



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:00 PM GMT

PDB ID : 4B73  
Title : Discovery of an allosteric mechanism for the regulation of HCV NS3 protein function  
Authors : Saalau-Bethell, S.M.; Woodhead, A.J.; Chessari, G.; Carr, M.G.; Coyle, J.; Graham, B.; Hiscock, S.D.; Murray, C.W.; Pathuri, P.; Rich, S.J.; Richardson, C.J.; Williams, P.A.; Jhoti, H.  
Deposited on : 2012-08-16  
Resolution : 2.50 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.

---

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

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

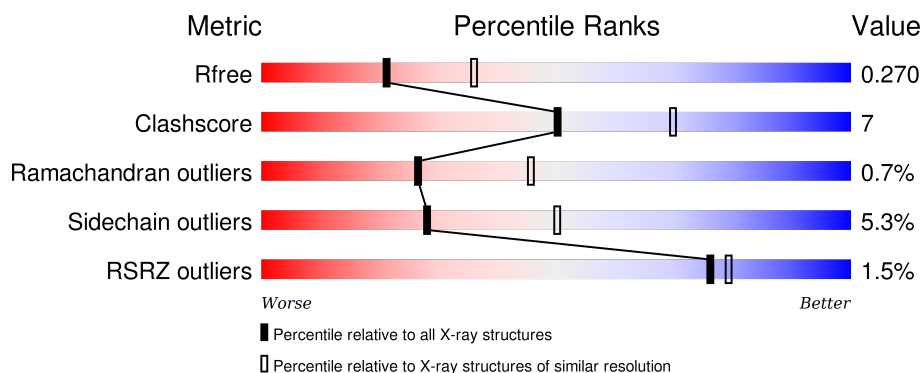
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

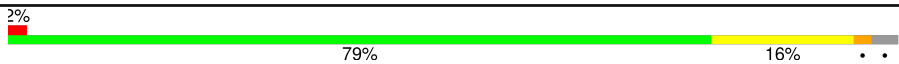

The reported resolution of this entry is 2.50 Å.

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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	666	
1	B	666	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	4VA	A	1721	-	-	-	X
2	4VA	B	1721	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9943 atoms, of which 46 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 NON-STRUCTURAL PROTEIN 4A, SERINE PROTEASE NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	645	Total	C	N	O	S	0	0	0
			4808	3026	834	918	30			
1	B	642	Total	C	N	O	S	0	0	0
			4794	3019	831	914	30			

There are 56 discrepancies between the modelled and reference sequences:

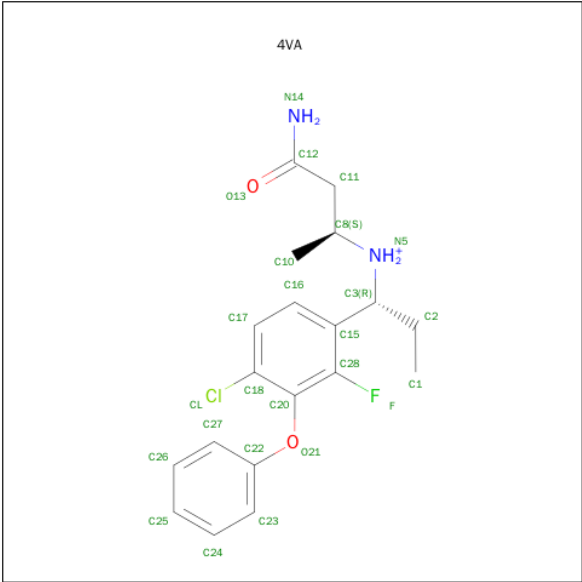
Chain	Residue	Modelled	Actual	Comment	Reference
A	684	MET	-	EXPRESSION TAG	UNP P26663
A	685	GLY	-	EXPRESSION TAG	UNP P26663
A	686	SER	-	EXPRESSION TAG	UNP P26663
A	687	SER	-	EXPRESSION TAG	UNP P26663
A	688	HIS	-	EXPRESSION TAG	UNP P26663
A	689	HIS	-	EXPRESSION TAG	UNP P26663
A	690	HIS	-	EXPRESSION TAG	UNP P26663
A	691	HIS	-	EXPRESSION TAG	UNP P26663
A	692	HIS	-	EXPRESSION TAG	UNP P26663
A	693	HIS	-	EXPRESSION TAG	UNP P26663
A	694	SER	-	EXPRESSION TAG	UNP P26663
A	695	SER	-	EXPRESSION TAG	UNP P26663
A	696	GLY	-	EXPRESSION TAG	UNP P26663
A	697	LEU	-	EXPRESSION TAG	UNP P26663
A	698	VAL	-	EXPRESSION TAG	UNP P26663
A	699	PRO	-	EXPRESSION TAG	UNP P26663
A	700	ARG	-	EXPRESSION TAG	UNP P26663
A	701	GLY	-	EXPRESSION TAG	UNP P26663
A	702	SER	-	EXPRESSION TAG	UNP P26663
A	703	HIS	-	EXPRESSION TAG	UNP P26663
A	704	MET	-	EXPRESSION TAG	UNP P26663
A	718	SER	-	LINKER	UNP P26663
A	719	GLY	-	LINKER	UNP P26663
A	720	SER	-	LINKER	UNP P26663

