



## Full wwPDB EM Validation Report ⓘ

Dec 9, 2024 – 08:07 PM JST

PDB ID : 8YFX  
EMDB ID : EMD-39232  
Title : Cryo EM structure of human phosphate channel XPR1 at inward-facing state  
Authors : Lu, Y.; Yue, C.; Zhang, L.; Yao, D.; Yu, Y.; Cao, Y.  
Deposited on : 2024-02-25  
Resolution : 3.56 Å(reported)

This is a Full wwPDB EM 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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : **FAILED**  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

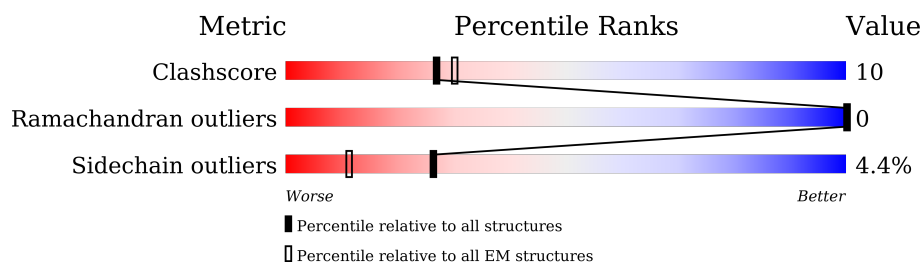
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.56 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	396	
1	B	396	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6588 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

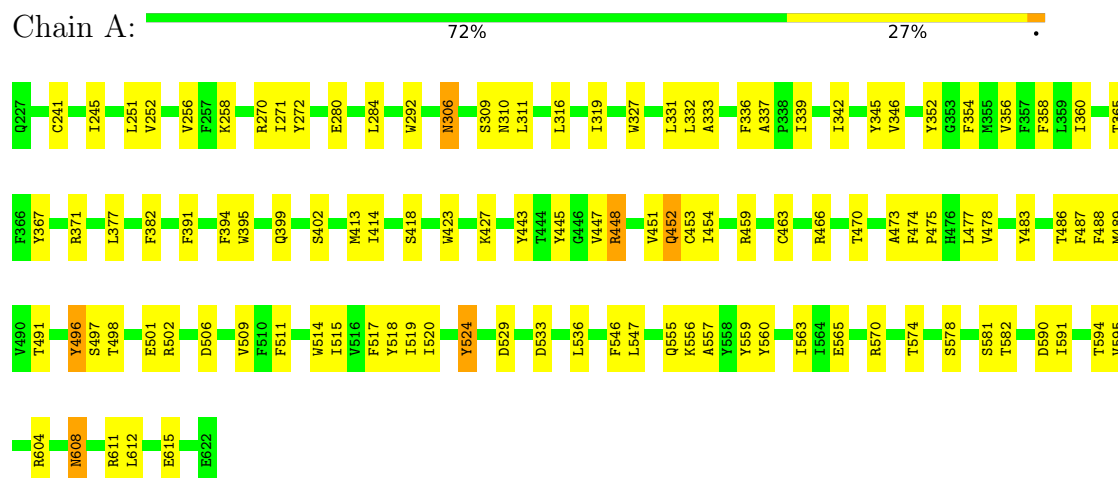
- Molecule 1 is a protein called Solute carrier family 53 member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	396	Total	C	N	O	S	0	0
			3294	2207	527	544	16		
1	B	396	Total	C	N	O	S	0	0
			3294	2207	527	544	16		

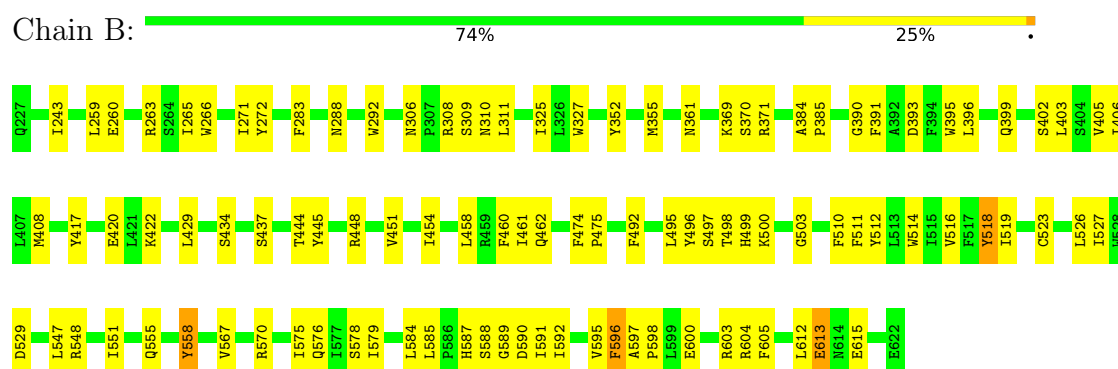
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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: Solute carrier family 53 member 1



