



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 15, 2017 – 09:13 AM EDT

PDB ID : 2QQP  
Title : Crystal Structure of Authentic Providence Virus  
Authors : Speir, J.A.; Taylor, D.J.; Johnson, J.E.  
Deposited on : unknown  
Resolution : 3.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

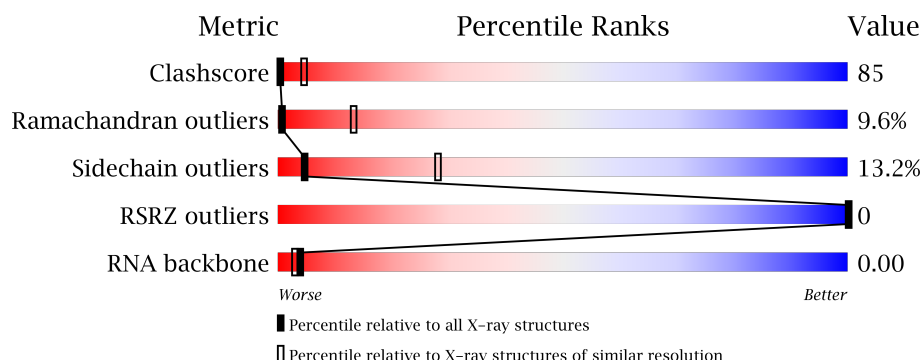
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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.






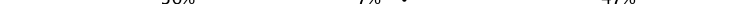
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1030 (4.04-3.56)
Ramachandran outliers	110173	1011 (4.06-3.54)
Sidechain outliers	110143	1005 (4.06-3.54)
RSRZ outliers	101464	1032 (4.08-3.52)
RNA backbone	2435	1016 (4.70-2.90)

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	556	
1	C	556	
1	E	556	
1	G	556	
2	B	75	

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Mol	Chain	Length	Quality of chain
2	D	75	
2	F	75	
2	H	75	
3	R	4	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 16634 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 Large Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3714	2359	604	740	11			
1	C	484	Total	C	N	O	S	0	0	0
			3714	2359	604	740	11			
1	E	517	Total	C	N	O	S	0	0	0
			3948	2505	645	785	13			
1	G	518	Total	C	N	O	S	0	0	0
			3957	2510	646	788	13			

- Molecule 2 is a protein called Small capsid protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	39	Total	C	N	O	0	0	0
			255	162	44	49			
2	D	40	Total	C	N	O	0	0	0
			263	166	46	51			
2	F	67	Total	C	N	O	0	0	0
			448	282	84	82			
2	H	38	Total	C	N	O	0	0	0
			250	159	43	48			

- Molecule 3 is a RNA chain called RNA (5'-R(\*UP\*UP\*UP\*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	R	4	Total	C	N	O	P	0	0	0
			77	36	8	30	3			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0