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	GLY	ALA	CONFLICT	UNP P26663
A	86	GLN	PRO	CONFLICT	UNP P26663
A	87	ALA	LYS	CONFLICT	UNP P26663
A	147	SER	PHE	CONFLICT	UNP P26663
B	684	MET	-	EXPRESSION TAG	UNP P26663
B	685	GLY	-	EXPRESSION TAG	UNP P26663
B	686	SER	-	EXPRESSION TAG	UNP P26663
B	687	SER	-	EXPRESSION TAG	UNP P26663
B	688	HIS	-	EXPRESSION TAG	UNP P26663
B	689	HIS	-	EXPRESSION TAG	UNP P26663
B	690	HIS	-	EXPRESSION TAG	UNP P26663
B	691	HIS	-	EXPRESSION TAG	UNP P26663
B	692	HIS	-	EXPRESSION TAG	UNP P26663
B	693	HIS	-	EXPRESSION TAG	UNP P26663
B	694	SER	-	EXPRESSION TAG	UNP P26663
B	695	SER	-	EXPRESSION TAG	UNP P26663
B	696	GLY	-	EXPRESSION TAG	UNP P26663
B	697	LEU	-	EXPRESSION TAG	UNP P26663
B	698	VAL	-	EXPRESSION TAG	UNP P26663
B	699	PRO	-	EXPRESSION TAG	UNP P26663
B	700	ARG	-	EXPRESSION TAG	UNP P26663
B	701	GLY	-	EXPRESSION TAG	UNP P26663
B	702	SER	-	EXPRESSION TAG	UNP P26663
B	703	HIS	-	EXPRESSION TAG	UNP P26663
B	704	MET	-	EXPRESSION TAG	UNP P26663
B	718	SER	-	LINKER	UNP P26663
B	719	GLY	-	LINKER	UNP P26663
B	720	SER	-	LINKER	UNP P26663
B	66	GLY	ALA	CONFLICT	UNP P26663
B	86	GLN	PRO	CONFLICT	UNP P26663
B	87	ALA	LYS	CONFLICT	UNP P26663
B	147	SER	PHE	CONFLICT	UNP P26663

- Molecule 2 is (2S)-4-AMINO-N-[(1R)-1-(4-CHLORO-2-FLUORO-3-PHENOXYPHENYL)PROPYL]-4-OXOBUTAN-2-AMINIUM (three-letter code: 4VA) (formula: C<sub>19</sub>H<sub>23</sub>ClFN<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	Cl	F	H	N	O	0	0
			48	19	1	1	23	2	2		
2	B	1	Total	C	Cl	F	H	N	O	0	0
			48	19	1	1	23	2	2		

