



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:27 AM GMT

PDB ID : 2QQP  
Title : Crystal Structure of Authentic Providence Virus  
Authors : Speir, J.A.; Taylor, D.J.; Johnson, J.E.  
Deposited on : 2007-07-26  
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  
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

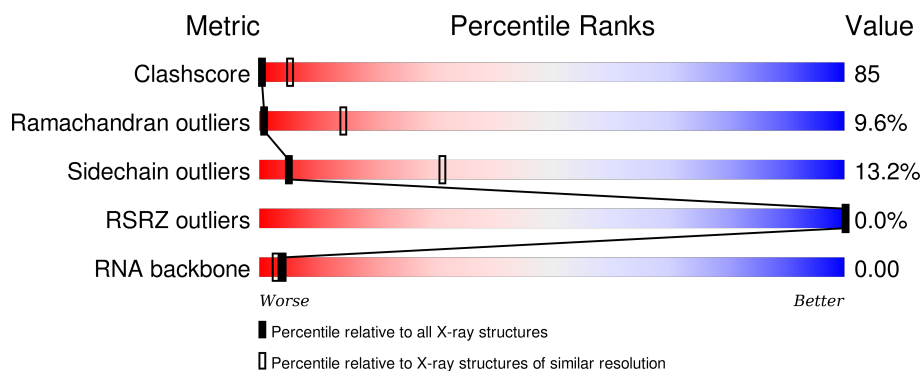
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)
RNA backbone	2183	1070 (4.76-2.80)

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	<div><div></div><div></div><div></div><div></div></div> <div>9%36%7%47%</div>
2	F	75	<div><div></div><div></div><div></div><div></div></div> <div>16%60%13%11%</div>
2	H	75	<div><div></div><div></div><div></div><div></div></div> <div>9%33%7%49%</div>
3	R	4	<div><div></div><div></div></div> <div>25%75%</div>

## 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	Ca	0	0
			1	1		

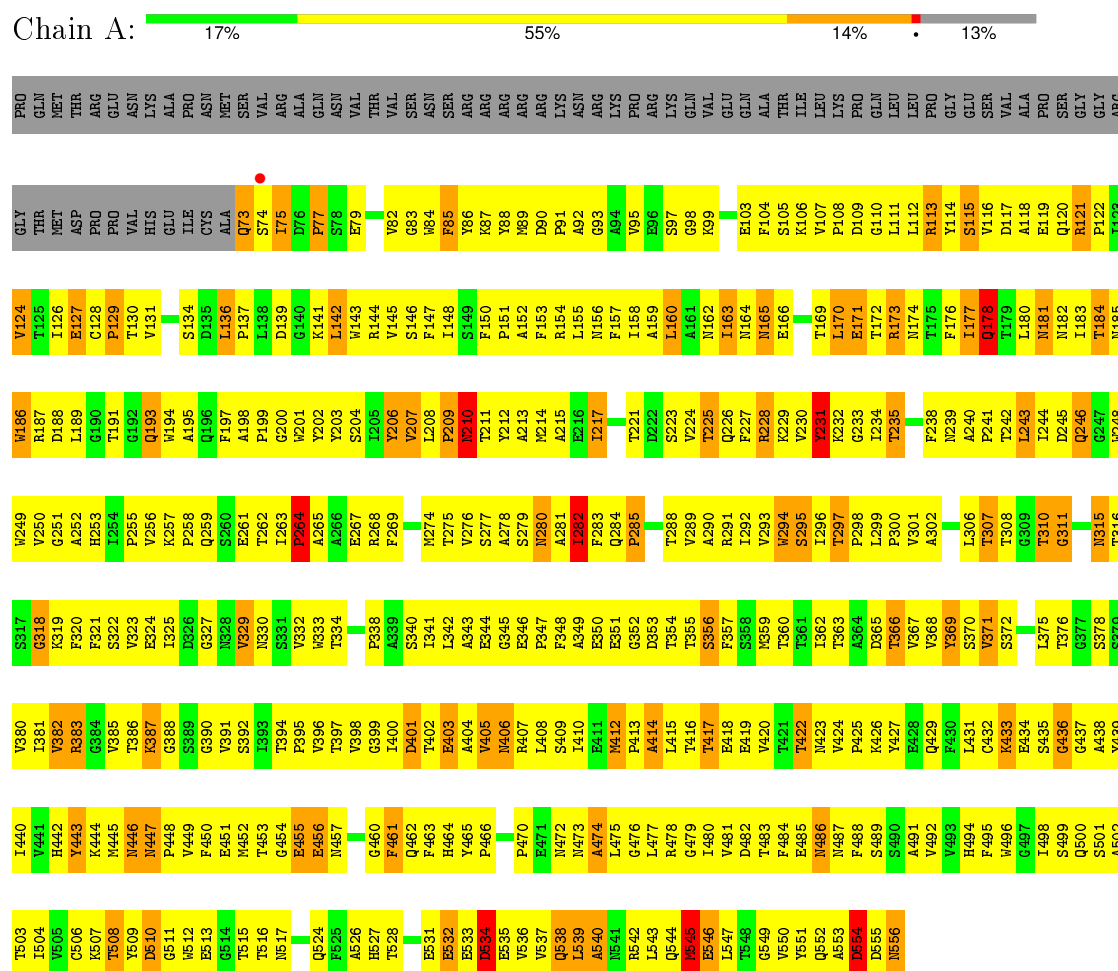
- Molecule 5 is water.