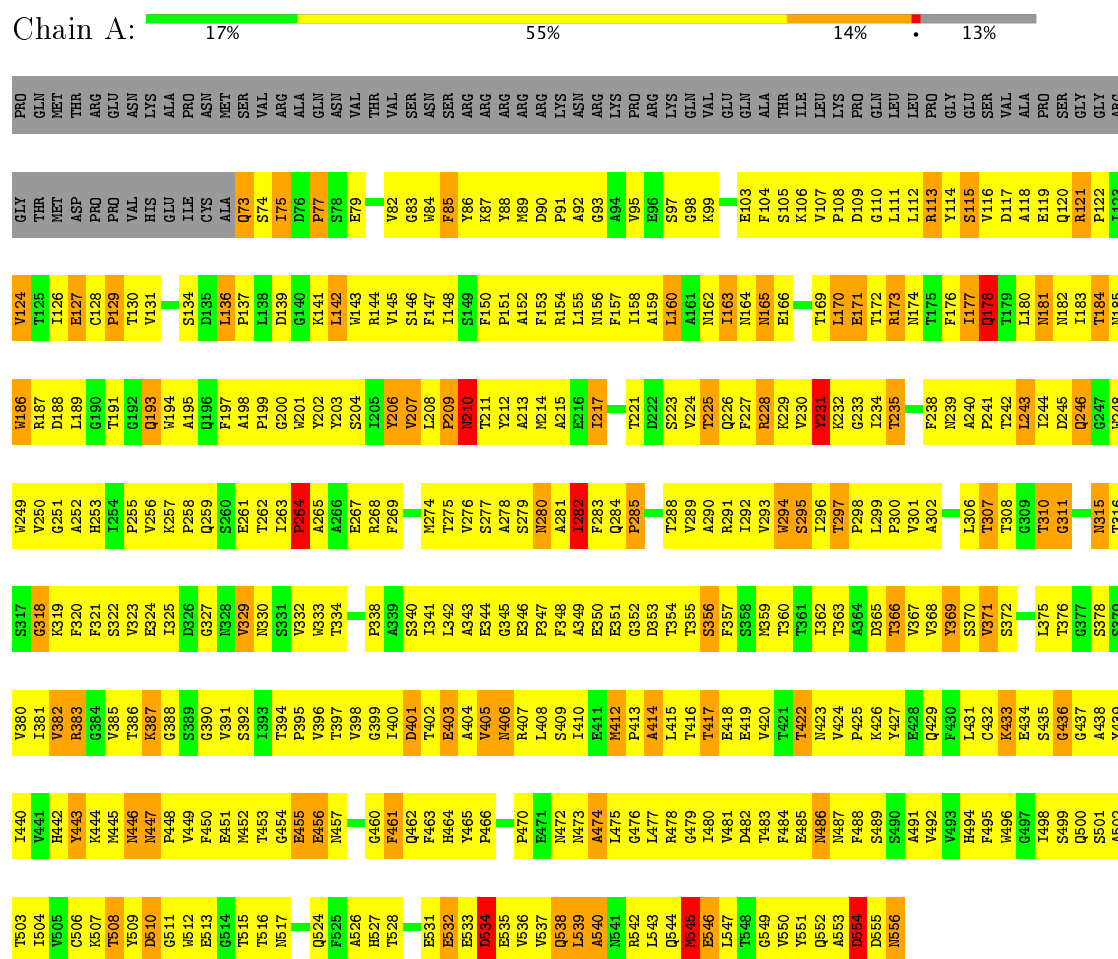
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	O 1	0	0
5	C	2	Total 2	O 2	0	0
5	E	2	Total 2	O 2	0	0
5	G	1	Total 1	O 1	0	0

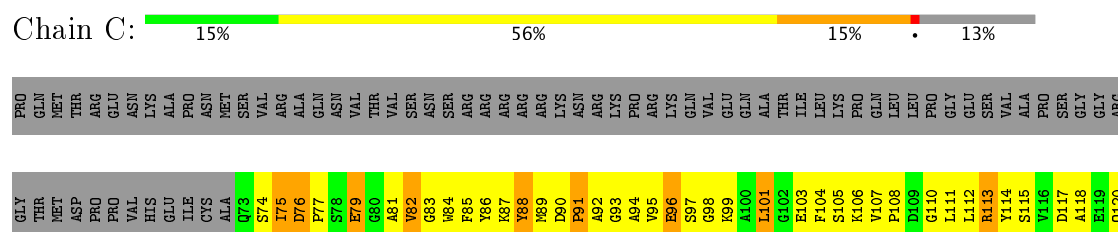
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Large Capsid protein