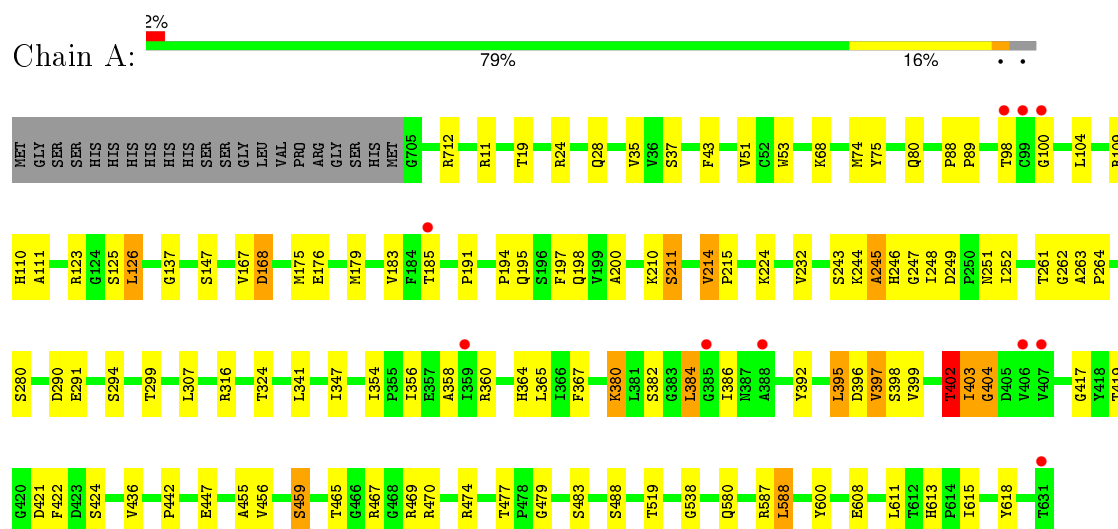
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	139	Total	O	0	0
			139	139		
3	B	106	Total	O	0	0
			106	106		

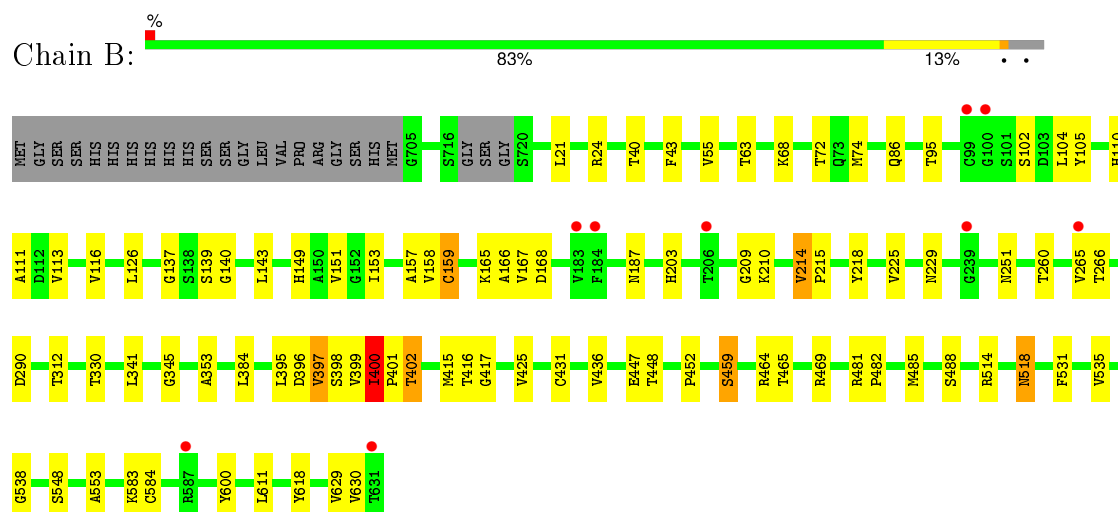
### 3 Residue-property plots

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: NON-STRUCTURAL PROTEIN 4A, SERINE PROTEASE NS3



- Molecule 1: NON-STRUCTURAL PROTEIN 4A, SERINE PROTEASE NS3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.84Å 109.50Å 141.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.49 – 2.50 62.64 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.3 (86.49-2.50) 97.3 (62.64-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.19 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.6.0062	Depositor
R, $R_{free}$	0.183 , 0.264 0.188 , 0.270	Depositor DCC
$R_{free}$ test set	2501 reflections (5.50%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.7	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 47905 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9943	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 4VA

