12	1:D:479:LEU:HD21	2.03	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	457/516 (89%)	437 (96%)	17 (4%)	3 (1%)	26	69
1	B	444/516 (86%)	432 (97%)	12 (3%)	0	100	100
1	C	455/516 (88%)	434 (95%)	15 (3%)	6 (1%)	15	55
1	D	441/516 (86%)	422 (96%)	15 (3%)	4 (1%)	21	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1797/2064 (87%)	1725 (96%)	59 (3%)	13 (1%)	26	69

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	458	VAL
1	C	432	GLU
1	C	454	ILE
1	C	455	GLU
1	C	458	VAL
1	D	432	GLU
1	D	458	VAL
1	C	430	SER
1	D	430	SER
1	A	381	GLY
1	A	456	SER
1	C	376	LYS
1	D	376	LYS

### 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	403/442 (91%)	361 (90%)	42 (10%)	9	34
1	B	397/442 (90%)	359 (90%)	38 (10%)	10	38
1	C	401/442 (91%)	354 (88%)	47 (12%)	7	29
1	D	392/442 (89%)	346 (88%)	46 (12%)	7	29
All	All	1593/1768 (90%)	1420 (89%)	173 (11%)	8	32

All (173) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	205	ASP
1	A	206	LEU

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Mol	Chain	Res	Type
1	A	207	THR
1	A	224	ILE
1	A	232	LYS
1	A	236	LEU
1	A	241	ILE
1	A	256	LEU
1	A	262	SER
1	A	283	MET
1	A	303	MET
1	A	342	GLU
1	A	362	GLN
1	A	368	GLU
1	A	378	GLU
1	A	380	LEU
1	A	383	GLU
1	A	392	ILE
1	A	405	VAL
1	A	460	LEU
1	A	462	ASP
1	A	476	ARG
1	A	478	ARG
1	A	487	VAL
1	A	490	LEU
1	A	493	MET
1	A	532	LEU
1	A	570	LEU
1	A	582	LEU
1	A	601	LEU
1	A	610	VAL
1	A	624	ASP
1	A	625	THR
1	A	628	ASN
1	A	633	ASN
1	A	637	LEU
1	A	641	VAL
1	A	646	TYR
1	A	648	THR
1	A	678	LYS
1	A	680	VAL
1	A	688	ASN
1	B	205	ASP
1	B	206	LEU

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Mol	Chain	Res	Type
1	B	207	THR
1	B	224	ILE
1	B	236	LEU
1	B	241	ILE
1	B	256	LEU
1	B	262	SER
1	B	283	MET
1	B	303	MET
1	B	324	HIS
1	B	342	GLU
1	B	362	GLN
1	B	368	GLU
1	B	383	GLU
1	B	405	VAL
1	B	436	ASN
1	B	459	THR
1	B	462	ASP
1	B	473	CYS
1	B	476	ARG
1	B	478	ARG
1	B	487	VAL
1	B	490	LEU
1	B	493	MET
1	B	570	LEU
1	B	582	LEU
1	B	592	ARG
1	B	601	LEU
1	B	610	VAL
1	B	624	ASP
1	B	625	THR
1	B	628	ASN
1	B	635	ARG
1	B	641	VAL
1	B	646	TYR
1	B	648	THR
1	B	680	VAL
1	C	207	THR
1	C	224	ILE
1	C	236	LEU
1	C	241	ILE
1	C	256	LEU
1	C	261	GLU

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Mol	Chain	Res	Type
1	C	262	SER
1	C	283	MET
1	C	303	MET
1	C	342	GLU
1	C	363	LYS
1	C	368	GLU
1	C	370	ILE
1	C	375	MET
1	C	378	GLU
1	C	379	ASP
1	C	383	GLU
1	C	392	ILE
1	C	402	LEU
1	C	405	VAL
1	C	429	TYR
1	C	430	SER
1	C	432	GLU
1	C	454	ILE
1	C	460	LEU
1	C	462	ASP
1	C	473	CYS
1	C	474	GLU
1	C	476	ARG
1	C	487	VAL
1	C	490	LEU
1	C	491	LYS
1	C	492	ARG
1	C	566	MET
1	C	570	LEU
1	C	582	LEU
1	C	584	MET
1	C	601	LEU
1	C	625	THR
1	C	628	ASN
1	C	633	ASN
1	C	637	LEU
1	C	641	VAL
1	C	646	TYR
1	C	648	THR
1	C	668	GLN
1	C	678	LYS
1	D	207	THR