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

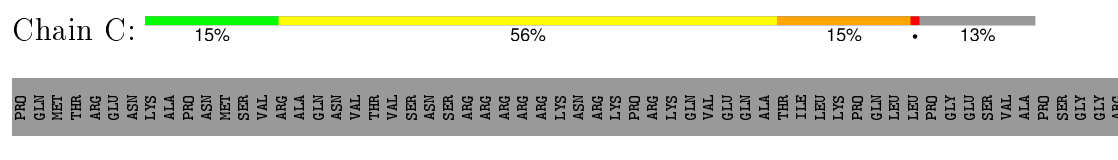
### 3 Residue-property plots

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: Large Capsid protein



#### • Molecule 1: Large Capsid protein

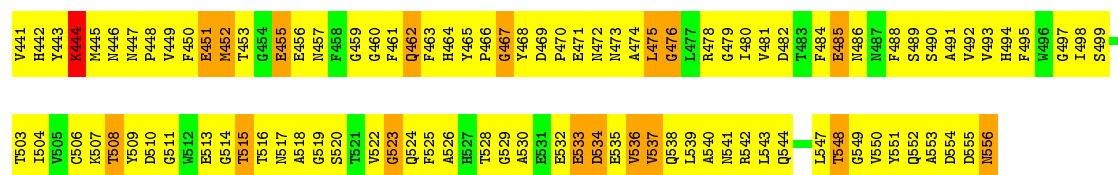


GLY	R121	R181	D245	L306	V371	S435	F495	N556	F495	N556
THR	P122	N182	Q246	L310	S372	G436	W496		W496	
MET	I123	I183	G247	T310	S373	G497	G497		G497	
ASP	I124	I184	W248	G311	S374	A438	A438		A438	
PRO	T125	N185	W249	G312	S375	Y439	S499		S499	
PRO	I126	N186	V250	T313	T376	I440	Q500		Q500	
VAL	E127	R187	G251	T314	G377	W441	S501		S501	
HIS	C128	D188	A252	N315	S378	H442	W442		W442	
GLU	P129	L189	H253	T316		Y443	T503		T503	
ILE	T130	G190	I254	S317	I381	K444	F504		F504	
CYS	I131	T191	P255	G318	V382	W445	V505		V505	
ALA	S132	G192	V256	T319	R363	N446	C506		C506	
ALA	E133	Q193	K257	F320	G384	N447	S507		S507	
S74	S134	W194	F258	F321	V385	P448	T508		T508	
I75	D135	A195	Q259	V322	K387	V449	F509		F509	
D76	L136	Q196	S260	V323	K387	F450	W510		W510	
P77	P137	F197	E261	G324	V391	E451	G511		G511	
S78	L138	A198	T262	T325	S392	W453	E512		E512	
E79	D139	P199	I263	G327	I393	G454	E513		E513	
G80	G140	G200	P264		V394	G455	G514		G514	
A81	K141	W201	A265	R328	P395	E456	T515		T515	
W82	L142	Y202	A266	V329	V396	N457	N517		N517	
G83	W143	Y203	E267		T397	F458	S520		S520	
W84	R144	S204	R268	V332	V397	G459	T521		T521	
F85	V145	T205	F269	R333	V398	G460	V522		V522	
H86	S146	Y206	S270	T334	G399	F461	G523		G523	