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	0.66	1/4917 (0.0%)	0.73	2/6714 (0.0%)
1	B	0.63	3/4902 (0.1%)	0.72	2/6693 (0.0%)
All	All	0.64	4/9819 (0.0%)	0.73	4/13407 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	447	GLU	CB-CG	6.55	1.64	1.52
1	B	447	GLU	CG-CD	5.89	1.60	1.51
1	A	447	GLU	CG-CD	5.19	1.59	1.51
1	B	159	CYS	CB-SG	-5.02	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	400	ILE	C-N-CD	-7.06	105.06	120.60
1	A	402	THR	C-N-CA	5.33	135.03	121.70
1	A	35	VAL	N-CA-C	-5.33	96.62	111.00
1	B	400	ILE	C-N-CA	5.27	144.12	122.00

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	4808	0	4784	72	0
1	B	4794	0	4772	66	0
2	A	25	23	23	0	0
2	B	25	23	23	0	0
3	A	139	0	0	1	0
3	B	106	0	0	1	0
All	All	9897	46	9602	135	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 7.

All (135) 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:400:ILE:HG22	1:B:401:PRO:CA	1.66	1.26
1:B:400:ILE:HG22	1:B:401:PRO:C	1.82	0.98
1:B:400:ILE:CG2	1:B:402:THR:HG23	1.95	0.97
1:B:400:ILE:HG21	1:B:402:THR:HG23	1.47	0.93
1:B:400:ILE:HG22	1:B:401:PRO:HA	1.51	0.89
1:B:209:GLY:O	1:B:214:VAL:HG12	1.74	0.86
1:B:400:ILE:HG22	1:B:402:THR:N	1.93	0.83
1:B:400:ILE:CG2	1:B:402:THR:N	2.46	0.78
1:B:400:ILE:CG2	1:B:401:PRO:CA	2.56	0.78
1:A:397:VAL:HG11	1:A:417:GLY:O	1.85	0.77
1:B:400:ILE:CG2	1:B:401:PRO:HA	2.15	0.76
1:B:400:ILE:HG22	1:B:401:PRO:N	1.98	0.74
1:A:436:VAL:HG11	1:A:488:SER:HB3	1.72	0.71
1:B:400:ILE:HG23	1:B:402:THR:HG23	1.73	0.69
1:B:400:ILE:CG2	1:B:401:PRO:C	2.61	0.67
1:B:209:GLY:O	1:B:214:VAL:CG1	2.42	0.67
1:A:477:THR:HG22	1:A:479:GLY:H	1.60	0.66
1:A:611:LEU:HD13	1:B:611:LEU:HD23	1.76	0.66
1:A:396:ASP:O	1:A:399:VAL:HG13	1.95	0.66
1:B:452:PRO:O	1:B:481:ARG:NH1	2.30	0.63
1:A:51:VAL:HG21	1:A:179:MET:HE3	1.81	0.63
1:B:397:VAL:HG21	1:B:417:GLY:O	1.99	0.62
1:B:398:SER:HA	1:B:400:ILE:HG12	1.83	0.61
1:B:126:LEU:HD11	1:B:167:VAL:HG13	1.82	0.61
1:A:587:ARG:HG3	1:A:588:LEU:HD13	1.81	0.61
1:B:210:LYS:HA	1:B:214:VAL:HG11	1.83	0.61
1:A:245:ALA:O	1:A:247:GLY:N	2.33	0.60
1:A:347:ILE:HD11	1:A:356:ILE:HG12	1.84	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:LYS:O	1:A:384:LEU:HD13	2.04	0.58
1:A:403:ILE:O	1:A:404:GLY:O	2.22	0.58
1:B:518:ASN:HD22	1:B:518:ASN:N	2.02	0.58
1:A:51:VAL:CG2	1:A:179:MET:CE	2.81	0.58