#### • Molecule 1: Large Capsid protein



N556	F495	S435	V371	L306	D245	N181	N121
	W496	G436	S372		Q246	M182	P122
	G497	G437	S373	T310	Q247	M183	I123
	T498	A438	S374	G311	W248	T184	N124
	S499	ARG	L375	G312	Y249	M185	T125
	Q500	I430	T376	G313	W250	W186	I126
	S501	ASN	G377	N314	Q251	M187	E127
	W502	LYS		N315	A252	D188	P128
	T503	ALA		T316	H253	L189	P129
	Q504	PRO	I381	G317	I254	G190	T130
	W505	ASN	V382	G318	P255	T191	V131
	C506	MET	R383	K319	V256	G192	S132
	W507	SER	G384	K320	K257	Q193	S133
	T508	VAL	V385	F321	P258	W194	S134
	Y509	ARG	V386	S322	S259	A195	D135
	D510	ALA	K387	V323	S260	Q196	L136
	G511	GLN		G324	E261	F197	P137
	E513	VAL	V391	I325	T262	A198	L138
	Q514	THR	S392	D326	T263	P199	D139
	T515	VAL	I393	G327	P264	G200	G140
	W516	SER	T394		A265	W201	L141
	N517	ASN	V395	V329	A266	Y202	L142
	S520	SER	V396		E267	Y203	W143
	T521	ARG	T397	V332	R268	S204	R144
	V522	ARG	V398	W333	V269	I205	V145
	G523	ARG	G399	T334	S270	Y206	S146
	Q524	ARG	I400	F335	A271	V207	F147
	A525	ARG	D401	T336	G272	L208	I148
	N526	LYS	T402	S337	S273	P209	S149
	W527	ASN	E403	P338	N274	N210	F150
	H528	ASN	A404	A339	T275	T211	P151
	T529	ARG	W405	S340	V276	Y212	A152
	G529	PRO	I406	I341	S277	A213	F153
	E530	ARG	R407	L342	A278	M214	R154
	E531	LYS			S279	A215	L155
	E532	GLN	I410	E346			N156
	E533	VAL	E411	P347	I282	G218	F157
	D534	GLU	N412	F348	F283		I158
	E535	Q40	P413	A349	Q284	D222	A159
	V536	A41	A414	E350	P285		
	W537	T42	L415	E351	S286	T225	A161
	Q538	T43	T416	G352	N287	Q226	N162
	L539	L44	T417	D353	T288	P227	I163
	A540		E418	T354	V289	R228	N164
	N541		E419	T355	A290	K229	N165
	N542	L48	V420	S356	R291	V230	E166
	L543	L49	T421	F357	I292	Y231	A167
	Q544	P50	T422	N423	V293	K232	L168
	N545	G51	N423	N359	Y294	G233	T169
	E546	E52	V424	T360	S295	I234	L170
	S547	S53	P425	T361	I296	T235	E171
	L547	V54	F426	I362	T297	P336	T172
	T548	A55	N466	T363	P298	E237	R173
	G549	P56	N467	Y427	L299	F238	N174
	W550	S57	E468	E428	Q429	N239	T175
	V551	G58	S469	S469	F430	V301	F176
	Q552	G59	A491	A491	A302	A240	P241
	A553	R60	V492	V492	T303	T242	L177
	D554	G61	V493	V493	V369	T243	T178
	D555	T62	H494	H494	S370	I244	T179

• Molecule 1: Large Capsid protein

Chain E: 