R87	F147	Y207	A271	F335	I400	Q462	G524		G524	
Y88	L148	L208	G272	T336	D401	F463	F525		F525	
N89	S149	P209	S273	A337	T402	W464	W526		W526	
D90	F150	N210	R274	P338	E403	A465	H527		H527	
P91	P151	T211	T275	A339	A404	Y466	L528		L528	
A92	A152	Y212	V276	G340	W405	G467	G529		G529	
G93	F153	A213	S277	L341	N406	L468	E531		E531	
A94	R154	N214	A278	L342	R407	D469	E532		E532	
V95	L155	A215	S279		I410	P470	E533		E533	
E96	N156			E346	E411	E471	D534		D534	
S97	F157	G218	I282	P347	M412	M472	E535		E535	
G98	L158		F283	F348	P413	W473	V536		V536	
K99	A159	D222	Q284	E350	A414	L474	V537		V537	
A100	A161	T225	S286	E351	T416	G476	Q538		Q538	
L101	M162	Q226	N287	G352	T417	L477	L539		L539	
E103	I163	F227	T288	D353	E418	R478	A540		A540	
F104	M164	R228	V289	T354	E419	G479	N541		N541	
S105	M165	K229	R291	T355	V420	L480	R542		R542	
K106	E166	Y230	I292	S356	T421	W481	L543		L543	
P107	A167	Y231	V293	S358	T422	D482	Q544		Q544	
P108	L168	K232	W294	N359	N423	T483	M545		M545	
D109	T169	G233	E294	T360	V424	F484	E546		E546	
G110	L170	I234	S295	T361	P425	E486	L547		L547	
L111	E171	T235	I296	T362	R426	W487	T548		T548	
L112	T172	F236	T297	A363	Y427	F488	G549		G549	
R113	R173	E237	P298	A364	E428	S489	V551		V551	
Y114	N174	F238	L299	D365	Q429	S490	Q552		Q552	
S115	T175	P300	P300	T366	F430	A491	A553		A553	
W116	F176	V301	A302	V367	L431	V492	D555		D555	
D117	I177	P241	A302	V367	C432	V493				
E118	Q178	T242	T303	V368	K433					
A119	T179	T243	V304	V369	E434					
Q120	L180	T244	A305	S370	E434					