1:A:442:PRO:HB3	1:A:611:LEU:HD22	1.87	0.57
1:B:397:VAL:O	1:B:400:ILE:HG12	2.04	0.56
1:A:19:THR:HG23	1:A:24:ARG:O	2.05	0.56
1:A:403:ILE:HG22	1:A:404:GLY:N	2.21	0.55
1:A:402:THR:HG23	1:A:403:ILE:HB	1.90	0.54
1:B:126:LEU:CD1	1:B:167:VAL:HG13	2.38	0.54
1:A:74:MET:CE	1:A:75:TYR:CE2	2.91	0.54
1:A:74:MET:HE2	1:A:75:TYR:CE2	2.44	0.53
1:A:51:VAL:CG2	1:A:179:MET:HE3	2.39	0.53
1:A:110:HIS:O	1:A:111:ALA:HB3	2.10	0.52
1:A:51:VAL:HG21	1:A:179:MET:CE	2.40	0.52
1:B:531:PHE:O	1:B:535:VAL:HG23	2.10	0.51
1:B:251:ASN:HD22	1:B:260:THR:HA	1.75	0.51
1:A:53:TRP:CD1	1:A:175:MET:HE1	2.46	0.51
1:A:436:VAL:CG1	1:A:488:SER:HB3	2.41	0.51
1:A:53:TRP:NE1	1:A:175:MET:HE3	2.26	0.51
1:B:425:VAL:HG23	1:B:465:THR:HB	1.93	0.51
1:B:553:ALA:HB2	1:B:583:LYS:HZ2	1.76	0.50
1:B:345:GLY:HA3	1:B:353:ALA:HB1	1.94	0.50
1:A:214:VAL:N	1:A:215:PRO:HD2	2.27	0.50
1:A:214:VAL:HG22	1:A:215:PRO:HD3	1.94	0.50
1:B:74:MET:HE3	1:B:86:GLN:HB2	1.93	0.50
1:A:611:LEU:HD13	1:B:611:LEU:CD2	2.41	0.49
1:B:140:GLY:HA2	1:B:153:ILE:HD12	1.94	0.49
1:A:341:LEU:CD1	1:A:474:ARG:HB3	2.43	0.49
1:B:225:VAL:CG1	1:B:265:VAL:HG22	2.43	0.48
1:B:158:VAL:HB	1:B:166:ALA:HB3	1.95	0.48
1:B:104:LEU:O	1:B:116:VAL:N	2.46	0.48
1:B:210:LYS:HA	1:B:214:VAL:CG1	2.43	0.48
1:B:126:LEU:HD11	1:B:167:VAL:CG1	2.44	0.48
1:A:364:HIS:ND1	1:A:424:SER:OG	2.38	0.48
1:A:251:ASN:HD21	1:A:262:GLY:H	1.62	0.48
1:B:436:VAL:CG1	1:B:488:SER:HB3	2.43	0.48
1:B:330:THR:HG22	1:B:459:SER:HB2	1.95	0.48
1:B:553:ALA:CB	1:B:583:LYS:HZ2	2.27	0.48
1:A:392:TYR:CZ	1:A:395:LEU:HD21	2.49	0.47
1:B:104:LEU:HD21	1:B:151:VAL:HG11	1.95	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:553:ALA:HB1	1:B:583:LYS:NZ	2.29	0.47
1:B:436:VAL:HG11	1:B:488:SER:HB3	1.96	0.47
1:B:229:ASN:HD22	1:B:290:ASP:HB3	1.80	0.47
1:B:538:GLY:HA3	1:B:618:TYR:CE2	2.50	0.47
1:B:482:PRO:HG2	1:B:485:MET:CE	2.45	0.47
1:A:382:SER:HA	1:A:386:ILE:O	2.14	0.47
1:B:43:PHE:HA	1:B:137:GLY:O	2.14	0.46
1:B:110:HIS:O	1:B:111:ALA:HB3	2.15	0.46
1:A:611:LEU:CD1	1:B:611:LEU:HD23	2.44	0.46
1:B:251:ASN:HB2	1:B:266:THR:HG23	1.96	0.46
1:A:358:ALA:HB1	1:A:474:ARG:NH2	2.30	0.46
1:B:95:THR:OG1	1:B:149:HIS:ND1	2.49	0.46
1:A:347:ILE:HD12	1:A:354:ILE:O	2.16	0.45
1:A:358:ALA:HB1	1:A:474:ARG:CZ	2.46	0.45
1:B:553:ALA:CB	1:B:583:LYS:NZ	2.80	0.45
1:A:538:GLY:HA3	1:A:618:TYR:CE2	2.52	0.45