- Molecule 1: Solute carrier family 53 member 1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	261912	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.29	0/3404	0.49	0/4634
1	B	0.30	0/3404	0.49	0/4634
All	All	0.29	0/6808	0.49	0/9268

There are no bond length outliers.

There are no bond angle outliers.

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	3294	0	3276	66	0
1	B	3294	0	3276	62	0
All	All	6588	0	6552	128	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 10.

All (128) 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:533:ASP:OD1	1:A:611:ARG:NH1	2.15	0.79
1:B:548:ARG:NH2	1:B:613:GLU:OE2	2.16	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:ILE:O	1:A:352:TYR:OH	2.07	0.72
1:B:272:TYR:HB3	1:B:327:TRP:HE1	1.56	0.71
1:A:306:ASN:O	1:A:310:ASN:ND2	2.27	0.67
1:B:306:ASN:ND2	1:B:309:SER:O	2.28	0.66
1:A:451:VAL:HA	1:A:454:ILE:HD12	1.76	0.66
1:A:445:TYR:HB2	1:A:448:ARG:HH22	1.60	0.65
1:B:444:THR:OG1	1:B:445:TYR:N	2.28	0.64
1:A:342:ILE:HD13	1:A:346:VAL:HB	1.80	0.63
1:A:466:ARG:O	1:A:470:THR:OG1	2.15	0.63
1:B:592:ILE:HG23	1:B:596:PHE:HE2	1.63	0.62
1:A:365:THR:O	1:A:371:ARG:NH2	2.31	0.62
1:B:306:ASN:HD21	1:B:369:LYS:HE3	1.64	0.61
1:B:361:ASN:HB3	1:B:371:ARG:HH12	1.66	0.61
1:B:592:ILE:HG23	1:B:596:PHE:CE2	2.36	0.60
1:B:584:LEU:HB3	1:B:585:LEU:HD22	1.84	0.59
1:A:489:MET:SD	1:A:574:THR:OG1	2.60	0.59
1:A:306:ASN:OD1	1:A:309:SER:N	2.36	0.59
1:A:591:ILE:O	1:A:595:VAL:HG23	2.02	0.59
1:A:241:CYS:O	1:A:245:ILE:HG12	2.02	0.58
1:A:252:VAL:O	1:A:256:VAL:HG22	2.02	0.58
1:A:452:GLN:NE2	1:A:581:SER:OG	2.34	0.58
1:B:259:LEU:HD21	1:B:265:ILE:HG21	1.87	0.57
1:B:588:SER:HA	1:B:591:ILE:HD12	1.85	0.57
1:A:511:PHE:O	1:A:514:TRP:HB3	2.03	0.57
1:B:518:TYR:HD1	1:B:519:ILE:HD13	1.68	0.57
1:B:591:ILE:O	1:B:595:VAL:HG22	2.04	0.56
1:A:272:TYR:HB3	1:A:327:TRP:HE1	1.71	0.56
1:B:458:LEU:O	1:B:462:GLN:HG3	2.06	0.56
1:B:402:SER:OG	1:B:604:ARG:NE	2.33	0.55
1:A:258:LYS:HG2	1:A:336:PHE:HE1	1.70	0.55
1:A:556:LYS:HE2	1:A:560:TYR:HE2	1.72	0.55
1:B:547:LEU:HD23	1:B:551:ILE:HG21	1.88	0.54
1:A:511:PHE:CD2	1:A:515:ILE:HD11	2.43	0.54
1:B:243:ILE:HB	1:B:325:ILE:HD11	1.90	0.53
1:A:517:PHE:HA	1:A:520:ILE:HG22	1.90	0.53
1:B:395:TRP:O	1:B:399:GLN:HG2	2.08	0.53
1:B:451:VAL:HA	1:B:454:ILE:HD12	1.91	0.53
1:A:271:ILE:HG12	1:A:413:MET:HG3	1.91	0.53
1:B:474:PHE:HB3	1:B:475:PRO:HD3	1.91	0.53
1:B:390:GLY:N	1:B:393:ASP:OD2	2.35	0.52
1:B:288:ASN:HD21	1:B:605:PHE:HD1	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:LEU:HD21	1:A:331:LEU:HD13	1.91	0.52
1:B:408:MET:HB3	1:B:448:ARG:HH12	1.73	0.52
1:A:399:GLN:HE22	1:A:608:ASN:ND2	2.08	0.52
1:A:529:ASP:HA	1:A:533:ASP:HB2	1.93	0.51
1:B:396:LEU:O	1:B:396:LEU:HD23	2.11	0.51
1:B:496:TYR:O	1:B:500:LYS:HG3	2.10	0.51
1:A:345:TYR:OH	1:A:423:TRP:O	2.27	0.51
1:B:514:TRP:O	1:B:518:TYR:N	2.44	0.50
1:A:395:TRP:O	1:A:399:GLN:HG2	2.11	0.50
1:A:515:ILE:HD12	1:A:515:ILE:H	1.76	0.50
1:A:515:ILE:O	1:A:518:TYR:HB3	2.10	0.50
1:B:310:ASN:OD1	1:B:311:LEU:N	2.44	0.50
1:B:266:TRP:CZ2	1:B:591:ILE:HG12	2.46	0.50
1:B:514:TRP:HZ2	1:B:578:SER:HB2	1.76	0.50
1:A:547:LEU:HD21	1:A:559:TYR:CG	2.48	0.49