• Molecule 1: Large Capsid protein

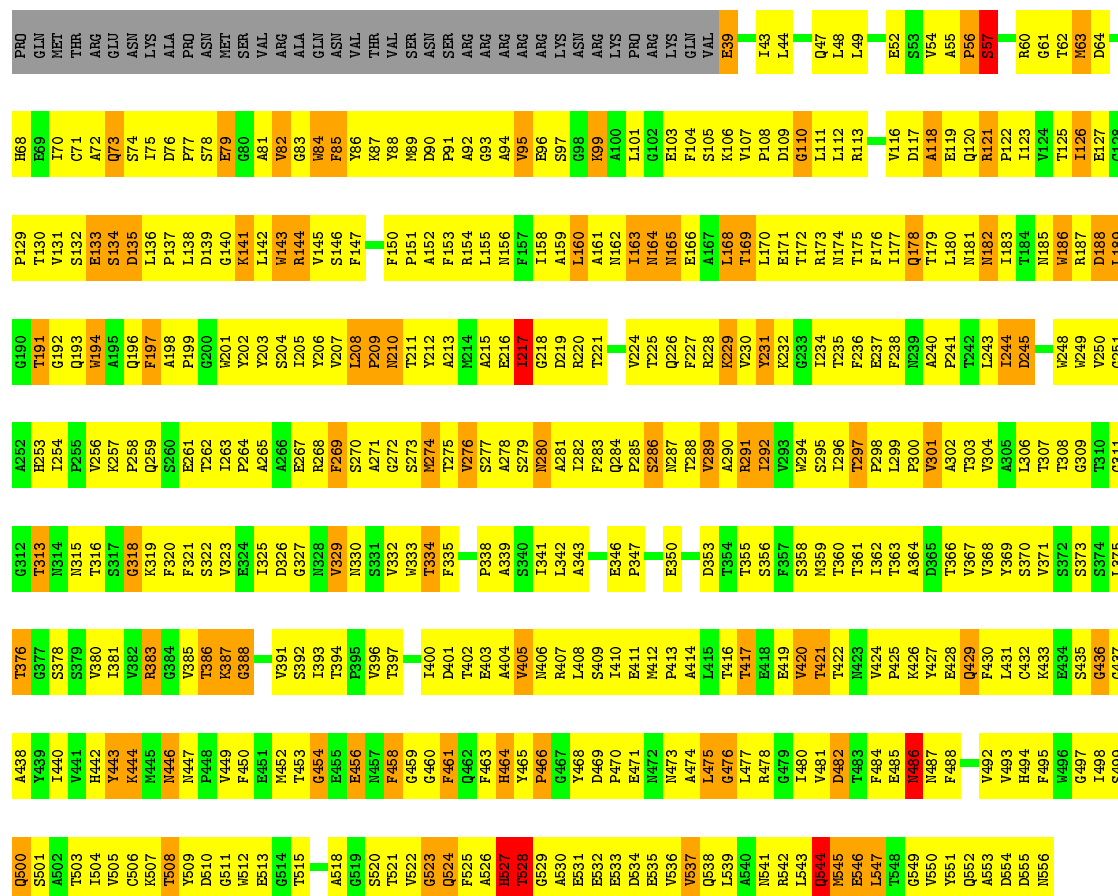
Chain E: 18% 63% 12% 7%

PRO	GLN	P63	Y124	R187	G247	G312	V380
GLN	D64	D64	T125	D188	W248	T313	I381
MET	P65	P65	I126	L189	W249	T314	V382
THR	P66	P66	E127	G190	W250	N315	
G191	V67	V67	G128	T191	G251	T316	V385
GLU	H68	H68	P129	G129	A252	G318	T386
ASN	R69	R69	T130	Q193	H253	R319	K387
LYS	T70	T70	V131	W194	I254	G319	G388
ALA	C71	C71	S132	A195	P255	F320	S389
ALA	Q73	Q73	S134	F197	V256	F321	G390
				G196	K257	S322	V391
				A198	P258	V323	S392
				P199	Q259	E324	I393
				G200	S260	I325	T394
				W201	E261	V329	P395
				Y202	T262	H330	V396
				T203	A265	S331	T397
				S204	A266	V332	V398
				T205	E267	W333	I400
				I206		T334	D401
				V207		F335	T402
				L208	S270	T336	E403
				P209	A271	A337	A404
				N210	G272	A404	W405
				T211	S273	V405	M406
				Y212	K274		
				A213	T275		
				N214	V276		
				A215	S277		
				E216	A278		
				T217			
				G218	F283		
				D219	Q284		
				R220	P285		
				T221	S286		
				D222	N287		
				S223	T288		
				Y224	V289		
				T225	A290		
				Q226	R291		
				F227	I292		
				K228	V293		
				K229	W294		
				V230	S295		
				Y231	I296		
				K232	T297		
				G233	P298		
				I234	L299		
				T235	P300		
				F236	V301		
				E237	A302		
				F238	T303		
				N239	V304		
				A240	A305		
				P241	T306		
				T242	N307		
				L243	T308		
				I244	G309		
				D245	S374		
				Q246	L375		
					G311		