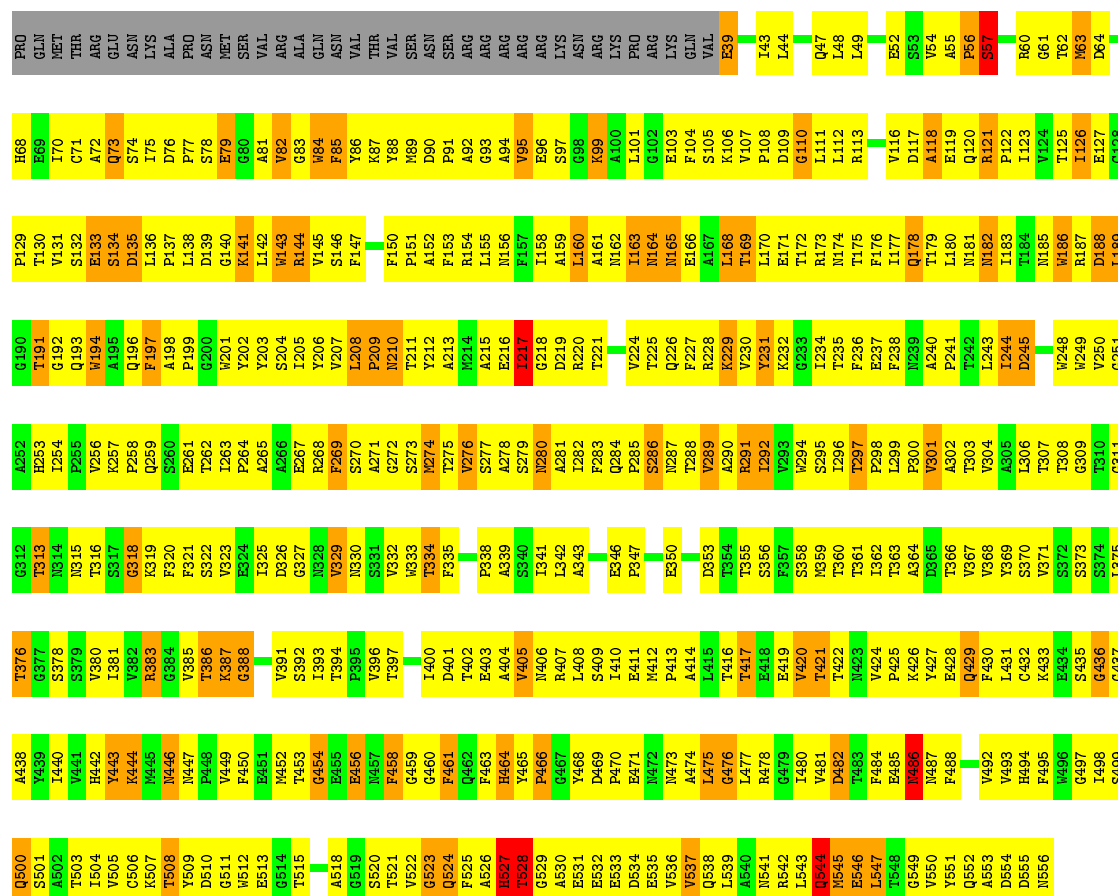
18%63%12%7%

PRO	M63	V124	R187	G247	G312	V380	V441
GLN	D64	T125	D188	W248	T313	I381	H442
MET	P65	I126	L189	W249	N314	V382	Y443
THR	P66	E127	G190	V250	N315		K444
ARG	H68	G128	T191	Q251	S317	T366	M445
GLU	E69	P129	G192	A252	G318	K387	M446
ASN	E70	T130	Q193	H253	F319	G388	M447
LYS	C71	V312	W194	I254	P320	S389	P448
ALA	Q73	S134		T255	F320	G390	V449
PRO				Q196	A72	V391	F450
GLN	D76	D139	G140	P258	V323	S392	M452
ASN	P77	G140	K141	S260	G324	I393	T453
VAL	E78	K141	W201	E261	V329	T394	G454
ARG	E79	L142	Y202	T262	N330	P395	E455
ALA	G80	W143	Y203		N331	T397	M457
GLN	V82	V145	S204	A265	V332	V398	F459
VAL	G83	S146	I205	A266	W333	G399	G459
THR	H84	F147	Y206	E267	T334	I400	G460
SER	F85	T148	V207		F335	D401	F461
ASN	Y86	S149	L208	S270	T336	T402	Q462
SER	K87	P209	P209	A271	A337	E403	H464
ARG	Y88	F150	N210	G272	W404	G404	H464
ARG	M89	P151	T211	S273	Y405	V405	V465
ARG	D90	A152	Y212	M274	P338	N406	P466
ARG	P91	F153	A213	T275	T341	R407	G467
ARG	G92	M154	M214	V276	L342	Y468	Y468
ARG	A93	L155	A215	S277	A343	S409	D469
LYS	N94	M156	E216	A278	E344	P470	P470
ASN	A94	F157	T217			E411	E471
ASN	V95	I158	G218	F283	F348	M412	M472
ARG	E96	A159	D219	Q284	A349	P413	M473
PRO	S97	L160	R220	P285	E350	A414	A474
ARG	G98	A161	T221	S286	L415	L415	A475
LYS	K99	M162	D222	N287	G352	T416	G476
GLN	A100	I163	S223	T288	D353	T417	L477
VAL	L101	M164	Y224	V289	T354	E418	R478
GLU	G102	M165	T225	A290	S355	E419	G479
		E166	Q226	R291	S356	A426	N486
		A167	F227	I292	F357	Y427	N487
		T168	R228	V293	S358	E428	F488
		T169	K229	W294	N359	Q429	S489
		V107	V230	S295	T360	F430	S490
		P108	Y231	I296	T361	F435	F484
		T172	K232	T297	I362	L431	E485
		R173	G233	P298	T363	C432	N486
		N174	I234	L299	A364	V420	N487
		T175	T235	P300	D365	Y427	F488
		F176	V236	V301	T366	Q429	D482
		I177	E237	A302	V367	F430	T483
		Q178	F238	T303	V368	L431	F484
		V116	M239	V304	Y369	C432	E485
		D117	L180	A305	S370	F433	N486
		A118	P241	L306	V371	E434	F488
		N182	T242	T307	G372	S435	S489
		I183	L243	T308	S373	G436	N496
		T184	I244	G309	L375	G437	G497
		M185	D245	T310		E438	I498
		G123	Q246	G311		S499	S499