1:A:28:GLN:N	1:A:28:GLN:OE1	2.50	0.45
1:B:398:SER:CA	1:B:400:ILE:HG12	2.47	0.45
1:A:251:ASN:HD22	1:A:261:THR:H	1.65	0.45
1:A:392:TYR:CZ	1:A:395:LEU:CD2	3.00	0.44
1:B:214:VAL:HG23	1:B:218:TYR:CE2	2.53	0.44
1:A:294:SER:HB2	1:A:299:THR:HG21	1.99	0.44
1:A:53:TRP:CD1	1:A:175:MET:CE	3.01	0.43
1:B:553:ALA:HB1	1:B:583:LYS:HZ1	1.83	0.43
1:A:307:LEU:HD13	1:A:519:THR:OG1	2.17	0.43
1:A:613:HIS:CE1	1:A:615:ILE:HG12	2.53	0.43
1:A:53:TRP:CE2	1:A:175:MET:HE3	2.53	0.43
1:A:341:LEU:HD13	1:A:474:ARG:HB3	2.00	0.43
1:A:477:THR:HG22	1:A:479:GLY:N	2.31	0.43
1:A:396:ASP:O	1:A:399:VAL:HG22	2.18	0.43
1:B:187:ASN:ND2	1:B:203:HIS:CE1	2.87	0.43
1:B:514:ARG:HH11	1:B:518:ASN:HD21	1.66	0.43
1:A:421:ASP:HB3	1:A:467:ARG:HD2	2.01	0.43
1:A:74:MET:HE3	1:A:75:TYR:CE2	2.54	0.43
1:B:400:ILE:CB	1:B:401:PRO:HA	2.49	0.43
1:A:397:VAL:O	1:A:398:SER:OG	2.34	0.43
1:B:63:THR:HG22	1:B:72:THR:HA	2.00	0.43
1:B:396:ASP:O	1:B:399:VAL:HG22	2.19	0.42
1:A:197:PHE:HA	1:A:316:ARG:O	2.20	0.42
1:A:194:PRO:HG3	1:A:198:GLN:HB2	2.01	0.42
1:A:263:ALA:HB1	1:A:264:PRO:HD2	2.00	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:VAL:HG22	1:B:215:PRO:HD3	2.02	0.42
1:A:324:THR:HB	1:A:456:VAL:HG22	2.01	0.42
1:B:157:ALA:HB3	1:B:629:VAL:HG23	2.01	0.42
1:B:24:ARG:NH2	1:B:68:LYS:O	2.53	0.42
1:B:415:MET:HA	1:B:464:ARG:NH2	2.35	0.42
1:A:211:SER:OG	1:A:290:ASP:OD2	2.35	0.42
1:A:43:PHE:HA	1:A:137:GLY:O	2.20	0.42
1:B:341:LEU:HD23	3:B:2055:HOH:O	2.20	0.42
1:A:291:GLU:HA	1:A:291:GLU:OE1	2.21	0.41
1:A:402:THR:HG23	1:A:403:ILE:CG1	2.50	0.41
1:A:244:LYS:HG3	1:A:245:ALA:N	2.36	0.41
1:A:126:LEU:HD11	1:A:167:VAL:HG13	2.01	0.41
1:A:365:LEU:HD21	1:A:367:PHE:CZ	2.55	0.41
1:B:105:TYR:HB3	1:B:113:VAL:HG12	2.02	0.41
1:A:243:SER:HA	1:A:248:ILE:O	2.21	0.41
1:A:183:VAL:HG23	3:A:2037:HOH:O	2.19	0.41
1:A:88:PRO:CB	1:A:89:PRO:HD2	2.50	0.41
1:A:455:ALA:HB3	1:A:483:SER:HB3	2.03	0.41
1:A:51:VAL:HG23	1:A:179:MET:CE	2.50	0.41
1:A:251:ASN:O	1:A:252:ILE:HD13	2.21	0.41
1:A:324:THR:HG21	1:A:459:SER:OG	2.21	0.40
1:A:422:PHE:O	1:A:465:THR:OG1	2.34	0.40
1:B:55:VAL:HG21	1:B:139:SER:HB3	2.03	0.40
1:A:123:ARG:NE	1:A:168:ASP:OD1	2.49	0.40
1:A:191:PRO:HG3	1:A:200:ALA:CB	2.52	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	643/666 (96%)	606 (94%)	32 (5%)	5 (1%)	24 41