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Mol	Chain	Res	Type
1	D	224	ILE
1	D	234	THR
1	D	236	LEU
1	D	241	ILE
1	D	256	LEU
1	D	261	GLU
1	D	262	SER
1	D	283	MET
1	D	303	MET
1	D	342	GLU
1	D	368	GLU
1	D	370	ILE
1	D	375	MET
1	D	378	GLU
1	D	379	ASP
1	D	382	SER
1	D	383	GLU
1	D	392	ILE
1	D	402	LEU
1	D	405	VAL
1	D	430	SER
1	D	454	ILE
1	D	460	LEU
1	D	462	ASP
1	D	473	CYS
1	D	474	GLU
1	D	476	ARG
1	D	487	VAL
1	D	490	LEU
1	D	525	SER
1	D	566	MET
1	D	570	LEU
1	D	582	LEU
1	D	584	MET
1	D	601	LEU
1	D	610	VAL
1	D	625	THR
1	D	628	ASN
1	D	633	ASN
1	D	637	LEU
1	D	641	VAL
1	D	646	TYR

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Mol	Chain	Res	Type
1	D	648	THR
1	D	668	GLN
1	D	678	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	GLN
1	A	324	HIS
1	A	338	HIS
1	A	343	ASN
1	A	362	GLN
1	A	536	GLN
1	A	574	ASN
1	A	595	HIS
1	B	343	ASN
1	B	536	GLN
1	B	574	ASN
1	B	588	ASN
1	B	595	HIS
1	C	223	GLN
1	C	324	HIS
1	C	338	HIS
1	C	343	ASN
1	C	536	GLN
1	C	574	ASN
1	C	595	HIS
1	D	223	GLN
1	D	324	HIS
1	D	338	HIS
1	D	343	ASN
1	D	536	GLN
1	D	574	ASN
1	D	595	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 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 ⓘ

### 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	467/516 (90%)	0.18	10 (2%) 67 58	23, 58, 96, 119	0
1	B	458/516 (88%)	0.24	15 (3%) 50 41	15, 60, 89, 116	0
1	C	461/516 (89%)	0.26	17 (3%) 45 36	25, 63, 96, 126	0
1	D	453/516 (87%)	0.43	24 (5%) 30 23	25, 67, 106, 135	0
All	All	1839/2064 (89%)	0.28	66 (3%) 46 37	15, 62, 98, 135	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	441	THR	4.1
1	C	454	ILE	4.1
1	C	363	LYS	4.0
1	D	461	PRO	3.9
1	D	442	SER	3.9
1	C	456	SER	3.7
1	A	456	SER	3.7
1	D	462	ASP	3.6
1	D	373	GLU	3.6
1	A	621	GLU	3.5
1	D	525	SER	3.5
1	D	324	HIS	3.5
1	B	351	ALA	3.4
1	B	375	MET	3.3
1	D	416	LYS	3.2
1	C	256	LEU	3.2
1	A	620	GLY	3.1
1	A	375	MET	3.0
1	D	666	GLY	3.0
1	B	436	ASN	3.0
1	C	666	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	226	LEU	2.9
1	C	272	PRO	2.9
1	C	592	ARG	2.9
1	D	430	SER	2.8
1	D	376	LYS	2.7
1	D	207	THR	2.7
1	B	282	GLU	2.6
1	C	525	SER	2.6
1	D	280	ILE	2.6
1	C	619	ASN	2.6
1	B	456	SER	2.6
1	D	443	GLN	2.6
1	A	233	THR	2.5
1	D	510	VAL	2.4
1	B	489	GLY	2.4
1	A	376	LYS	2.4
1	C	621	GLU	2.4
1	B	324	HIS	2.4
1	D	456	SER	2.4
1	B	395	GLU	2.4
1	B	382	SER	2.4
1	B	273	SER	2.4
1	C	324	HIS	2.4
1	B	407	THR	2.3
1	D	382	SER	2.3
1	D	596	PRO	2.3
1	D	523	VAL	2.3
1	C	593	THR	2.3
1	B	269	GLN	2.2
1	D	459	THR	2.2
1	C	668	GLN	2.2
1	A	521	THR	2.2
1	C	481	PRO	2.2
1	B	381	GLY	2.2
1	A	381	GLY	2.2
1	C	438	ARG	2.1
1	C	258	ALA	2.1
1	D	508	GLY	2.1
1	B	640	ASP	2.1
1	B	668	GLN	2.0
1	A	204	THR	2.0
1	C	293	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	421	LYS	2.0
1	D	246	ARG	2.0
1	D	679	GLN	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.