1:B:271:ILE:O	1:B:352:TYR:OH	2.30	0.49
1:A:536:LEU:HD13	1:A:563:ILE:HD11	1.93	0.49
1:B:529:ASP:CG	1:B:570:ARG:HH21	2.15	0.49
1:A:578:SER:O	1:A:582:THR:OG1	2.18	0.49
1:B:263:ARG:HH21	1:B:429:LEU:HB3	1.77	0.49
1:A:496:TYR:CE1	1:A:511:PHE:HD1	2.31	0.49
1:B:391:PHE:HE2	1:B:615:GLU:HG3	1.78	0.49
1:B:369:LYS:HD3	1:B:370:SER:N	2.29	0.48
1:A:333:ALA:O	1:A:337:ALA:N	2.47	0.47
1:A:497:SER:O	1:A:501:GLU:HG2	2.14	0.47
1:A:352:TYR:O	1:A:356:VAL:HG23	2.15	0.47
1:A:498:THR:O	1:A:502:ARG:HG3	2.15	0.47
1:B:575:ILE:O	1:B:579:ILE:HG13	2.14	0.47
1:A:447:VAL:HG12	1:A:448:ARG:NH1	2.30	0.47
1:B:579:ILE:HD12	1:B:592:ILE:HG21	1.97	0.47
1:A:258:LYS:HG2	1:A:336:PHE:CE1	2.50	0.46
1:B:444:THR:HG1	1:B:445:TYR:H	1.61	0.46
1:A:402:SER:OG	1:A:604:ARG:NH2	2.46	0.46
1:B:308:ARG:HA	1:B:308:ARG:HE	1.80	0.46
1:B:405:VAL:HA	1:B:408:MET:HE2	1.97	0.46
1:A:319:ILE:HD11	1:A:367:TYR:HE2	1.80	0.46
1:A:555:GLN:HG2	1:A:557:ALA:HB3	1.97	0.46
1:B:499:HIS:O	1:B:503:GLY:N	2.47	0.46
1:B:518:TYR:CD1	1:B:519:ILE:HD13	2.49	0.46
1:B:266:TRP:HZ2	1:B:591:ILE:HG12	1.81	0.46
1:B:420:GLU:O	1:B:422:LYS:NZ	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:TYR:O	1:A:486:THR:HG22	2.17	0.45
1:A:520:ILE:O	1:A:524:TYR:HB2	2.17	0.45
1:A:280:GLU:O	1:A:284:LEU:HG	2.16	0.45
1:A:487:PHE:O	1:A:491:THR:HG22	2.16	0.45
1:A:332:LEU:HD12	1:A:332:LEU:HA	1.83	0.44
1:A:590:ASP:O	1:A:594:THR:OG1	2.33	0.44
1:B:597:ALA:HB3	1:B:598:PRO:HD3	1.99	0.44
1:B:570:ARG:HD3	1:B:603:ARG:NH1	2.32	0.44
1:B:308:ARG:HA	1:B:308:ARG:NE	2.33	0.44
1:A:443:TYR:HA	1:A:448:ARG:HH21	1.82	0.44
1:B:292:TRP:CZ2	1:B:612:LEU:HD22	2.53	0.44
1:B:403:LEU:HB3	1:B:406:ILE:HD12	2.00	0.44
1:B:408:MET:HB3	1:B:448:ARG:NH1	2.33	0.44
1:A:496:TYR:CE1	1:A:511:PHE:CD1	3.06	0.43
1:B:306:ASN:ND2	1:B:369:LYS:HE3	2.32	0.43
1:A:474:PHE:HB3	1:A:475:PRO:HD3	2.00	0.43
1:A:311:LEU:HD21	1:A:316:LEU:HG	2.01	0.43
1:A:506:ASP:O	1:A:509:VAL:HB	2.18	0.43
1:B:555:GLN:HB3	1:B:558:TYR:CE2	2.53	0.43
1:A:474:PHE:O	1:A:478:VAL:HG23	2.19	0.43
1:B:434:SER:O	1:B:437:SER:OG	2.30	0.43
1:A:546:PHE:O	1:A:547:LEU:HD12	2.18	0.42
1:B:512:TYR:O	1:B:516:VAL:HG23	2.19	0.42
1:A:473:ALA:O	1:A:477:LEU:HB2	2.19	0.42
1:A:356:VAL:O	1:A:360:ILE:HG12	2.19	0.42
1:B:384:ALA:N	1:B:385:PRO:HD2	2.33	0.42
1:B:518:TYR:HE2	1:B:575:ILE:HG13	1.84	0.42
1:A:414:ILE:O	1:A:418:SER:OG	2.22	0.42
1:A:452:GLN:NE2	1:A:581:SER:HG	2.16	0.41
1:B:497:SER:HA	1:B:500:LYS:NZ	2.35	0.41
1:B:495:LEU:O	1:B:498:THR:HG22	2.20	0.41
1:B:497:SER:HA	1:B:500:LYS:HZ3	1.85	0.41
1:B:585:LEU:O	1:B:589:GLY:N	2.52	0.41
1:A:391:PHE:HE2	1:A:615:GLU:HG3	1.85	0.41
1:B:523:CYS:O	1:B:527:ILE:HG12	2.20	0.41
1:B:458:LEU:O	1:B:461:ILE:HG22	2.20	0.41
1:A:459:ARG:HG2	1:A:483:TYR:CE1	2.56	0.41
1:A:519:ILE:H	1:A:519:ILE:HG13	1.62	0.41
1:A:270:ARG:NE	1:A:590:ASP:OD1	2.54	0.41
1:A:292:TRP:CE2	1:A:612:LEU:HD22	2.56	0.41
1:A:377:LEU:HD12	1:A:377:LEU:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:PHE:HA	1:A:491:THR:HG22	2.03	0.40
1:B:526:LEU:HD11	1:B:567:VAL:HA	2.03	0.40
1:A:339:ILE:HD12	1:A:339:ILE:HA	1.80	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 PDB entries followed by that with respect to all EM entries.