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	638/666 (96%)	612 (96%)	22 (3%)	4 (1%)	30	50
All	All	1281/1332 (96%)	1218 (95%)	54 (4%)	9 (1%)	26	46

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	246	HIS
1	A	403	ILE
1	B	400	ILE
1	A	404	GLY
1	A	245	ALA
1	B	402	THR
1	B	469	ARG
1	B	584	CYS
1	A	100	GLY

### 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	526/544 (97%)	490 (93%)	36 (7%)	20	36
1	B	525/544 (96%)	505 (96%)	20 (4%)	40	67
All	All	1051/1088 (97%)	995 (95%)	56 (5%)	28	50

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	712	ARG
1	A	11	ARG
1	A	37	SER
1	A	68	LYS
1	A	80	GLN
1	A	98	THR
1	A	104	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	109	ARG
1	A	125	SER
1	A	126	LEU
1	A	147	SER
1	A	168	ASP
1	A	176	GLU
1	A	185	THR
1	A	195	GLN
1	A	210	LYS
1	A	211	SER
1	A	214	VAL
1	A	224	LYS
1	A	232	VAL
1	A	249	ASP
1	A	280	SER
1	A	360	ARG
1	A	380	LYS
1	A	384	LEU
1	A	395	LEU
1	A	397	VAL
1	A	402	THR
1	A	419	THR
1	A	459	SER
1	A	469	ARG
1	A	470	ARG
1	A	580	GLN
1	A	588	LEU
1	A	600	TYR
1	A	608	GLU
1	B	21	LEU
1	B	40	THR
1	B	102	SER
1	B	143	LEU
1	B	159	CYS
1	B	165	LYS
1	B	168	ASP
1	B	214	VAL
1	B	312	THR
1	B	384	LEU
1	B	395	LEU
1	B	397	VAL
1	B	416	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	431	CYS
1	B	448	THR
1	B	459	SER
1	B	518	ASN
1	B	548	SER
1	B	600	TYR
1	B	630	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	195	GLN
1	A	251	ASN
1	A	541	HIS
1	A	606	GLN
1	B	27	ASN
1	B	187	ASN
1	B	229	ASN
1	B	251	ASN
1	B	293	HIS
1	B	518	ASN

### 5.3.3 RNA [i](#)

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](#)

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	4VA	A	1721	-	24,26,26	0.86	1 (4%)	25,35,35	0.85	2 (8%)
2	4VA	B	1721	-	25,26,26	0.70	1 (4%)	30,35,35	0.86	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4VA	A	1721	-	-	0/18/18/18	0/2/2/2
2	4VA	B	1721	-	-	0/18/18/18	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1721	4VA	C15-C28	2.15	1.41	1.38
2	A	1721	4VA	C3-N5	2.51	1.51	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1721	4VA	C20-C18-CL	2.05	120.95	118.43
2	B	1721	4VA	C20-C18-CL	2.46	121.45	118.43
2	B	1721	4VA	C22-O21-C20	2.82	123.38	118.46
2	A	1721	4VA	C22-O21-C20	2.88	123.48	118.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [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	645/666 (96%)	0.08	10 (1%) 74 78	24, 47, 84, 121	0
1	B	642/666 (96%)	0.08	9 (1%) 78 80	30, 50, 80, 121	0
All	All	1287/1332 (96%)	0.08	19 (1%) 76 79	24, 49, 82, 121	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	98	THR	6.1
1	A	99	CYS	5.6
1	B	239	GLY	3.8
1	B	631	THR	3.4
1	A	388	ALA	3.3
1	B	184	PHE	3.2
1	B	183	VAL	2.9
1	A	631	THR	2.8
1	A	407	VAL	2.7
1	A	406	VAL	2.6
1	B	206	THR	2.5
1	A	100	GLY	2.4
1	B	265	VAL	2.2
1	B	99	CYS	2.2
1	A	185	THR	2.2
1	A	359	ILE	2.2
1	B	100	GLY	2.1
1	A	385	GLY	2.1
1	B	587	ARG	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	4VA	A	1721	25/25	0.96	0.20	2.65	22,24,30,47	48
2	4VA	B	1721	25/25	0.96	0.24	2.48	30,33,36,61	48

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

There are no such residues in this entry.