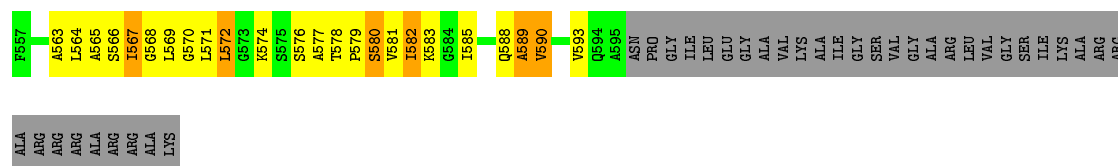
• Molecule 1: Large Capsid protein

Chain G: 18% 58% 15% 7%



• Molecule 2: Small capsid protein

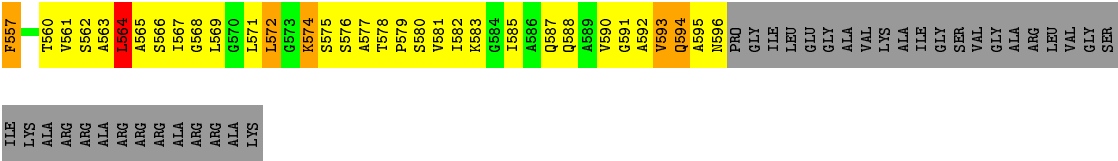
Chain B: 20% 24% 8% 48%



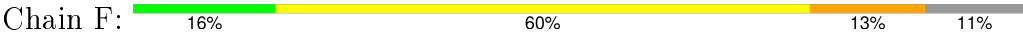
• Molecule 2: Small capsid protein

Chain D: 9% 36% 7% 47%

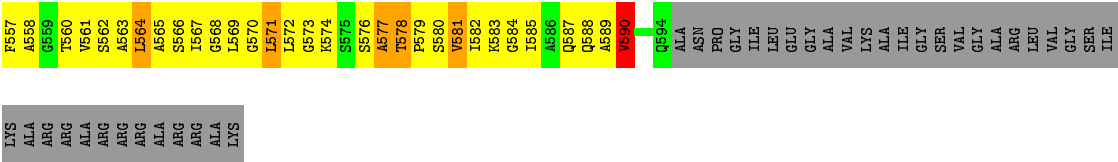




• Molecule 2: Small capsid protein



• Molecule 2: Small capsid protein



• Molecule 3: RNA (5'-R(\*UP\*UP\*UP\*U)-3')



## 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) 26.5 (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 1.2	Depositor
R, $R_{free}$	0.285 , (Not available) 0.265 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	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> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.059 for -h-2*k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	1 of 272211 reflections (0.000%)	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, 0.375 respectively for untwinned datasets, and 0.333, 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 [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	482/556 (87%)	357 (74%)	80 (17%)	45 (9%)	1	15
1	C	482/556 (87%)	358 (74%)	74 (15%)	50 (10%)	1	12
1	E	515/556 (93%)	379 (74%)	95 (18%)	41 (8%)	1	19
1	G	516/556 (93%)	373 (72%)	87 (17%)	56 (11%)	0	11
2	B	37/75 (49%)	21 (57%)	12 (32%)	4 (11%)	0	11
2	D	38/75 (51%)	30 (79%)	6 (16%)	2 (5%)	2	30
2	F	65/75 (87%)	47 (72%)	12 (18%)	6 (9%)	1	16
2	H	36/75 (48%)	16 (44%)	16 (44%)	4 (11%)	0	10
All	All	2171/2524 (86%)	1581 (73%)	382 (18%)	208 (10%)	1	14

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 [i](#)

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	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	403/466 (86%)	348 (86%)	55 (14%)	5	30
1	E	429/466 (92%)	385 (90%)	44 (10%)	9	42
1	G	430/466 (92%)	376 (87%)	54 (13%)	5	32
2	B	25/49 (51%)	22 (88%)	3 (12%)	6	34
2	D	26/49 (53%)	21 (81%)	5 (19%)	2	13
2	F	43/49 (88%)	36 (84%)	7 (16%)	3	21
2	H	25/49 (51%)	21 (84%)	4 (16%)	3	22
All	All	1784/2060 (87%)	1548 (87%)	236 (13%)	5	31

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

*Continued on next page...*

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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 ⓘ

### 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	484/556 (87%)	-0.27	1 (0%) 95 91	7, 20, 30, 48	0
1	C	484/556 (87%)	-0.27	0 100 100	8, 19, 30, 43	0
1	E	517/556 (92%)	-0.28	0 100 100	7, 21, 33, 52	0
1	G	518/556 (93%)	-0.28	0 100 100	7, 20, 31, 53	0
2	B	39/75 (52%)	-0.21	0 100 100	10, 20, 36, 40	0
2	D	40/75 (53%)	-0.26	0 100 100	10, 21, 35, 40	0
2	F	67/75 (89%)	-0.16	0 100 100	13, 20, 35, 39	0
2	H	38/75 (50%)	-0.35	0 100 100	11, 18, 29, 38	0
3	R	4/4 (100%)	0.56	0 100 100	54, 56, 57, 61	0
All	All	2191/2528 (86%)	-0.27	1 (0%) 100 100	7, 20, 32, 61	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	SER	2.2

### 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 ⓘ

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	0.95	0.09	-4.91	44,44,44,44	0
4	CA	G	557	1/1	0.99	0.08	-	73,73,73,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.