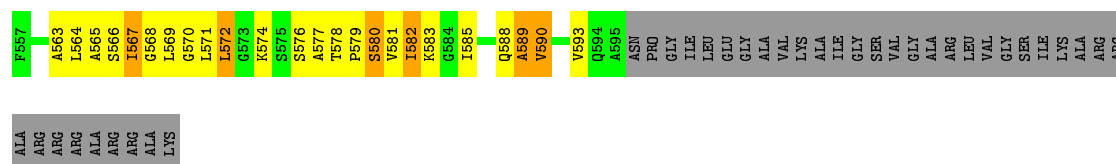
• Molecule 1: Large Capsid protein

Chain G: 18% 58% 15% 7%



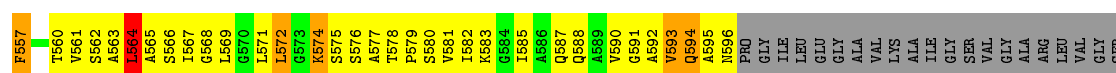
• Molecule 2: Small capsid protein

Chain B: 20% 24% 8% 48%



• Molecule 2: Small capsid protein

Chain D: 9% 36% 7% 47%





U1	U2	U3	U4
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	659.79Å 434.07Å 415.85Å 90.00° 126.13° 90.00°	Depositor
Resolution (Å)	49.42 – 3.80 50.01 – 3.80	Depositor EDS
% Data completeness (in resolution range)	28.6 (49.42-3.80) 28.6 (50.01-3.80)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 3.77Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.285 , (Not available) (Not available) , (Not available)	Depositor DCC
$R_{free}$ test set	NotAvailable	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 34.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.059 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.74	EDS
Total number of atoms	16634	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.81% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.54	0/3807	0.78	0/5203
1	C	0.53	0/3807	0.78	0/5203
1	E	0.55	0/4047	0.78	0/5532
1	G	0.52	0/4056	0.79	0/5544
2	B	0.60	0/256	0.72	0/346
2	D	0.55	0/264	0.83	0/357
2	F	0.58	0/450	0.85	0/606
2	H	0.51	0/251	0.74	0/339
3	R	1.57	0/84	0.91	0/128
All	All	0.55	0/17022	0.78	0/23258

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	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	TYR	Sidechain
1	C	206	TYR	Sidechain

## 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	3714	0	3548	661	0
1	C	3714	0	3548	689	0
1	E	3948	0	3786	744	0
1	G	3957	0	3792	703	0
2	B	255	0	275	40	0
2	D	263	0	281	66	0
2	F	448	0	491	90	0
2	H	250	0	270	47	0
3	R	77	0	42	4	0
4	A	1	0	0	0	0
4	G	1	0	0	0	0
5	A	1	0	0	0	0
5	C	2	0	0	0	0
5	E	2	0	0	0	0
5	G	1	0	0	0	0
All	All	16634	0	16033	2780	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 85.