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	394/396 (100%)	369 (94%)	25 (6%)	0	100	100
1	B	394/396 (100%)	371 (94%)	23 (6%)	0	100	100
All	All	788/792 (100%)	740 (94%)	48 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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 PDB entries followed by that with respect to all EM entries.

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	352/352 (100%)	337 (96%)	15 (4%)	25	54
1	B	352/352 (100%)	336 (96%)	16 (4%)	23	53
All	All	704/704 (100%)	673 (96%)	31 (4%)	26	53

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	ASN
1	A	354	PHE
1	A	358	PHE
1	A	382	PHE
1	A	394	PHE
1	A	427	LYS
1	A	448	ARG
1	A	452	GLN
1	A	453	CYS
1	A	463	CYS
1	A	496	TYR
1	A	524	TYR
1	A	565	GLU
1	A	570	ARG
1	A	608	ASN
1	B	260	GLU
1	B	283	PHE
1	B	355	MET
1	B	417	TYR
1	B	460	PHE
1	B	492	PHE
1	B	510	PHE
1	B	511	PHE
1	B	518	TYR
1	B	558	TYR
1	B	576	GLN
1	B	587	HIS
1	B	590	ASP
1	B	596	PHE
1	B	600	GLU
1	B	613	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	608	ASN

### 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 oligosaccharides 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.