The worst 5 of 2780 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:C:475:LEU:HD11	1:E:267:GLU:CG	1.36	1.52
1:C:297:THR:HG23	1:C:476:GLY:CA	1.55	1.35
1:C:120:GLN:NE2	1:C:208:LEU:HB3	1.45	1.29
1:E:297:THR:HG22	1:E:298:PRO:CD	1.64	1.27
1:C:475:LEU:HD11	1:E:267:GLU:CB	1.68	1.21

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	482/556 (87%)	357 (74%)	80 (17%)	45 (9%)	1	14
1	C	482/556 (87%)	358 (74%)	74 (15%)	50 (10%)	0	11
1	E	515/556 (93%)	379 (74%)	95 (18%)	41 (8%)	1	18
1	G	516/556 (93%)	373 (72%)	87 (17%)	56 (11%)	0	10
2	B	37/75 (49%)	21 (57%)	12 (32%)	4 (11%)	0	10
2	D	38/75 (51%)	30 (79%)	6 (16%)	2 (5%)	2	29
2	F	65/75 (87%)	47 (72%)	12 (18%)	6 (9%)	1	15
2	H	36/75 (48%)	16 (44%)	16 (44%)	4 (11%)	0	9
All	All	2171/2524 (86%)	1581 (73%)	382 (18%)	208 (10%)	1	13

5 of 208 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	PRO
1	A	297	THR
1	A	318	GLY
1	A	405	VAL
1	A	455	GLU

### 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	403/466 (86%)	339 (84%)	64 (16%)	3	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	403/466 (86%)	348 (86%)	55 (14%)	4	27
1	E	429/466 (92%)	385 (90%)	44 (10%)	8	38
1	G	430/466 (92%)	376 (87%)	54 (13%)	5	29
2	B	25/49 (51%)	22 (88%)	3 (12%)	6	31
2	D	26/49 (53%)	21 (81%)	5 (19%)	1	12
2	F	43/49 (88%)	36 (84%)	7 (16%)	3	20
2	H	25/49 (51%)	21 (84%)	4 (16%)	3	20
All	All	1784/2060 (87%)	1548 (87%)	236 (13%)	5	28

5 of 236 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	405	VAL
1	E	124	VAL
1	G	456	GLU
1	C	453	THR
1	C	548	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	181	ASN
1	G	120	GLN
1	C	464	HIS
1	C	120	GLN
1	C	462	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	R	3/4 (75%)	3 (100%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	R	2	U
3	R	3	U

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Mol	Chain	Res	Type
3	R	4	U

There are no RNA pucker outliers to report.

## 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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	484/556 (87%)	-0.69	0 100 100	7, 20, 30, 48	0
1	C	484/556 (87%)	-0.72	0 100 100	8, 19, 30, 43	0
1	E	517/556 (92%)	-0.71	0 100 100	7, 21, 33, 52	0
1	G	518/556 (93%)	-0.83	0 100 100	7, 20, 31, 53	0
2	B	39/75 (52%)	-0.66	0 100 100	10, 20, 36, 40	0
2	D	40/75 (53%)	-0.65	0 100 100	10, 21, 35, 40	0
2	F	67/75 (89%)	-0.64	0 100 100	13, 20, 35, 39	0
2	H	38/75 (50%)	-0.58	0 100 100	11, 18, 29, 38	0
3	R	4/4 (100%)	0.85	0 100 100	54, 56, 57, 61	0
All	All	2191/2528 (86%)	-0.73	0 100 100	7, 20, 32, 61	0

There are no RSRZ outliers to report.

### 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](#)

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
4	CA	A	557	1/1	0.97	0.17	0.53	44,44,44,44	0
4	CA	G	557	1/1	0.98	0.06	-	73,73,73,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.